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(54) Title: MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE

(57) Abstract: Human HM genes are identified as modulators of the p53 pathway, and thus are therapeutic targets for disorders associated with defective p53 function. Methods for identifying modulators of p53, comprising screening for agents that modulate the activity of HM are provided.

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MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE

REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. provisional patent applications 60/296,076
5 filed 6/5/2001, 60/328,605 filed 10/10/2001, and 60/357,253 filed 2/15/2002. The
contents of the prior applications are hereby incorporated in their entirety.

BACKGROUND OF THE INVENTION

The p53 gene is mutated in over 50 different types of human cancers, including
10 familial and spontaneous cancers, and is believed to be the most commonly mutated gene
in human cancer (Zambetti and Levine, FASEB (1993) 7:855-865; Hollstein, *et al.*,
Nucleic Acids Res. (1994) 22:3551-3555). Greater than 90% of mutations in the p53 gene
are missense mutations that alter a single amino acid that inactivates p53 function.
Aberrant forms of human p53 are associated with poor prognosis, more aggressive tumors,
15 metastasis, and short survival rates (Mitsudomi *et al.*, Clin Cancer Res 2000 Oct;
6(10):4055-63; Koshland, Science (1993) 262:1953).

The human p53 protein normally functions as a central integrator of signals including
DNA damage, hypoxia, nucleotide deprivation, and oncogene activation (Prives, Cell
(1998) 95:5-8). In response to these signals, p53 protein levels are greatly increased with
20 the result that the accumulated p53 activates cell cycle arrest or apoptosis depending on
the nature and strength of these signals. Indeed, multiple lines of experimental evidence
have pointed to a key role for p53 as a tumor suppressor (Levine, Cell (1997) 88:323-331).
For example, homozygous p53 "knockout" mice are developmentally normal but exhibit
nearly 100% incidence of neoplasia in the first year of life (Donehower *et al.*, Nature
25 (1992) 356:215-221).

The biochemical mechanisms and pathways through which p53 functions in normal
and cancerous cells are not fully understood, but one clearly important aspect of p53
function is its activity as a gene-specific transcriptional activator. Among the genes with
known p53-response elements are several with well-characterized roles in either regulation
30 of the cell cycle or apoptosis, including GADD45, p21/Waf1/Cip1, cyclin G, Bax, IGF-
BP3, and MDM2 (Levine, Cell (1997) 88:323-331).

The ability to manipulate the genomes of model organisms such as *Drosophila*
provides a powerful means to analyze biochemical processes that, due to significant
evolutionary conservation, have direct relevance to more complex vertebrate organisms.

Due to a high level of gene and pathway conservation, the strong similarity of cellular processes, and the functional conservation of genes between these model organisms and mammals, identification of the involvement of novel genes in particular pathways and their functions in such model organisms can directly contribute to the understanding of the correlative pathways and methods of modulating them in mammals (see, for example, Mechler BM et al., 1985 EMBO J 4:1551-1557; Gateff E. 1982 Adv. Cancer Res. 37: 33-74; Watson KL., et al., 1994 J Cell Sci. 18: 19-33; Miklos GL, and Rubin GM. 1996 Cell 86:521-529; Wassarman DA, et al., 1995 Curr Opin Gen Dev 5: 44-50; and Booth DR. 1999 Cancer Metastasis Rev. 18: 261-284). For example, a genetic screen can be carried out in an invertebrate model organism having underexpression (e.g. knockout) or overexpression of a gene (referred to as a "genetic entry point") that yields a visible phenotype. Additional genes are mutated in a random or targeted manner. When a gene mutation changes the original phenotype caused by the mutation in the genetic entry point, the gene is identified as a "modifier" involved in the same or overlapping pathway as the genetic entry point. When the genetic entry point is an ortholog of a human gene implicated in a disease pathway, such as p53, modifier genes can be identified that may be attractive candidate targets for novel therapeutics.

All references cited herein, including sequence information in referenced Genbank identifier numbers and website references, are incorporated herein in their entireties.

SUMMARY OF THE INVENTION

We have discovered genes that modify the p53 pathway in *Drosophila*, and identified their human orthologs, hereinafter referred to as HM. The invention provides methods for utilizing these p53 modifier genes and polypeptides to identify candidate therapeutic agents that can be used in the treatment of disorders associated with defective p53 function. Preferred HM-modulating agents specifically bind to HM polypeptides and restore p53 function. Other preferred HM-modulating agents are nucleic acid modulators such as antisense oligomers and RNAi that repress HM gene expression or product activity by, for example, binding to and inhibiting the respective nucleic acid (i.e. DNA or mRNA).

HM-specific modulating agents may be evaluated by any convenient *in vitro* or *in vivo* assay for molecular interaction with an HM polypeptide or nucleic acid. In one embodiment, candidate p53 modulating agents are tested with an assay system comprising a HM polypeptide or nucleic acid. Candidate agents that produce a change in the activity

of the assay system relative to controls are identified as candidate p53 modulating agents. The assay system may be cell-based or cell-free. HM-modulating agents include HM related proteins (e.g. dominant negative mutants, and biotherapeutics); HM-specific antibodies; HM-specific antisense oligomers and other nucleic acid modulators; and
5 chemical agents that specifically bind HM or compete with HM binding target. In specific embodiments, the screening assay system is selected from a binding assay, an apoptosis assay, a cell proliferation assay, an angiogenesis assay, and a hypoxic induction assay.

In another embodiment, candidate p53 pathway modulating agents are further tested using a second assay system that detects changes in the p53 pathway, such as angiogenic,
10 apoptotic, or cell proliferation changes produced by the originally identified candidate agent or an agent derived from the original agent. The second assay system may use cultured cells or non-human animals. In specific embodiments, the secondary assay system uses non-human animals, including animals predetermined to have a disease or disorder implicating the p53 pathway, such as an angiogenic, apoptotic, or cell
15 proliferation disorder (e.g. cancer).

The invention further provides methods for modulating the p53 pathway in a mammalian cell by contacting the mammalian cell with an agent that specifically binds a HM polypeptide or nucleic acid. The agent may be a small molecule modulator, a nucleic acid modulator, or an antibody and may be administered to a mammalian animal
20 predetermined to have a pathology associated the p53 pathway.

DETAILED DESCRIPTION OF THE INVENTION

Genetic screens were designed to identify modifiers of the p53 pathway in *Drosophila* in which p53 was overexpressed in the wing (Ollmann M, et al., Cell 2000 101: 91-101).
25 Modifiers of the wing phenotype were identified as a modifier of the p53 pathway. Accordingly, vertebrate orthologs of these modifiers, and preferably the human orthologs, HM genes (i.e., nucleic acids and polypeptides) are attractive drug targets for the treatment of pathologies associated with a defective p53 signaling pathway, such as cancer. Table 1 lists the modifiers and their orthologs.

30 In vitro and in vivo methods of assessing HM function are provided herein. Modulation of the HM or their respective binding partners is useful for understanding the association of the p53 pathway and its members in normal and disease conditions and for developing diagnostics and therapeutic modalities for p53 related pathologies. HM-modulating agents that act by inhibiting or enhancing HM expression, directly or

indirectly, for example, by affecting an HM function such as enzymatic (e.g., catalytic) or binding activity, can be identified using methods provided herein. HM modulating agents are useful in diagnosis, therapy and pharmaceutical development.

5 **Nucleic acids and polypeptides of the invention**

Sequences related to HM nucleic acids and polypeptides that can be used in the invention are disclosed in Genbank (referenced by Genbank identifier (GI) number), shown in Table 1 and in the sequence listing .

10 A review of the nucleic acids and polypeptides of the invention reveals several categories of proteins, and their functional domains. Preferred HMs are enzymes or soluble proteins with ligand binding sites, including protein kinases, protein phosphatases, proteases, protease inhibitors, helicases, polymerases, prolyl isomerases, GTPase activating proteins (GAPs), guanine nucleotide exchange factors (GEFs), a range of metabolic enzymes, proteins involved in ubiquitination, DNA methylation and metabolism, RNA
15 processing or binding, and adapters, among others. Alternative preferred targets are membrane proteins, such as G protein coupled receptors (GPCRs), protein kinase receptors, transporters, and ligand-gated ion channels, among others.

The term "HM polypeptide" refers to a full-length HM protein or a functionally active fragment or derivative thereof. A "functionally active" HM fragment or derivative
20 exhibits one or more functional activities associated with a full-length, wild-type HM protein, such as antigenic or immunogenic activity, enzymatic activity, ability to bind natural cellular substrates, etc. The functional activity of HM proteins, derivatives and fragments can be assayed by various methods known to one skilled in the art (Current Protocols in Protein Science (1998) Coligan *et al.*, eds., John Wiley & Sons, Inc.,
25 Somerset, New Jersey) and as further discussed below. For purposes herein, functionally active fragments also include those fragments that comprise one or more structural domains of an HM, such as a kinase domain or a binding domain. Protein domains can be identified using the PFAM program (Bateman A., et al., Nucleic Acids Res, 1999, 27:260-2; <http://pfam.wustl.edu>). Methods for obtaining HM polypeptides are also further
30 described below. In some embodiments, preferred fragments are functionally active, domain-containing fragments comprising at least 25 contiguous amino acids, preferably at least 50, more preferably 75, and most preferably at least 100 contiguous amino acids of a domain-encoding region of an HM protein.

The term "HM nucleic acid" refers to a DNA or RNA molecule that encodes a HM polypeptide. Preferably, the HM polypeptide or nucleic acid or fragment thereof is from a human, but can also be an ortholog, or derivative thereof with at least 70% sequence identity, preferably at least 80%, more preferably 85%, still more preferably 90%, and most preferably at least 95% sequence identity with HM. Normally, orthologs in different species retain the same function, due to presence of one or more protein motifs and/or 3-dimensional structures. Orthologs are generally identified by sequence homology analysis, such as BLAST analysis, usually using protein bait sequences. Sequences are assigned as a potential ortholog if the best hit sequence from the forward BLAST result retrieves the original query sequence in the reverse BLAST (Huynen MA and Bork P, Proc Natl Acad Sci (1998) 95:5849-5856; Huynen MA *et al.*, Genome Research (2000) 10:1204-1210). Programs for multiple sequence alignment, such as CLUSTAL (Thompson JD *et al.*, 1994, Nucleic Acids Res 22:4673-4680) may be used to highlight conserved regions and/or residues of orthologous proteins and to generate phylogenetic trees. In a phylogenetic tree representing multiple homologous sequences from diverse species (e.g., retrieved through BLAST analysis), orthologous sequences from two species generally appear closest on the tree with respect to all other sequences from these two species. Structural threading or other analysis of protein folding (e.g., using software by ProCeryon, Biosciences, Salzburg, Austria) may also identify potential orthologs. In evolution, when a gene duplication event follows speciation, a single gene in one species, such as *Drosophila*, may correspond to multiple genes (paralogs) in another, such as human. As used herein, the term "orthologs" encompasses paralogs. As used herein, "percent (%) sequence identity" with respect to a subject sequence, or a specified portion of a subject sequence, is defined as the percentage of nucleotides or amino acids in the candidate derivative sequence identical with the nucleotides or amino acids in the subject sequence (or specified portion thereof), after aligning the sequences and introducing gaps, if necessary to achieve the maximum percent sequence identity, as generated by the program WU-BLAST-2.0a19 (Altschul *et al.*, J. Mol. Biol. (1997) 215:403-410; <http://blast.wustl.edu/blast/README.html>) with all the search parameters set to default values. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched. A % identity value is determined by the number of matching identical nucleotides or amino acids divided by the sequence length for which the percent identity is being reported.

"Percent (%) amino acid sequence similarity" is determined by doing the same calculation as for determining % amino acid sequence identity, but including conservative amino acid substitutions in addition to identical amino acids in the computation.

A conservative amino acid substitution is one in which an amino acid is substituted for another amino acid having similar properties such that the folding or activity of the protein is not significantly affected. Aromatic amino acids that can be substituted for each other are phenylalanine, tryptophan, and tyrosine; interchangeable hydrophobic amino acids are leucine, isoleucine, methionine, and valine; interchangeable polar amino acids are glutamine and asparagine; interchangeable basic amino acids are arginine, lysine and histidine; interchangeable acidic amino acids are aspartic acid and glutamic acid; and interchangeable small amino acids are alanine, serine, threonine, cysteine and glycine.

Alternatively, an alignment for nucleic acid sequences is provided by the local homology algorithm of Smith and Waterman (Smith and Waterman, 1981, *Advances in Applied Mathematics* 2:482-489; database: European Bioinformatics Institute <http://www.ebi.ac.uk/MPsrch/>; Smith and Waterman, 1981, *J. of Molec.Biol.*, 147:195-197; Nicholas et al., 1998, "A Tutorial on Searching Sequence Databases and Sequence Scoring Methods" (www.psc.edu) and references cited therein.; W.R. Pearson, 1991, *Genomics* 11:635-650). This algorithm can be applied to amino acid sequences by using the scoring matrix developed by Dayhoff (Dayhoff: *Atlas of Protein Sequences and Structure*, M. O. Dayhoff ed., 5 suppl. 3:353-358, National Biomedical Research Foundation, Washington, D.C., USA), and normalized by Gribskov (Gribskov 1986 *Nucl. Acids Res.* 14(6):6745-6763). The Smith-Waterman algorithm may be employed where default parameters are used for scoring (for example, gap open penalty of 12, gap extension penalty of two). From the data generated, the "Match" value reflects "sequence identity."

Derivative nucleic acid molecules of the subject nucleic acid molecules include sequences that hybridize to the nucleic acid sequence of an HM. The stringency of hybridization can be controlled by temperature, ionic strength, pH, and the presence of denaturing agents such as formamide during hybridization and washing. Conditions routinely used are set out in readily available procedure texts (*e.g.*, *Current Protocol in Molecular Biology*, Vol. 1, Chap. 2.10, John Wiley & Sons, Publishers (1994); Sambrook *et al.*, *Molecular Cloning*, Cold Spring Harbor (1989)). In some embodiments, a nucleic acid molecule of the invention is capable of hybridizing to a nucleic acid molecule containing the nucleotide sequence of an HM under stringent hybridization conditions that

comprise: prehybridization of filters containing nucleic acid for 8 hours to overnight at 65° C in a solution comprising 6X single strength citrate (SSC) (1X SSC is 0.15 M NaCl, 0.015 M Na citrate; pH 7.0), 5X Denhardt's solution, 0.05% sodium pyrophosphate and 100 µg/ml herring sperm DNA; hybridization for 18-20 hours at 65° C in a solution
5 containing 6X SSC, 1X Denhardt's solution, 100 µg/ml yeast tRNA and 0.05% sodium pyrophosphate; and washing of filters at 65° C for 1h in a solution containing 0.2X SSC and 0.1% SDS (sodium dodecyl sulfate).

In other embodiments, moderately stringent hybridization conditions are used that comprise: pretreatment of filters containing nucleic acid for 6 h at 40° C in a solution
10 containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH7.5), 5mM EDTA, 0.1% PVP, 0.1% Ficoll, 1% BSA, and 500 µg/ml denatured salmon sperm DNA; hybridization for 18-20h at 40° C in a solution containing 35% formamide, 5X SSC, 50 mM Tris-HCl (pH7.5), 5mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 µg/ml salmon sperm DNA, and 10% (wt/vol) dextran sulfate; followed by washing twice for 1 hour at 55° C in
15 a solution containing 2X SSC and 0.1% SDS.

Alternatively, low stringency conditions can be used that comprise: incubation for 8 hours to overnight at 37° C in a solution comprising 20% formamide, 5 x SSC, 50 mM sodium phosphate (pH 7.6), 5X Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured sheared salmon sperm DNA; hybridization in the same buffer for 18 to 20
20 hours; and washing of filters in 1 x SSC at about 37° C for 1 hour.

Isolation, Production, Expression, and Mis-expression of HM Nucleic Acids and Polypeptides

HM nucleic acids and polypeptides, useful for identifying and testing agents that
25 modulate HM function and for other applications related to the involvement of HM in the p53 pathway. HM nucleic acids and derivatives and orthologs thereof may be obtained using any available method. For instance, techniques for isolating cDNA or genomic DNA sequences of interest by screening DNA libraries or by using polymerase chain reaction (PCR) are well known in the art. In general, the particular use for the protein will
30 dictate the particulars of expression, production, and purification methods. For instance, production of proteins for use in screening for modulating agents may require methods that preserve specific biological activities of these proteins, whereas production of proteins for antibody generation may require structural integrity of particular epitopes. Expression of proteins to be purified for screening or antibody production may require the addition of

specific tags (*e.g.*, generation of fusion proteins). Overexpression of an HM protein for assays used to assess HM function, such as involvement in cell cycle regulation or hypoxic response, may require expression in eukaryotic cell lines capable of these cellular activities. Techniques for the expression, production, and purification of proteins are well known in the art; any suitable means therefore may be used (*e.g.*, Higgins SJ and Hames BD (eds.) *Protein Expression: A Practical Approach*, Oxford University Press Inc., New York 1999; Stanbury PF et al., *Principles of Fermentation Technology*, 2nd edition, Elsevier Science, New York, 1995; Doonan S (ed.) *Protein Purification Protocols*, Humana Press, New Jersey, 1996; Coligan JE et al, *Current Protocols in Protein Science* (eds.), 1999, John Wiley & Sons, New York). In particular embodiments, recombinant HM is expressed in a cell line known to have defective p53 function (*e.g.* SAOS-2 osteoblasts, H1299 lung cancer cells, C33A and HT3 cervical cancer cells, HT-29 and DLD-1 colon cancer cells, among others, available from American Type Culture Collection (ATCC), Manassas, VA). The recombinant cells are used in cell-based screening assay systems of the invention, as described further below.

The nucleotide sequence encoding an HM polypeptide can be inserted into any appropriate expression vector. The necessary transcriptional and translational signals, including promoter/enhancer element, can derive from the native HM gene and/or its flanking regions or can be heterologous. A variety of host-vector expression systems may be utilized, such as mammalian cell systems infected with virus (*e.g.* vaccinia virus, adenovirus, *etc.*); insect cell systems infected with virus (*e.g.* baculovirus); microorganisms such as yeast containing yeast vectors, or bacteria transformed with bacteriophage, plasmid, or cosmid DNA. A host cell strain that modulates the expression of, modifies, and/or specifically processes the gene product may be used.

To detect expression of the HM gene product, the expression vector can comprise a promoter operably linked to an HM gene nucleic acid, one or more origins of replication, and, one or more selectable markers (*e.g.* thymidine kinase activity, resistance to antibiotics, *etc.*). Alternatively, recombinant expression vectors can be identified by assaying for the expression of the HM gene product based on the physical or functional properties of the HM protein in *in vitro* assay systems (*e.g.* immunoassays).

The HM protein, fragment, or derivative may be optionally expressed as a fusion, or chimeric protein product (*i.e.* it is joined via a peptide bond to a heterologous protein sequence of a different protein), for example to facilitate purification or detection. A chimeric product can be made by ligating the appropriate nucleic acid sequences encoding

the desired amino acid sequences to each other using standard methods and expressing the chimeric product. A chimeric product may also be made by protein synthetic techniques, *e.g.* by use of a peptide synthesizer (Hunkapiller *et al.*, Nature (1984) 310:105-111).

Once a recombinant cell that expresses the HM gene sequence is identified, the gene product can be isolated and purified using standard methods (*e.g.* ion exchange, affinity, and gel exclusion chromatography; centrifugation; differential solubility; electrophoresis, cite purification reference). Alternatively, native HM proteins can be purified from natural sources, by standard methods (*e.g.* immunoaffinity purification). Once a protein is obtained, it may be quantified and its activity measured by appropriate methods, such as immunoassay, bioassay, or other measurements of physical properties, such as crystallography.

The methods of this invention may also use cells that have been engineered for altered expression (mis-expression) of HM or other genes associated with the p53 pathway. As used herein, mis-expression encompasses ectopic expression, over-expression, under-expression, and non-expression (*e.g.* by gene knock-out or blocking expression that would otherwise normally occur).

Genetically modified animals

Animal models that have been genetically modified to alter HM expression may be used in *in vivo* assays to test for activity of a candidate p53 modulating agent, or to further assess the role of HM in a p53 pathway process such as apoptosis or cell proliferation. Preferably, the altered HM expression results in a detectable phenotype, such as decreased or increased levels of cell proliferation, angiogenesis, or apoptosis compared to control animals having normal HM expression. The genetically modified animal may additionally have altered p53 expression (*e.g.* p53 knockout). Preferred genetically modified animals are mammals such as primates, rodents (preferably mice), cows, horses, goats, sheep, pigs, dogs and cats. Preferred non-mammalian species include zebrafish, *C. elegans*, and *Drosophila*. Preferred genetically modified animals are transgenic animals having a heterologous nucleic acid sequence present as an extrachromosomal element in a portion of its cells, *i.e.* mosaic animals (see, for example, techniques described by Jakobovits, 1994, Curr. Biol. 4:761-763.) or stably integrated into its germ line DNA (*i.e.*, in the genomic sequence of most or all of its cells). Heterologous nucleic acid is introduced into the germ line of such transgenic animals by genetic manipulation of, for example, embryos or embryonic stem cells of the host animal.

Methods of making transgenic animals are well-known in the art (for transgenic mice see Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442 (1985), U.S. Pat. Nos. 4,736,866 and 4,870,009, both by Leder *et al.*, U.S. Pat. No. 4,873,191 by Wagner *et al.*, and Hogan, B., Manipulating the Mouse Embryo, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1986); for particle bombardment see U.S. Pat. No., 4,945,050, by Sandford *et al.*; for transgenic *Drosophila* see Rubin and Spradling, Science (1982) 218:348-53 and U.S. Pat. No. 4,670,388; for transgenic insects see Berghammer A.J. *et al.*, A Universal Marker for Transgenic Insects (1999) Nature 402:370-371; for transgenic Zebrafish see Lin S., Transgenic Zebrafish, Methods Mol Biol. (2000);136:375-3830); for microinjection procedures for fish, amphibian eggs and birds see Houdebine and Chourrout, Experientia (1991) 47:897-905; for transgenic rats see Hammer *et al.*, Cell (1990) 63:1099-1112; and for culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection see, e.g., Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E. J. Robertson, ed., IRL Press (1987)). Clones of the nonhuman transgenic animals can be produced according to available methods (see Wilmut, I. *et al.* (1997) Nature 385:810-813; and PCT International Publication Nos. WO 97/07668 and WO 97/07669).

In one embodiment, the transgenic animal is a "knock-out" animal having a heterozygous or homozygous alteration in the sequence of an endogenous HM gene that results in a decrease of HM function, preferably such that HM expression is undetectable or insignificant. Knock-out animals are typically generated by homologous recombination with a vector comprising a transgene having at least a portion of the gene to be knocked out. Typically a deletion, addition or substitution has been introduced into the transgene to functionally disrupt it. The transgene can be a human gene (e.g., from a human genomic clone) but more preferably is an ortholog of the human gene derived from the transgenic host species. For example, a mouse HM gene is used to construct a homologous recombination vector suitable for altering an endogenous HM gene in the mouse genome. Detailed methodologies for homologous recombination in mice are available (see Capecchi, Science (1989) 244:1288-1292; Joyner *et al.*, Nature (1989) 338:153-156). Procedures for the production of non-rodent transgenic mammals and other animals are also available (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science (1989) 244:1281-1288; Simms *et al.*, Bio/Technology (1988) 6:179-183). In a preferred embodiment, knock-out animals, such as mice harboring a knockout of a specific gene,

may be used to produce antibodies against the human counterpart of the gene that has been knocked out (Claesson MH et al., (1994) *Scan J Immunol* 40:257-264; Declerck PJ et al., (1995) *J Biol Chem.* 270:8397-400).

5 In another embodiment, the transgenic animal is a "knock-in" animal having an alteration in its genome that results in altered expression (e.g., increased (including ectopic) or decreased expression) of the HM gene, e.g., by introduction of additional copies of HM, or by operatively inserting a regulatory sequence that provides for altered expression of an endogenous copy of the HM gene. Such regulatory sequences include inducible, tissue-specific, and constitutive promoters and enhancer elements. The knock-
10 in can be homozygous or heterozygous.

Transgenic nonhuman animals can also be produced that contain selected systems allowing for regulated expression of the transgene. One example of such a system that may be produced is the cre/loxP recombinase system of bacteriophage P1 (Lakso *et al.*, PNAS (1992) 89:6232-6236; U.S. Pat. No. 4,959,317). If a cre/loxP recombinase system
15 is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase. Another example of a recombinase
20 system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman et al. (1991) *Science* 251:1351-1355; U.S. Pat. No. 5,654,182). In a preferred embodiment, both Cre-LoxP and Flp-Frt are used in the same system to regulate expression of the transgene, and for sequential deletion of vector sequences in the same cell (Sun X et al (2000) *Nat Genet* 25:83-6).

25 The genetically modified animals can be used in genetic studies to further elucidate the p53 pathway, as animal models of disease and disorders implicating defective p53 function, and for *in vivo* testing of candidate therapeutic agents, such as those identified in screens described below. The candidate therapeutic agents are administered to a genetically modified animal having altered HM function and phenotypic changes are
30 compared with appropriate control animals such as genetically modified animals that receive placebo treatment, and/or animals with unaltered HM expression that receive candidate therapeutic agent.

In addition to the above-described genetically modified animals having altered HM function, animal models having defective p53 function (and otherwise normal HM

function), can be used in the methods of the present invention. For example, a p53 knockout mouse can be used to assess, *in vivo*, the activity of a candidate p53 modulating agent identified in one of the *in vitro* assays described below. p53 knockout mice are described in the literature (Jacks et al., Nature 2001;410:1111-1116, 1043-1044;

- 5 Donehower *et al.*, supra). Preferably, the candidate p53 modulating agent when administered to a model system with cells defective in p53 function, produces a detectable phenotypic change in the model system indicating that the p53 function is restored, i.e., the cells exhibit normal cell cycle progression.

10 Modulating Agents

- The invention provides methods to identify agents that interact with and/or modulate the function of HM and/or the p53 pathway. Such agents are useful in a variety of diagnostic and therapeutic applications associated with the p53 pathway, as well as in further analysis of the HM protein and its contribution to the p53 pathway. Accordingly, 15 the invention also provides methods for modulating the p53 pathway comprising the step of specifically modulating HM activity by administering a HM-interacting or -modulating agent.

- In a preferred embodiment, HM-modulating agents inhibit or enhance HM activity or otherwise affect normal HM function, including transcription, protein expression, protein 20 localization, and cellular or extra-cellular activity. In a further preferred embodiment, the candidate p53 pathway- modulating agent specifically modulates the function of the HM. The phrases "specific modulating agent", "specifically modulates", etc., are used herein to refer to modulating agents that directly bind to the HM polypeptide or nucleic acid, and preferably inhibit, enhance, or otherwise alter, the function of the HM. The term also 25 encompasses modulating agents that alter the interaction of the HM with a binding partner or substrate (e.g. by binding to a binding partner of an HM, or to a protein/binding partner complex, and inhibiting function).

- Preferred HM-modulating agents include small molecule compounds; HM-interacting proteins, including antibodies and other biotherapeutics; and nucleic acid modulators such 30 as antisense and RNA inhibitors. The modulating agents may be formulated in pharmaceutical compositions, for example, as compositions that may comprise other active ingredients, as in combination therapy, and/or suitable carriers or excipients. Techniques for formulation and administration of the compounds may be found in "Remington's Pharmaceutical Sciences" Mack Publishing Co., Easton, PA, 19th edition.

Small molecule modulators

Small molecule modulators are preferred where the identified HM has enzymatic function, and/or contains protein interaction domains. Such HMs are represented, for example, in rows 1-23, 26-29, 33-35, 37, 43-66, and 70-115 of Table 1.

5 Small molecules are often preferred to modulate function of proteins with enzymatic function, and/or containing protein interaction domains. Chemical agents, referred to in the art as "small molecule" compounds are typically organic, non-peptide molecules, having a molecular weight less than 10,000, preferably less than 5,000, more preferably less than 1,000, and most preferably less than 500. This class of modulators includes
10 chemically synthesized molecules, for instance, compounds from combinatorial chemical libraries. Synthetic compounds may be rationally designed or identified based on known or inferred properties of the HM protein or may be identified by screening compound libraries. Alternative appropriate modulators of this class are natural products, particularly secondary metabolites from organisms such as plants or fungi, which can also be
15 identified by screening compound libraries for HM-modulating activity. Methods for generating and obtaining compounds are well known in the art (Schreiber SL, Science (2000) 151: 1964-1969; Radmann J and Gunther J, Science (2000) 151:1947-1948).

Small molecule modulators identified from screening assays, as described below, can be used as lead compounds from which candidate clinical compounds may be designed,
20 optimized, and synthesized. Such clinical compounds may have utility in treating pathologies associated with the p53 pathway. The activity of candidate small molecule modulating agents may be improved several-fold through iterative secondary functional validation, as further described below, structure determination, and candidate modulator modification and testing. Additionally, candidate clinical compounds are generated with
25 specific regard to clinical and pharmacological properties. For example, the reagents may be derivatized and re-screened using *in vitro* and *in vivo* assays to optimize activity and minimize toxicity for pharmaceutical development.

Protein Modulators

30 Specific HM-interacting proteins are useful in a variety of diagnostic and therapeutic applications related to the p53 pathway and related disorders, as well as in validation assays for other HM-modulating agents. In a preferred embodiment, HM-interacting proteins affect normal HM function, including transcription, protein expression, protein localization, and cellular or extra-cellular activity. In another embodiment, HM-

interacting proteins are useful in detecting and providing information about the function of HM proteins, as is relevant to p53 related disorders, such as cancer (e.g., for diagnostic means).

5 An HM-interacting protein may be endogenous, i.e. one that naturally interacts genetically or biochemically with an HM, such as a member of the HM pathway that modulates HM expression, localization, and/or activity. HM-modulators include dominant negative forms of HM-interacting proteins and of HM proteins themselves. Yeast two-hybrid and variant screens offer preferred methods for identifying endogenous HM-interacting proteins (Finley, R. L. et al. (1996) in DNA Cloning-Expression Systems: A
10 Practical Approach, eds. Glover D. & Hames B. D (Oxford University Press, Oxford, England), pp. 169-203; Fashema SF et al., Gene (2000) 250:1-14; Drees BL Curr Opin Chem Biol (1999) 3:64-70; Vidal M and Legrain P Nucleic Acids Res (1999) 27:919-29; and U.S. Pat. No. 5,928,868). Mass spectrometry is an alternative preferred method for the elucidation of protein complexes (reviewed in, e.g., Pandley A and Mann M, Nature
15 (2000) 405:837-846; Yates JR 3rd, Trends Genet (2000) 16:5-8).

An HM-interacting protein may be an exogenous protein, such as an HM-specific antibody or a T-cell antigen receptor (see, e.g., Harlow and Lane (1988) Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory; Harlow and Lane (1999) Using antibodies: a laboratory manual. Cold Spring Harbor, NY: Cold Spring Harbor Laboratory
20 Press). HM antibodies are further discussed below.

In preferred embodiments, an HM-interacting protein specifically binds an HM protein. In alternative preferred embodiments, an HM-modulating agent binds an HM substrate, binding partner, or cofactor.

25 ***Antibodies***

In another embodiment, the protein modulator is an HM specific antibody agonist or antagonist. While antibodies may be produced against any protein to dissect cellular processes, preferred HM candidates for antibody production for therapeutic applications include cell surface proteins, proteins with transmembrane domains, proteins with
30 extracellular Ig or fibronectin domains, or proteins with no cytoplasmic retention domains. Such HM proteins are found, for example, in rows 22-23, 29, 36, 38-39, 41-42, 62, 65-69, 76, 79, 85-87, 95, and 103-107 of Table 1.

The antibodies have therapeutic and diagnostic utilities, and can be used in screening assays to identify HM modulators. The antibodies can also be used in dissecting the

portions of the HM pathway responsible for various cellular responses and in the general processing and maturation of the HM.

Antibodies that specifically bind HM polypeptides can be generated using known methods. Preferably the antibody is specific to a mammalian ortholog of HM polypeptide, and more preferably, to human HM. Antibodies may be polyclonal, monoclonal (mAbs), humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab')₂ fragments, fragments produced by a FAb expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. Epitopes of HM which are particularly antigenic can be selected, for example, by routine screening of HM polypeptides for antigenicity or by applying a theoretical method for selecting antigenic regions of a protein (Hopp and Wood (1981), Proc. Natl. Acad. Sci. U.S.A. 78:3824-28; Hopp and Wood, (1983) Mol. Immunol. 20:483-89; Sutcliffe et al., (1983) Science 219:660-66) to the amino acid sequence of an HM. Monoclonal antibodies with affinities of 10^8 M^{-1} preferably 10^9 M^{-1} to 10^{10} M^{-1} , or stronger can be made by standard procedures as described (Harlow and Lane, *supra*; Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed) Academic Press, New York; and U.S. Pat. Nos. 4,381,292; 4,451,570; and 4,618,577). Antibodies may be generated against crude cell extracts of HM or substantially purified fragments thereof. If HM fragments are used, they preferably comprise at least 10, and more preferably, at least 20 contiguous amino acids of an HM protein. In a particular embodiment, HM-specific antigens and/or immunogens are coupled to carrier proteins that stimulate the immune response. For example, the subject polypeptides are covalently coupled to the keyhole limpet hemocyanin (KLH) carrier, and the conjugate is emulsified in Freund's complete adjuvant, which enhances the immune response. An appropriate immune system such as a laboratory rabbit or mouse is immunized according to conventional protocols.

The presence of HM-specific antibodies is assayed by an appropriate assay such as a solid phase enzyme-linked immunosorbant assay (ELISA) using immobilized corresponding HM polypeptides. Other assays, such as radioimmunoassays or fluorescent assays might also be used.

Chimeric antibodies specific to HM polypeptides can be made that contain different portions from different animal species. For instance, a human immunoglobulin constant region may be linked to a variable region of a murine mAb, such that the antibody derives its biological activity from the human antibody, and its binding specificity from the murine fragment. Chimeric antibodies are produced by splicing together genes that

encode the appropriate regions from each species (Morrison et al., Proc. Natl. Acad. Sci. (1984) 81:6851-6855; Neuberger et al., Nature (1984) 312:604-608; Takeda et al., Nature (1985) 31:452-454). Humanized antibodies, which are a form of chimeric antibodies, can be generated by grafting complementary-determining regions (CDRs) (Carlos, T. M., J. M. Harlan. 1994. Blood 84:2068-2101) of mouse antibodies into a background of human framework regions and constant regions by recombinant DNA technology (Riechmann LM, et al., 1988 Nature 323: 323-327). Humanized antibodies contain ~10% murine sequences and ~90% human sequences, and thus further reduce or eliminate immunogenicity, while retaining the antibody specificities (Co MS, and Queen C. 1991 Nature 351: 501-501; Morrison SL. 1992 Ann. Rev. Immun. 10:239-265). Humanized antibodies and methods of their production are well-known in the art (U.S. Pat. Nos. 5,530,101, 5,585,089, 5,693,762, and 6,180,370).

HM-specific single chain antibodies which are recombinant, single chain polypeptides formed by linking the heavy and light chain fragments of the Fv regions via an amino acid bridge, can be produced by methods known in the art (U.S. Pat. No. 4,946,778; Bird, Science (1988) 242:423-426; Huston et al., Proc. Natl. Acad. Sci. USA (1988) 85:5879-5883; and Ward et al., Nature (1989) 334:544-546).

Other suitable techniques for antibody production involve in vitro exposure of lymphocytes to the antigenic polypeptides or alternatively to selection of libraries of antibodies in phage or similar vectors (Huse et al., Science (1989) 246:1275-1281). As used herein, T-cell antigen receptors are included within the scope of antibody modulators (Harlow and Lane, 1988, *supra*).

The polypeptides and antibodies of the present invention may be used with or without modification. Frequently, antibodies will be labeled by joining, either covalently or non-covalently, a substance that provides for a detectable signal, or that is toxic to cells that express the targeted protein (Menard S, et al., Int J. Biol Markers (1989) 4:131-134). A wide variety of labels and conjugation techniques are known and are reported extensively in both the scientific and patent literature. Suitable labels include radionuclides, enzymes, substrates, cofactors, inhibitors, fluorescent moieties, fluorescent emitting lanthanide metals, chemiluminescent moieties, bioluminescent moieties, magnetic particles, and the like (U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149; and 4,366,241). Also, recombinant immunoglobulins may be produced (U.S. Pat. No. 4,816,567). Antibodies to cytoplasmic polypeptides may be delivered and reach their

targets by conjugation with membrane-penetrating toxin proteins (U.S. Pat. No. 6,086,900).

When used therapeutically in a patient, the antibodies of the subject invention are typically administered parenterally, when possible at the target site, or intravenously. The therapeutically effective dose and dosage regimen is determined by clinical studies. Typically, the amount of antibody administered is in the range of about 0.1 mg/kg –to about 10 mg/kg of patient weight. For parenteral administration, the antibodies are formulated in a unit dosage injectable form (e.g., solution, suspension, emulsion) in association with a pharmaceutically acceptable vehicle. Such vehicles are inherently nontoxic and non-therapeutic. Examples are water, saline, Ringer's solution, dextrose solution, and 5% human serum albumin. Nonaqueous vehicles such as fixed oils, ethyl oleate, or liposome carriers may also be used. The vehicle may contain minor amounts of additives, such as buffers and preservatives, which enhance isotonicity and chemical stability or otherwise enhance therapeutic potential. The antibodies' concentrations in such vehicles are typically in the range of about 1 mg/ml to about 10 mg/ml. Immunotherapeutic methods are further described in the literature (US Pat. No. 5,859,206; WO0073469).

Specific biotherapeutics

In a preferred embodiment, an HM-interacting protein may have biotherapeutic applications. Biotherapeutic agents formulated in pharmaceutically acceptable carriers and dosages may be used to activate or inhibit signal transduction pathways. This modulation may be accomplished by binding a ligand, thus inhibiting the activity of the pathway; or by binding a receptor, either to inhibit activation of, or to activate, the receptor. Alternatively, the biotherapeutic may itself be a ligand capable of activating or inhibiting a receptor. Biotherapeutic agents and methods of producing them are described in detail in U.S. Pat. No. 6,146,628.

When the HM is a ligand, it may be used as a biotherapeutic agent to activate or inhibit its natural receptor. Alternatively, antibodies against HM, as described in the previous section, may be used as biotherapeutic agents.

When the HM is a receptor, its ligand(s), antibodies to the ligand(s) or the HM itself may be used as biotherapeutics to modulate the activity of HM in the p53 pathway.

Nucleic Acid Modulators

Other preferred HM-modulating agents comprise nucleic acid molecules, such as antisense oligomers or double stranded RNA (dsRNA), which generally inhibit HM activity. Preferred nucleic acid modulators interfere with the function of the HM nucleic acid such as DNA replication, transcription, translocation of the HM RNA to the site of protein translation, translation of protein from the HM RNA, splicing of the HM RNA to yield one or more mRNA species, or catalytic activity which may be engaged in or facilitated by the HM RNA. All HM proteins may be targeted by nucleic acid modulators, but preferred targets include transcription factors and cytoplasmic proteins. Thus, all HMs on Table 1, for example, can be targets for nucleic acid modulators.

In one embodiment, the antisense oligomer is an oligonucleotide that is sufficiently complementary to an HM mRNA to bind to and prevent translation, preferably by binding to the 5' untranslated region. HM-specific antisense oligonucleotides, preferably range from at least 6 to about 200 nucleotides. In some embodiments the oligonucleotide is preferably at least 10, 15, or 20 nucleotides in length. In other embodiments, the oligonucleotide is preferably less than 50, 40, or 30 nucleotides in length. The oligonucleotide can be DNA or RNA or a chimeric mixture or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, agents that facilitate transport across the cell membrane, hybridization-triggered cleavage agents, and intercalating agents.

In another embodiment, the antisense oligomer is a phosphothioate morpholino oligomer (PMO). PMOs are assembled from four different morpholino subunits, each of which contain one of four genetic bases (A, C, G, or T) linked to a six-membered morpholine ring. Polymers of these subunits are joined by non-ionic phosphodiamidate intersubunit linkages. Details of how to make and use PMOs and other antisense oligomers are well known in the art (e.g. see WO99/18193; Probst JC, Antisense Oligodeoxynucleotide and Ribozyme Design, Methods. (2000) 22(3):271-281; Summerton J, and Weller D. 1997 Antisense Nucleic Acid Drug Dev. :7:187-95; US Pat. No. 5,235,033; and US Pat No. 5,378,841).

Alternative preferred HM nucleic acid modulators are double-stranded RNA species mediating RNA interference (RNAi). RNAi is the process of sequence-specific, post-transcriptional gene silencing in animals and plants, initiated by double-stranded RNA (dsRNA) that is homologous in sequence to the silenced gene. Methods relating to the use

of RNAi to silence genes in *C. elegans*, *Drosophila*, plants, and humans are known in the art (Fire A, et al., 1998 Nature 391:806-811; Fire, A. Trends Genet. 15, 358-363 (1999); Sharp, P. A. RNA interference 2001. Genes Dev. 15, 485-490 (2001); Hammond, S. M., et al., Nature Rev. Genet. 2, 110-1119 (2001); Tuschl, T. Chem. Biochem. 2, 239-245 (2001); Hamilton, A. et al., Science 286, 950-952 (1999); Hammond, S. M., et al., Nature 404, 293-296 (2000); Zamore, P. D., et al., Cell 101, 25-33 (2000); Bernstein, E., et al., Nature 409, 363-366 (2001); Elbashir, S. M., et al., Genes Dev. 15, 188-200 (2001); WO0129058; WO9932619; Elbashir SM, et al., 2001 Nature 411:494-498).

Nucleic acid modulators are commonly used as research reagents, diagnostics, and therapeutics. For example, antisense oligonucleotides, which are able to inhibit gene expression with exquisite specificity, are often used to elucidate the function of particular genes (see, for example, U.S. Pat. No. 6,165,790). Nucleic acid modulators are also used, for example, to distinguish between functions of various members of a biological pathway. For example, antisense oligomers have been employed as therapeutic moieties in the treatment of disease states in animals and man and have been demonstrated in numerous clinical trials to be safe and effective (Milligan JF, *et al*, Current Concepts in Antisense Drug Design, J Med Chem. (1993) 36:1923-1937; Tonkinson JL *et al.*, Antisense Oligodeoxynucleotides as Clinical Therapeutic Agents, Cancer Invest. (1996) 14:54-65). Accordingly, in one aspect of the invention, an HM-specific nucleic acid modulator is used in an assay to further elucidate the role of the HM in the p53 pathway, and/or its relationship to other members of the pathway. In another aspect of the invention, an HM-specific antisense oligomer is used as a therapeutic agent for treatment of p53-related disease states.

Assay Systems

The invention provides assay systems and screening methods for identifying specific modulators of HM activity. As used herein, an "assay system" encompasses all the components required for performing and analyzing results of an assay that detects and/or measures a particular event. In general, primary assays are used to identify or confirm a modulator's specific biochemical or molecular effect with respect to the HM nucleic acid or protein. In general, secondary assays further assess the activity of a HM modulating agent identified by a primary assay and may confirm that the modulating agent affects HM in a manner relevant to the p53 pathway. In some cases, HM modulators will be directly tested in a secondary assay.

In a preferred embodiment, the screening method comprises contacting a suitable assay system comprising an HM polypeptide with a candidate agent under conditions whereby, but for the presence of the agent, the system provides a reference activity (e.g. kinase activity), which is based on the particular molecular event the screening method
5 detects. A statistically significant difference between the agent-biased activity and the reference activity indicates that the candidate agent modulates HM activity, and hence the p53 pathway.

Primary Assays

10 The type of modulator tested generally determines the type of primary assay.

Primary assays for small molecule modulators

For small molecule modulators, screening assays are used to identify candidate modulators. Screening assays may be cell-based or may use a cell-free system that
15 recreates or retains the relevant biochemical reaction of the target protein (reviewed in Sittampalam GS *et al.*, Curr Opin Chem Biol (1997) 1:384-91 and accompanying references). As used herein the term "cell-based" refers to assays using live cells, dead cells, or a particular cellular fraction, such as a membrane, endoplasmic reticulum, or mitochondrial fraction. The term "cell free" encompasses assays using substantially
20 purified protein (either endogenous or recombinantly produced), partially purified or crude cellular extracts. Screening assays may detect a variety of molecular events, including protein-DNA interactions, protein-protein interactions (e.g., receptor-ligand binding), transcriptional activity (e.g., using a reporter gene), enzymatic activity (e.g., via a property of the substrate), activity of second messengers, immunogenicity and changes in cellular
25 morphology or other cellular characteristics. Appropriate screening assays may use a wide range of detection methods including fluorescent, radioactive, colorimetric, spectrophotometric, and amperometric methods, to provide a read-out for the particular molecular event detected.

Cell-based screening assays usually require systems for recombinant expression of
30 HM and any auxiliary proteins demanded by the particular assay. Appropriate methods for generating recombinant proteins produce sufficient quantities of proteins that retain their relevant biological activities and are of sufficient purity to optimize activity and assure assay reproducibility. Yeast two-hybrid and variant screens, and mass spectrometry provide preferred methods for determining protein-protein interactions and elucidation of

protein complexes. In certain applications, when HM-interacting proteins are used in screens to identify small molecule modulators, the binding specificity of the interacting protein to the HM protein may be assayed by various known methods such as substrate processing (e.g. ability of the candidate HM-specific binding agents to function as negative effectors in HM-expressing cells), binding equilibrium constants (usually at least about 10^7 M^{-1} , preferably at least about 10^8 M^{-1} , more preferably at least about 10^9 M^{-1}), and immunogenicity (e.g. ability to elicit HM specific antibody in a heterologous host such as a mouse, rat, goat or rabbit). For enzymes and receptors, binding may be assayed by, respectively, substrate and ligand processing.

10 The screening assay may measure a candidate agent's ability to specifically bind to or modulate activity of a HM polypeptide, a fusion protein thereof, or to cells or membranes bearing the polypeptide or fusion protein. The HM polypeptide can be full length or a fragment thereof that retains functional HM activity. The HM polypeptide may be fused to another polypeptide, such as a peptide tag for detection or anchoring, or to another tag.

15 The HM polypeptide is preferably human HM, or is an ortholog or derivative thereof as described above. In a preferred embodiment, the screening assay detects candidate agent-based modulation of HM interaction with a binding target, such as an endogenous or exogenous protein or other substrate that has HM-specific binding activity, and can be used to assess normal HM gene function.

20 Suitable assay formats that may be adapted to screen for HM modulators are known in the art. Preferred screening assays are high throughput or ultra high throughput and thus provide automated, cost-effective means of screening compound libraries for lead compounds (Fernandes PB, Curr Opin Chem Biol (1998) 2:597-603; Sundberg SA, Curr Opin Biotechnol 2000, 11:47-53). In one preferred embodiment, screening assays uses

25 fluorescence technologies, including fluorescence polarization, time-resolved fluorescence, and fluorescence resonance energy transfer. These systems offer means to monitor protein-protein or DNA-protein interactions in which the intensity of the signal emitted from dye-labeled molecules depends upon their interactions with partner molecules (e.g., Selvin PR, Nat Struct Biol (2000) 7:730-4; Fernandes PB, *supra*;

30 Hertzberg RP and Pope AJ, Curr Opin Chem Biol (2000) 4:445-451).

A variety of suitable assay systems may be used to identify candidate HM and p53 pathway modulators (e.g. U.S. Pat. No. 6,165,992 (kinase assays); U.S. Pat. Nos. 5,550,019 and 6,133,437 (apoptosis assays); U.S. Pat. No. 6,020,135 (p53 modulation),

WO 01/25487 (Helicase assays), U.S. Pat. No. 6,114,132 (phosphatase and protease assays), among others). Specific preferred assays are described in more detail below.

As seen from Table 1, preferred HMs are enzymes or soluble proteins with ligand binding sites, including protein kinases, protein phosphatases, proteases, protease inhibitors, helicases, polymerases, prolylisomerases, hydrolases, reductases, GTPase activating proteins (GAPs), guanine nucleotide exchange factors (GEFs), a range of metabolic enzymes, proteins involved in ubiquitination, DNA methylation and metabolism, RNA processing or binding, and adapters, among others. Alternative preferred targets are membrane proteins, such as G protein coupled receptors (GPCRs), protein kinase receptors, transporters, and ligand-gated ion channels, among others.

Protein kinases, key signal transduction proteins that may be either membrane-associated or intracellular, catalyze the transfer of gamma phosphate from adenosine triphosphate (ATP) to a serine, threonine or tyrosine residue in a protein substrate. Radioassays, which monitor the transfer from [γ - ^{32}P or ^{33}P]ATP, are frequently used to assay kinase activity. For instance, a scintillation assay for p56 (lck) kinase activity monitors the transfer of the gamma phosphate from [γ - ^{33}P] ATP to a biotinylated peptide substrate. The substrate is captured on a streptavidin coated bead that transmits the signal (Beveridge M *et al.*, J Biomol Screen (2000) 5:205-212). This assay uses the scintillation proximity assay (SPA), in which only radio-ligand bound to receptors tethered to the surface of an SPA bead are detected by the scintillant immobilized within it, allowing binding to be measured without separation of bound from free ligand. Other assays for protein kinase activity may use antibodies that specifically recognize phosphorylated substrates. For instance, the kinase receptor activation (KIRA) assay measures receptor tyrosine kinase activity by ligand stimulating the intact receptor in cultured cells, then capturing solubilized receptor with specific antibodies and quantifying phosphorylation via phosphotyrosine ELISA (Sadick MD, Dev Biol Stand (1999) 97:121-133). Another example of antibody based assays for protein kinase activity is TRF (time-resolved fluorometry). This method utilizes europium chelate-labeled anti-phosphotyrosine antibodies to detect phosphate transfer to a polymeric substrate coated onto microtiter plate wells. The amount of phosphorylation is then detected using time-resolved, dissociation-enhanced fluorescence (Braunwalder AF, et al., Anal Biochem 1996 Jul 1;238(2):159-64).

Protein phosphatases catalyze the removal of a gamma phosphate from a serine, threonine or tyrosine residue in a protein substrate. Since phosphatases act in opposition

to kinases, appropriate assays measure the same parameters as kinase assays. In one example, the dephosphorylation of a fluorescently labeled peptide substrate allows trypsin cleavage of the substrate, which in turn renders the cleaved substrate significantly more fluorescent (Nishikata M *et al.*, Biochem J (1999) 343:35-391). In another example, fluorescence polarization (FP), a solution-based, homogeneous technique requiring no immobilization or separation of reaction components, is used to develop high throughput screening (HTS) assays for protein phosphatases. This assay uses direct binding of the phosphatase with the target, and increasing concentrations of target- phosphatase increase the rate of dephosphorylation, leading to a change in polarization (Parker GJ *et al.*, (2000) J Biomol Screen 5:77-88).

Proteases are enzymes that cleave protein substrates at specific sites. Exemplary assays detect the alterations in the spectral properties of an artificial substrate that occur upon protease-mediated cleavage. In one example, synthetic caspase substrates containing four amino acid proteolysis recognition sequences, separating two different fluorescent tags are employed; fluorescence resonance energy transfer detects the proximity of these fluorophores, which indicates whether the substrate is cleaved (Mahajan NP *et al.*, Chem Biol (1999) 6:401-409).

Endogenous protease inhibitors may inhibit protease activity. In an example of an assay developed for either proteases or protease inhibitors, a biotinylated substrate is coated on a titer plate and hydrolyzed with the protease; the unhydrolyzed substrate is quantified by reaction with alkaline phosphatase-streptavidin complex and detection of the reaction product. The activity of protease inhibitors correlates with the activity of the alkaline phosphatase indicator enzyme (Gan Z *et al.*, Anal Biochem 1999) 268:151-156).

Helicases are involved in unwinding double stranded DNA and RNA. In one embodiment, an assay for DNA helicase activity detects the displacement of a radio-labeled oligonucleotide from single stranded DNA upon initiation of unwinding (Sivaraja M *et al.*, Anal Biochem (1998) 265:22-27). An assay for RNA helicase activity uses the scintillation proximity (SPA) assay to detect the displacement of a radio-labeled oligonucleotide from single stranded RNA (Kyono K *et al.*, Anal Biochem (1998) 257:120-126).

Polymerases catalyze the extension of newly synthesized DNA or RNA chains. Their activity may be monitored in an assay that uses labeled nucleotide analogs. For instance, a colorimetric polymerase assay monitors RNA synthesis using labeled ATP and GTP (Vassiliou W *et al.*, Virology (2000) 274:429-437).

Peptidyl-prolyl isomerase (PPIase) proteins, which include cyclophilins, FK506 binding proteins and paravulins, catalyze the isomerization of *cis-trans* proline peptide bonds in oligopeptides and are thought to be essential for protein folding during protein synthesis in the cell. Spectrophotometric assays for PPIase activity can detect

5 isomerization of labeled peptide substrates, either by direct measurement of isomer-specific absorbance, or by coupling isomerization to isomer-specific cleavage by chymotrypsin (Scholz C *et al.*, FEBS Lett (1997) 414:69-73; Janowski B *et al.*, Anal Biochem (1997) 252:299-307; Kullertz G *et al.*, Clin Chem (1998) 44:502-8). Alternative assays use the scintillation proximity or fluorescence polarization assay to screen for

10 ligands of specific PPIases (Graziani F *et al.*, J Biolmol Screen (1999) 4:3-7; Dubowchik GM *et al.*, Bioorg Med Chem Lett (2000) 10:559-562). Assays for 3,2-trans-enoyl-CoA isomerase activity have also been described (Binstock, J. F., and Schulz, H. (1981) Methods Enzymol. 71:403-411; Geisbrecht BV *et al* (1999) J Biol Chem. 274:21797-803). These assays use 3-cis-octenoyl-CoA as a substrate, and reaction progress is

15 monitored spectrophotometrically using a coupled assay for the isomerization of 3-cis-octenoyl-CoA to 2-trans-octenoyl-CoA.

The proteins used in the methods of this invention include enzymes involved in lipid, nucleic acid, and protein metabolism. Many different metabolic enzymes are amenable to high throughput assay development, due to well-characterized substrates and active sites,

20 generally simple reaction mechanisms, and a general conservation in reaction mechanism. Numerous assays for metabolic enzymes (e.g., fatty acid desaturases, glycosyltransferases, mitochondrial enzymes, histone deacetylases, purine biosynthetic enzymes, etc.) have been developed.

Fatty acid desaturases catalyze the insertion of double bonds into saturated fatty acid

25 molecules. In one application, radioassays for inhibitors of delta-5 and delta-6 fatty acid desaturase activity use thin layer chromatography to detect conversion of fatty acid substrates (Obukowicz *et al.*, Biochem Pharmacol (1998) 55:1045-1058).

Glycosyltransferases mediate changes in glycosylation patterns that, in turn, may affect the function of glycoproteins and/or glycolipids and, further downstream, processes

30 of development, differentiation, transformation and cell-cell recognition. An assay for glycosyltransferase uses scintillation methods to measure the transfer of carbohydrate from radiolabeled sugar-nucleotide donor to a synthetic glycopolymer acceptor that is coupled to polyacrylamide and coated on plastic microtiter plates (Donovan RS *et al.*, Glycoconj J (1999) 16:607-615).

Histone deacetylation and acetylation proteins are involved in regulating chromatin structure during transcription and thus function in gene regulation. In one example, a histone deacetylase assay uses the scintillation proximity assay (SPA) and biotinylated [3H]acetyl histone H4 peptide substrate (Nare B et al., Anal Biochem 1999, 267:390-396).

5 Upon binding to streptavidin-coated SPA beads, the peptide substrate generates a radioactive signal, which decreases as a result of histone deacetylase activity.

The purH protein is a bifunctional enzyme that is responsible for key steps in de novo purine biosynthesis, having AICAR transformylase and IMP cyclohydrolase activities. In one application, a radioassay uses 3H-labeled intermediates and scintillation methods to
10 measure enzyme activity (Szabados E and Christopherson RI, Anal Biochem 1994, 221:401-4).

Ubiquitination is a process of attaching ubiquitin to a protein prior to the selective proteolysis of that protein in the cell. Assays based on fluorescence resonance energy transfer to screen for ubiquitination inhibitors are known in the art (Boisclair MD et al., J
15 Biomol Screen 2000 5:319-328).

DNA methylation is an epigenetic DNA modification that participates in genome stability and gene repression in vertebrates, and is involved in various stages of neoplasia. Measurements of DNA methylation may be based on immunoassays for biomarkers of methylation (Harrison KL, et al., Chem Res Toxicol 2001 14:295-301), or alternatively,
20 based on fluorescence-based real-time PCR (Eads CA, et al., Nucleic Acids Res 2000 28:E32). Assays for DNA metabolism might include assays for DNA cleavage (Biggins JB, et al., Proc Natl Acad Sci U S A. 2000 97:13537-42), or for polymerization (Lin K, and Ricciardi RP. J Virol Methods. 2000 88:219-25).

RNA folds into a myriad of tertiary structures that are responsible for its diverse
25 functions in cells. In most instances, RNA is associated with RNA-binding proteins (RBPs) that protect, stabilize, package or transport RNA, mediate RNA interactions with other biomolecules or act catalytically on RNA. The structural information obtained for RNA alone and RNA-protein complexes has elucidated a variety of RNA tertiary structures and diverse modes for RNA-protein interaction. The specific interaction of
30 proteins with highly structured RNAs makes it possible to target unique RNA motifs with small molecules, thus making RNA an interesting target for therapeutic intervention. Assays for RNA binding or processing may be based on homogeneous scintillation proximity (Liu J, et al., Anal Biochem 2001 289:239-245), chemiluminescence

(Mazumder A, *Nucleic Acids Res* 1998 26:1996-2000), gel shift (Stull RA, et al., *Antisense Nucleic Acid Drug Dev* 1996 6:221-228; U.S. Pat. No: 6004749).

Adapter proteins are involved in a wide range of signaling and other cellular processes and generally facilitate protein-protein or protein-nucleic acid interactions via certain conserved motifs, including PDZ, SH2, SH3, PH, TRAF, WD40, LIM, ankyrin repeat, KH and annexin domains, etc. Assays for adapter protein activity may measure protein binding at the conserved motifs. For instance, exemplary assays for SH2 domain-containing proteins have measured binding using fluorescently labeled peptide substrate and fluorescence polarization or laser-scanning techniques (Lynch BA et al., *Anal Biochem* 1999, 275:62-73; Zuck P et al., *Proc Natl Acad Sci USA* 1999, 96: 11122-11127). An alternative SH2 binding assay uses radiolabeled peptide. An assay for protein-protein interaction at the LIM domain has used fluorescently labeled LIM-containing proteins (FHL2 and FHL3) and the fluorescence resonance energy transfer (FRET) technique (Li HY, *J Cell Biochem* 2001, 80:293-303).

G-protein-coupled receptors (GPCRs) comprise a large family of cell surface receptors that mediate a diverse array of biological functions. They selectively respond to a wide variety of extracellular chemical stimuli to activate specific signaling cascades. Assays may measure reporter gene activity or changes in intracellular calcium ions, or other second messengers (Durocher Y *et al.*, *Anal Biochem* (2000) 284: 316-326; Miller TR *et al.*, *J Biomol Screen* (1999) 4:249-258). Such assays may utilize chimeric Gα proteins that will couple to many different GPCRs and thus facilitate "universal" screening assays (Coward P *et al.*, *Anal Biochem* (1999) 270:242-248; Milligan G and Rees S *et al.*, *Trends Pharmacol Sci* (1999) 20:118-124).

GPCRs exert their effects through heterotrimeric G proteins, which cycle between active GTP- and inactive GDP-bound forms. Receptors catalyze the activation of G proteins by promoting exchange of GDP for GTP, while G proteins catalyze their own deactivation through their intrinsic GTPase activity. GEFs accelerate GDP dissociation and GTP binding, while GAPs stimulate GTP hydrolysis to GDP. The same assays used to monitor GPCR activity may thus be applied to monitor the activity of GEFs or GAPs. Alternatively, GEF activity may be assayed by the release of labeled GDP from the appropriate GTPase or by the uptake of labelled GTP. GAP activity may be monitored via a GTP hydrolysis assay using labeled GTP (*e.g.*, Jones S *et al.*, *Molec Biol Cell* (1998) 9:2819-2837).

Transporter proteins carry a range of substrates, including nutrients, ions, amino acids, and drugs, across cell membranes. Assays for modulators of transporters may use labeled substrates. For instance, exemplary high throughput screens to identify compounds that interact with different peptide and anion transporters both use fluorescently labeled
5 substrates; the assay for peptide transport additionally uses multiscreen filtration plates (Blevitt JM et al., J Biomol Screen 1999, 4:87-91; Cihlar T and Ho ES, Anal Biochem 2000, 283:49-55).

Ion channels mediate essential physiological functions, including fluid secretion, electrolyte balance, bioenergetics, and membrane excitability. Assays for channel activity
10 can incorporate ion-sensitive dyes or proteins or voltage-sensitive dyes or proteins, as reviewed in Gonzalez JE *et al.* (Drug Discovery Today (1999) 4:431-439). Alternative methods measure the displacement of known ligands, which may be radio-labeled or fluorescently labeled (*e.g.*, ScHMid EL *et al.*, Anal Chem (1998) 70:1331-1338).

Transcription factors control gene transcription. Electrophoretic mobility shift assay
15 (EMSA) or gel shift assay is one of the most powerful methods for studying protein-DNA interactions. High throughput gel shift assays for transcription factors may involve fluorescence (Cyano dye Cy5) labeled oligodeoxynucleotide duplexes as specific probes and an automatic DNA sequencer for analysis (Ruscher K, et al., (2000) J Biotechnol 78:163-70). Alternatively high throughput methods involve colorimetric assays (Renard
20 P, et al. (2001) Nucleic Acids Res 29(4):E21), or homogeneous fluorescence assays for the detection and quantification of sequence-specific DNA-binding proteins (Heyduk T, and Heyduk E (2001) Nat Biotechnol 20:171-6.)

Nuclear receptors (NRs) are a superfamily of ligand-dependent transcription factors that mediate the effects of hormones and other endogenous ligands to regulate the
25 expression of specific genes. High throughput assays for nuclear receptors include fluorescent polarization binding assays (Lin S, et al. (2002) Anal Biochem 300(1):15-21), and homogeneous time-resolved fluorescence energy transfer (Zhou G, et al. (2001) Methods 25:54-61), among others.

Reductases are enzymes of oxidoreductase class that catalyze reactions in which
30 metabolites are reduced. High throughput screening assays for reductases may involve scintillation (Fernandes PB. (1998) Curr Opin Chem Biol 2:597-603; Delaporte E et al. (2001) J Biomol Screen 6:225-231).

Hydrolases catalyze the hydrolysis of a substrate such as esterases, lipases, peptidases, nucleotidases, and phosphatases, among others. Enzyme activity assays may be used to

measure hydrolase activity. The activity of the enzyme is determined in presence of excess substrate, by spectrophotometrically measuring the rate of appearance of reaction products. High throughput arrays and assays for hydrolases are known to those skilled in the art (Park CB and Clark DS (2002) Biotech Bioeng 78:229-235).

- 5 If an existent high-throughput assay is not available for a particular HM, its activity can be monitored using cell-based or cell-free methods. Since noncovalently associated multi-protein complexes mediate many biological processes, many effective chemical modulators will function by disrupting such complexes. If the HM belongs to a complex that is essential for protein function, appropriate assays may monitor complex formation or
- 10 survival, instead of function *per se*. For instance, an appropriate cell-based assay is based on protein complementation, in which two proteins in a complex are fused to complementary fragments of the enzyme dihydrofolate reductase (DHFR). Enzyme activity of DHFR depends on proper folding of the two fragments, which in turn depends upon binding of the two complexed proteins. Two properties of DHFR can be assayed:
- 15 DHFR confers viability to DHFR-negative cells in a cell survival assay, or DHFR binds a fluorescent substrate in a reporter assay (Remy I and Michnick SW, Proc Natl Acad Sci (1999) 96:5394-5399).

- Apoptosis assays.** Assays for apoptosis may be performed by terminal
- 20 deoxynucleotidyl transferase-mediated digoxigenin-11-dUTP nick end labeling (TUNEL) assay. The TUNEL assay is used to measure nuclear DNA fragmentation characteristic of apoptosis (Lazebnik *et al.*, 1994, Nature 371, 346), by following the incorporation of fluorescein-dUTP (Yonehara *et al.*, 1989, J. Exp. Med. 169, 1747). Apoptosis may further be assayed by acridine orange staining of tissue culture cells (Lucas, R., et al., 1998, Blood
- 25 15:4730-41). An apoptosis assay system may comprise a cell that expresses an HM, and that optionally has defective p53 function (e.g. p53 is over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the apoptosis assay system and changes in induction of apoptosis relative to controls where no test agent is added, identify candidate p53 modulating agents. In some embodiments of the invention, an apoptosis
- 30 assay may be used as a secondary assay to test a candidate p53 modulating agents that is initially identified using a cell-free assay system. An apoptosis assay may also be used to test whether HM function plays a direct role in apoptosis. For example, an apoptosis assay may be performed on cells that over- or under-express HM relative to wild type cells. Differences in apoptotic response compared to wild type cells suggests that the HM plays

a direct role in the apoptotic response. Apoptosis assays are described further in US Pat. No. 6,133,437.

- Cell proliferation and cell cycle assays.** Cell proliferation may be assayed via
- 5 bromodeoxyuridine (BRDU) incorporation. This assay identifies a cell population undergoing DNA synthesis by incorporation of BRDU into newly-synthesized DNA. Newly-synthesized DNA may then be detected using an anti-BRDU antibody (Hoshino *et al.*, 1986, *Int. J. Cancer* 38, 369; Campana *et al.*, 1988, *J. Immunol. Meth.* 107, 79), or by other means.
- 10 Cell Proliferation may also be examined using [³H]-thymidine incorporation (Chen, J., 1996, *Oncogene* 13:1395-403; Jeoung, J., 1995, *J. Biol. Chem.* 270:18367-73). This assay allows for quantitative characterization of S-phase DNA syntheses. In this assay, cells synthesizing DNA will incorporate [³H]-thymidine into newly synthesized DNA. Incorporation can then be measured by standard techniques such as by counting of
- 15 radioisotope in a scintillation counter (e.g., Beckman LS 3800 Liquid Scintillation Counter).

- Cell proliferation may also be assayed by colony formation in soft agar (Sambrook *et al.*, *Molecular Cloning*, Cold Spring Harbor (1989)). For example, cells transformed with HM are seeded in soft agar plates, and colonies are measured and counted after two weeks
- 20 incubation.

- Involvement of a gene in the cell cycle may be assayed by flow cytometry (Gray JW *et al.* (1986) *Int J Radiat Biol Relat Stud Phys Chem Med* 49:237-55). Cells transfected with an HM may be stained with propidium iodide and evaluated in a flow cytometer (available from Becton Dickinson).

- 25 Accordingly, a cell proliferation or cell cycle assay system may comprise a cell that expresses an HM, and that optionally has defective p53 function (e.g. p53 is over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the assay system and changes in cell proliferation or cell cycle relative to controls where no test agent is added, identify candidate p53 modulating agents. In some embodiments of
- 30 the invention, the cell proliferation or cell cycle assay may be used as a secondary assay to test a candidate p53 modulating agents that is initially identified using another assay system such as a cell-free assay system. A cell proliferation assay may also be used to test whether HM function plays a direct role in cell proliferation or cell cycle. For example, a cell proliferation or cell cycle assay may be performed on cells that over- or under-express

HM relative to wild type cells. Differences in proliferation or cell cycle compared to wild type cells suggests that the HM plays a direct role in cell proliferation or cell cycle.

Angiogenesis. Angiogenesis may be assayed using various human endothelial cell systems, such as umbilical vein, coronary artery, or dermal cells. Suitable assays include Alamar Blue based assays (available from Biosource International) to measure proliferation; migration assays using fluorescent molecules, such as the use of Becton Dickinson Falcon HTS FluoroBlock cell culture inserts to measure migration of cells through membranes in presence or absence of angiogenesis enhancer or suppressors; and tubule formation assays based on the formation of tubular structures by endothelial cells on Matrigel® (Becton Dickinson). Accordingly, an angiogenesis assay system may comprise a cell that expresses an HM, and that optionally has defective p53 function (e.g. p53 is over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the angiogenesis assay system and changes in angiogenesis relative to controls where no test agent is added, identify candidate p53 modulating agents. In some embodiments of the invention, the angiogenesis assay may be used as a secondary assay to test a candidate p53 modulating agents that is initially identified using another assay system. An angiogenesis assay may also be used to test whether HM function plays a direct role in cell proliferation. For example, an angiogenesis assay may be performed on cells that over- or under-express HM relative to wild type cells. Differences in angiogenesis compared to wild type cells suggests that the HM plays a direct role in angiogenesis.

Hypoxic induction. The alpha subunit of the transcription factor, hypoxia inducible factor-1 (HIF-1), is upregulated in tumor cells following exposure to hypoxia in vitro. Under hypoxic conditions, HIF-1 stimulates the expression of genes known to be important in tumour cell survival, such as those encoding glycolytic enzymes and VEGF. Induction of such genes by hypoxic conditions may be assayed by growing cells transfected with HM in hypoxic conditions (such as with 0.1% O₂, 5% CO₂, and balance N₂, generated in a Napco 7001 incubator (Precision Scientific)) and normoxic conditions, followed by assessment of gene activity or expression by Taqman®. For example, a hypoxic induction assay system may comprise a cell that expresses an HM, and that optionally has a mutated p53 (e.g. p53 is over-expressed or under-expressed relative to wild-type cells). A test agent can be added to the hypoxic induction assay system and

changes in hypoxic response relative to controls where no test agent is added, identify candidate p53 modulating agents. In some embodiments of the invention, the hypoxic induction assay may be used as a secondary assay to test a candidate p53 modulating agents that is initially identified using another assay system. A hypoxic induction assay
5 may also be used to test whether HM function plays a direct role in the hypoxic response. For example, a hypoxic induction assay may be performed on cells that over- or under-express HM relative to wild type cells. Differences in hypoxic response compared to wild type cells suggests that the HM plays a direct role in hypoxic induction.

10 **Cell adhesion.** Cell adhesion assays measure adhesion of cells to purified adhesion proteins, or adhesion of cells to each other, in presence or absence of candidate modulating agents. Cell-protein adhesion assays measure the ability of agents to modulate the adhesion of cells to purified proteins. For example, recombinant proteins are produced, diluted to 2.5g/mL in PBS, and used to coat the wells of a microtiter plate. The
15 wells used for negative control are not coated. Coated wells are then washed; blocked with 1% BSA, and washed again. Compounds are diluted to 2× final test concentration and added to the blocked, coated wells. Cells are then added to the wells, and the unbound cells are washed off. Retained cells are labeled directly on the plate by adding a membrane-permeable fluorescent dye, such as calcein-AM, and the signal is quantified in
20 a fluorescent microplate reader.

Cell-cell adhesion assays measure the ability of agents to modulate binding of cell adhesion proteins with their native ligands. These assays use cells that naturally or recombinantly express the adhesion protein of choice. In an exemplary assay, cells expressing the cell adhesion protein are plated in wells of a multiwell plate. Cells
25 expressing the ligand are labeled with a membrane-permeable fluorescent dye, such as BCECF, and allowed to adhere to the monolayers in the presence of candidate agents. Unbound cells are washed off, and bound cells are detected using a fluorescence plate reader.

High-throughput cell adhesion assays have also been described. In one such assay,
30 small molecule ligands and peptides are bound to the surface of microscope slides using a microarray spotter, intact cells are then contacted with the slides, and unbound cells are washed off. In this assay, not only the binding specificity of the peptides and modulators against cell lines are determined, but also the functional cell signaling of attached cells

using immunofluorescence techniques in situ on the microchip is measured (Falsey JR et al., Bioconjug Chem. 2001 May-Jun;12(3):346-53).

Primary assays for antibody modulators

5 For antibody modulators, appropriate primary assays test is a binding assay that tests the antibody's affinity to and specificity for the HM protein. Methods for testing antibody affinity and specificity are well known in the art (Harlow and Lane, 1988, 1999, *supra*). The enzyme-linked immunosorbant assay (ELISA) is a preferred method for detecting HM-specific antibodies; others include FACS assays, radioimmunoassays, and fluorescent
10 assays.

Primary assays for nucleic acid modulators

For nucleic acid modulators, primary assays may test the ability of the nucleic acid modulator to inhibit or enhance HM gene expression, preferably mRNA expression. In
15 general, expression analysis comprises comparing HM expression in like populations of cells (*e.g.*, two pools of cells that endogenously or recombinantly express HM) in the presence and absence of the nucleic acid modulator. Methods for analyzing mRNA and protein expression are well known in the art. For instance, Northern blotting, slot blotting, ribonuclease protection, quantitative RT-PCR (*e.g.*, using the TaqMan®, PE Applied
20 Biosystems), or microarray analysis may be used to confirm that HM mRNA expression is reduced in cells treated with the nucleic acid modulator (*e.g.*, Current Protocols in Molecular Biology (1994) Ausubel FM *et al.*, eds., John Wiley & Sons, Inc., chapter 4; Freeman WM *et al.*, Biotechniques (1999) 26:112-125; Kallioniemi OP, Ann Med 2001, 33:142-147; Blohm DH and Guiseppi-Elie, A Curr Opin Biotechnol 2001, 12:41-47).
25 Protein expression may also be monitored. Proteins are most commonly detected with specific antibodies or antisera directed against either the HM protein or specific peptides. A variety of means including Western blotting, ELISA, or in situ detection, are available (Harlow E and Lane D, 1988 and 1999, *supra*).

30 **Secondary Assays**

Secondary assays may be used to further assess the activity of HM-modulating agent identified by any of the above methods to confirm that the modulating agent affects HM in a manner relevant to the p53 pathway. As used herein, HM-modulating agents encompass candidate clinical compounds or other agents derived from previously identified

modulating agent. Secondary assays can also be used to test the activity of a modulating agent on a particular genetic or biochemical pathway or to test the specificity of the modulating agent's interaction with HM.

5 Secondary assays generally compare like populations of cells or animals (*e.g.*, two pools of cells or animals that endogenously or recombinantly express HM) in the presence and absence of the candidate modulator. In general, such assays test whether treatment of cells or animals with a candidate HM-modulating agent results in changes in the p53 pathway in comparison to untreated (or mock- or placebo-treated) cells or animals. Certain assays use "sensitized genetic backgrounds", which, as used herein, describe cells
10 or animals engineered for altered expression of genes in the p53 or interacting pathways.

Cell-based assays

Cell based assays may use a variety of mammalian cell lines known to have defective p53 function (*e.g.* SAOS-2 osteoblasts, H1299 lung cancer cells, C33A and HT3 cervical
15 cancer cells, HT-29 and DLD-1 colon cancer cells, among others, available from American Type Culture Collection (ATCC), Manassas, VA). Cell based assays may detect endogenous p53 pathway activity or may rely on recombinant expression of p53 pathway components. Any of the aforementioned assays may be used in this cell-based format. Candidate modulators are typically added to the cell media but may also be
20 injected into cells or delivered by any other efficacious means.

Animal Assays

A variety of non-human animal models of normal or defective p53 pathway may be used to test candidate HM modulators. Models for defective p53 pathway typically use
25 genetically modified animals that have been engineered to mis-express (*e.g.*, over-express or lack expression in) genes involved in the p53 pathway. Assays generally require systemic delivery of the candidate modulators, such as by oral administration, injection, etc.

In a preferred embodiment, p53 pathway activity is assessed by monitoring
30 neovascularization and angiogenesis. Animal models with defective and normal p53 are used to test the candidate modulator's affect on HM in Matrigel® assays. Matrigel® is an extract of basement membrane proteins, and is composed primarily of laminin, collagen IV, and heparin sulfate proteoglycan. It is provided as a sterile liquid at 4° C, but rapidly forms a solid gel at 37° C. Liquid Matrigel® is mixed with various angiogenic agents,

such as bFGF and VEGF, or with human tumor cells which over-express the HM. The mixture is then injected subcutaneously(SC) into female athymic nude mice (Taconic, Germantown, NY) to support an intense vascular response. Mice with Matrigel® pellets may be dosed via oral (PO), intraperitoneal (IP), or intravenous (IV) routes with the candidate modulator. Mice are euthanized 5 - 12 days post-injection, and the Matrigel® pellet is harvested for hemoglobin analysis (Sigma plasma hemoglobin kit). Hemoglobin content of the gel is found to correlate the degree of neovascularization in the gel.

In another preferred embodiment, the effect of the candidate modulator on HM is assessed via tumorigenicity assays. In one example, xenograft human tumors are implanted SC into female athymic mice, 6-7 week old, as single cell suspensions either from a pre-existing tumor or from *in vitro* culture. The tumors which express the HM endogenously are injected in the flank, 1×10^5 to 1×10^7 cells per mouse in a volume of 100 μ L using a 27gauge needle. Mice are then ear tagged and tumors are measured twice weekly. Candidate modulator treatment is initiated on the day the mean tumor weight reaches 100 mg. Candidate modulator is delivered IV, SC, IP, or PO by bolus administration. Depending upon the pharmacokinetics of each unique candidate modulator, dosing can be performed multiple times per day. The tumor weight is assessed by measuring perpendicular diameters with a caliper and calculated by multiplying the measurements of diameters in two dimensions. At the end of the experiment, the excised tumors maybe utilized for biomarker identification or further analyses. For immunohistochemistry staining, xenograft tumors are fixed in 4% paraformaldehyde, 0.1M phosphate, pH 7.2, for 6 hours at 4°C, immersed in 30% sucrose in PBS, and rapidly frozen in isopentane cooled with liquid nitrogen.

Diagnostic and therapeutic uses

Specific HM-modulating agents are useful in a variety of diagnostic and therapeutic applications where disease or disease prognosis is related to defects in the p53 pathway, such as angiogenic, apoptotic, or cell proliferation disorders. Accordingly, the invention also provides methods for modulating the p53 pathway in a cell, preferably a cell pre-determined to have defective p53 function, comprising the step of administering an agent to the cell that specifically modulates HM activity. Preferably, the modulating agent produces a detectable phenotypic change in the cell indicating that the p53 function is restored, i.e., for example, the cell undergoes normal proliferation or progression through the cell cycle.

The discovery that HM is implicated in p53 pathway provides for a variety of methods that can be employed for the diagnostic and prognostic evaluation of diseases and disorders involving defects in the p53 pathway and for the identification of subjects having a predisposition to such diseases and disorders.

5 Various expression analysis methods can be used to diagnose whether HM expression occurs in a particular sample, including Northern blotting, slot blotting, ribonuclease protection, quantitative RT-PCR, and microarray analysis. (*e.g.*, Current Protocols in Molecular Biology (1994) Ausubel FM *et al.*, eds., John Wiley & Sons, Inc., chapter 4; Freeman WM *et al.*, Biotechniques (1999) 26:112-125; Kallioniemi OP, Ann Med 2001, 10 33:142-147; Blohm and Guiseppi-Elie, Curr Opin Biotechnol 2001, 12:41-47). Tissues having a disease or disorder implicating defective p53 signaling that express an HM, are identified as amenable to treatment with an HM modulating agent. In a preferred application, the p53 defective tissue overexpresses an HM relative to normal tissue. For example, a Northern blot analysis of mRNA from tumor and normal cell lines, or from 15 tumor and matching normal tissue samples from the same patient, using full or partial HM cDNA sequences as probes, can determine whether particular tumors express or overexpress HM. Alternatively, the TaqMan® is used for quantitative RT-PCR analysis of HM expression in cell lines, normal tissues and tumor samples (PE Applied Biosystems).

20 Various other diagnostic methods may be performed, for example, utilizing reagents such as the HM oligonucleotides, and antibodies directed against an HM, as described above for: (1) the detection of the presence of HM gene mutations, or the detection of either over- or under-expression of HM mRNA relative to the non-disorder state; (2) the detection of either an over- or an under-abundance of HM gene product relative to the 25 non-disorder state; and (3) the detection of perturbations or abnormalities in the signal transduction pathway mediated by HM.

Thus, in a specific embodiment, the invention is drawn to a method for diagnosing a disease in a patient, the method comprising: a) obtaining a biological sample from the patient; b) contacting the sample with a probe for HM expression; c) comparing results 30 from step (b) with a control; and d) determining whether step (c) indicates a likelihood of disease. Preferably, the disease is cancer, most preferably a cancer as shown in TABLE 2. The probe may be either DNA or protein, including an antibody.

EXAMPLES

The following experimental section and examples are offered by way of illustration and not by way of limitation.

5 I. Drosophila p53 screen

The *Drosophila* p53 gene was overexpressed specifically in the wing using the vestigial margin quadrant enhancer. Increasing quantities of *Drosophila* p53 (titrated using different strength transgenic inserts in 1 or 2 copies) caused deterioration of normal wing morphology from mild to strong, with phenotypes including disruption of pattern and
 10 polarity of wing hairs, shortening and thickening of wing veins, progressive crumpling of the wing and appearance of dark “death” inclusions in wing blade. In a screen designed to identify enhancers and suppressors of *Drosophila* p53, homozygous females carrying two copies of p53 were crossed to 5663 males carrying random insertions of a piggyBac transposon (Fraser M *et al.*, Virology (1985) 145:356-361). Progeny containing insertions
 15 were compared to non-insertion-bearing sibling progeny for enhancement or suppression of the p53 phenotypes. Sequence information surrounding the piggyBac insertion site was used to identify the modifier genes. Modifiers of the wing phenotype were identified as members of the p53 pathway. Human orthologs of the modifiers are referred to herein as HM.

20

II. Analysis of Table 1

BLAST analysis (Altschul *et al.*, *supra*) was employed to identify Targets from *Drosophila* modifiers. The column “HM name” provides the known name abbreviations for the Targets, where available, from Genbank. “HM Acc#” and “HM Description”
 25 provide the Target protein Genbank identifier number (GI#) and description from Genbank, respectively. The length of each amino acid is in the “HM Length” column.

As discussed above, various classes of proteins are preferred targets for specific modulator types. “Target Type” column identifies each Target as a preferred target for one or more types of modulators. For example, TRIM2 (row 24) is a preferred target for
 30 antisense (AS), FBL3 (row 26) is a preferred target for both small molecule (SM) and antisense (AS), and PL6 (row 29) is a preferred target for antibody (Ab), small molecule (SM), and antisense (AS) modulators.

The “Category” column places each Target into a protein family, such as kinase, phosphatase, etc. These families were chosen based on the available literature, and

detailed protein domain and motif analysis for each Target. Various domains, signals, and functional subunits in proteins were analyzed using the PSORT (Nakai K., and Horton P., Trends Biochem Sci, 1999, 24:34-6; Kenta Nakai, Protein sorting signals and prediction of subcellular localization, Adv. Protein Chem. 54, 277-344 (2000)), PFAM (Bateman A., et al., Nucleic Acids Res, 1999, 27:260-2; <http://pfam.wustl.edu>), SMART (Ponting CP, et al., SMART: identification and annotation of domains from signaling and extracellular protein sequences. Nucleic Acids Res. 1999 Jan 1;27(1):229-32), TM-HMM (Erik L.L. Sonnhammer, Gunnar von Heijne, and Anders Krogh: A hidden Markov model for predicting transmembrane helices in protein sequences. In Proc. of Sixth Int. Conf. on Intelligent Systems for Molecular Biology, p 175-182 Ed J. Glasgow, T. Littlejohn, F. Major, R. Lathrop, D. Sankoff, and C. Sensen Menlo Park, CA: AAAI Press, 1998), and clust (Remm M, and Sonnhammer E. Classification of transmembrane protein families in the Caenorhabditis elegans genome and identification of human orthologs. Genome Res. 2000 Nov;10(11):1679-89) programs. The identified functional units for each protein are represented in the "Motif-H", "Psort-TM", and "TM-HMM" columns. The "Psort-TM", and "TM-TargetM" columns refer to predictions for possible transmembrane domains for each Target.

Protein sequences of Drosophila modifiers of p53 from screen (Example I), are represented in the "Fly Gene Acc" column by GI#, followed by the length of each Drosophila modifier protein ("Fly aa" column), their functional domains and motifs ("Motif Fly" column), and the type of interaction each modifier exhibits with the p53 pathway. The "PSCORE" column provides the BLAST score of each Target versus its Drosophila ortholog.

25 III. High-Throughput In Vitro Fluorescence Polarization Assay

Fluorescently-labeled HM peptide/substrate are added to each well of a 96-well microtiter plate, along with a test agent in a test buffer (10 mM HEPES, 10 mM NaCl, 6 mM magnesium chloride, pH 7.6). Changes in fluorescence polarization, determined by using a Fluorolite FPM-2 Fluorescence Polarization Microtiter System (Dynatech Laboratories, Inc), relative to control values indicates the test compound is a candidate modifier of HM activity.

IV. High-Throughput In Vitro Binding Assay.

³³P-labeled HM peptide is added in an assay buffer (100 mM KCl, 20 mM HEPES pH 7.6, 1 mM MgCl₂, 1% glycerol, 0.5% NP-40, 50 mM beta-mercaptoethanol, 1 mg/ml BSA, cocktail of protease inhibitors) along with a test agent to the wells of a Neutralite-avidin coated assay plate and incubated at 25°C for 1 hour. Biotinylated substrate is then added to each well and incubated for 1 hour. Reactions are stopped by washing with PBS, and counted in a scintillation counter. Test agents that cause a difference in activity relative to control without test agent are identified as candidate p53 modulating agents.

V. Immunoprecipitations and Immunoblotting

For coprecipitation of transfected proteins, 3×10^6 appropriate recombinant cells containing the HM proteins are plated on 10-cm dishes and transfected on the following day with expression constructs. The total amount of DNA is kept constant in each transfection by adding empty vector. After 24 h, cells are collected, washed once with phosphate-buffered saline and lysed for 20 min on ice in 1 ml of lysis buffer containing 50 mM Hepes, pH 7.9, 250 mM NaCl, 20 mM -glycerophosphate, 1 mM sodium orthovanadate, 5 mM p-nitrophenyl phosphate, 2 mM dithiothreitol, protease inhibitors (complete, Roche Molecular Biochemicals), and 1% Nonidet P-40. Cellular debris is removed by centrifugation twice at $15,000 \times g$ for 15 min. The cell lysate is incubated with 25 μ l of M2 beads (Sigma) for 2 h at 4 °C with gentle rocking.

After extensive washing with lysis buffer, proteins bound to the beads are solubilized by boiling in SDS sample buffer, fractionated by SDS-polyacrylamide gel electrophoresis, transferred to polyvinylidene difluoride membrane and blotted with the indicated antibodies. The reactive bands are visualized with horseradish peroxidase coupled to the appropriate secondary antibodies and the enhanced chemiluminescence (ECL) Western blotting detection system (Amersham Pharmacia Biotech).

VI. Kinase assay

A purified or partially purified HM is diluted in a suitable reaction buffer, e.g., 50 mM Hepes, pH 7.5, containing magnesium chloride or manganese chloride (1-20 mM) and a peptide or polypeptide substrate, such as myelin basic protein or casein (1-10 μ g/ml). The final concentration of the kinase is 1-20 nM. The enzyme reaction is conducted in microtiter plates to facilitate optimization of reaction conditions by increasing assay throughput. A 96-well microtiter plate is employed using a final volume 30-100 μ l. The reaction is initiated by the addition of ³³P-gamma-ATP (0.5 μ Ci/ml) and incubated for 0.5

to 3 hours at room temperature. Negative controls are provided by the addition of EDTA, which chelates the divalent cation (Mg^{2+} or Mn^{2+}) required for enzymatic activity. Following the incubation, the enzyme reaction is quenched using EDTA. Samples of the reaction are transferred to a 96-well glass fiber filter plate (MultiScreen, Millipore). The filters are subsequently washed with phosphate-buffered saline, dilute phosphoric acid (0.5%) or other suitable medium to remove excess radiolabeled ATP. Scintillation cocktail is added to the filter plate and the incorporated radioactivity is quantitated by scintillation counting (Wallac/Perkin Elmer). Activity is defined by the amount of radioactivity detected following subtraction of the negative control reaction value (EDTA quench).

VII. Expression analysis

All cell lines used in the following experiments are NCI (National Cancer Institute) lines, and are available from ATCC (American Type Culture Collection, Manassas, VA 20110-2209). Normal and tumor tissues were obtained from Impath, UC Davis, Clontech, Stratagene, and Ambion.

TaqMan analysis was used to assess expression levels of the disclosed genes in various samples.

RNA was extracted from each tissue sample using Qiagen (Valencia, CA) RNeasy kits, following manufacturer's protocols, to a final concentration of 50ng/ μ l. Single stranded cDNA was then synthesized by reverse transcribing the RNA samples using random hexamers and 500ng of total RNA per reaction, following protocol 4304965 of Applied Biosystems (Foster City, CA, <http://www.appliedbiosystems.com/>).

Primers for expression analysis using TaqMan assay (Applied Biosystems, Foster City, CA) were prepared according to the TaqMan protocols, and the following criteria: a) primer pairs were designed to span introns to eliminate genomic contamination, and b) each primer pair produced only one product.

Taqman reactions were carried out following manufacturer's protocols, in 25 μ l total volume for 96-well plates and 10 μ l total volume for 384-well plates, using 300nM primer and 250 nM probe, and approximately 25ng of cDNA. The standard curve for result analysis was prepared using a universal pool of human cDNA samples, which is a mixture of cDNAs from a wide variety of tissues so that the chance that a target will be present in appreciable amounts is good. The raw data were normalized using 18S rRNA (universally expressed in all tissues and cells).

For each expression analysis, tumor tissue samples were compared with matched normal tissues from the same patient. A gene was considered overexpressed in a tumor when the level of expression of the gene was 2 fold or higher in the tumor compared with its matched normal sample. In cases where normal tissue was not available, a universal pool of cDNA samples was used instead. In these cases, a gene was considered overexpressed in a tumor sample when the difference of expression levels between a tumor sample and the average of all normal samples from the same tissue type was greater than 2 times the standard deviation of all normal samples (i.e., $\text{Tumor} - \text{average}(\text{all normal samples}) > 2 \times \text{STDEV}(\text{all normal samples})$).

Results are shown in Table 2. Data presented in bold indicate that greater than 50% of tested tumor samples of the tissue type indicated in row 1 exhibited over expression of the gene listed in column 1, relative to normal samples. Underlined data indicates that between 25% to 49% of tested tumor samples exhibited over expression. A modulator identified by an assay described herein can be further validated for therapeutic effect by administration to a tumor in which the gene is overexpressed. A decrease in tumor growth confirms therapeutic utility of the modulator. Prior to treating a patient with the modulator, the likelihood that the patient will respond to treatment can be diagnosed by obtaining a tumor sample from the patient, and assaying for expression of the gene targeted by the modulator. The expression data for the gene(s) can also be used as a diagnostic marker for disease progression. The assay can be performed by expression analysis as described above, by antibody directed to the gene target, or by any other available detection method.

Table 1

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
1	Parkin1	gi 4758884 ref NP_004553.1	gi 4758884 ref NP_004553.1	116	gi 4758883 ref NM_004562.1 Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 1, mRNA	1	parkin isoform 1; parkin [Homo sapiens]; gi 3063388 dbj BAA25751.1 Parkin [Homo sapiens]	465
2	Parkin2	gi 7669538 ref NP_054642.1	gi 7669538 ref NP_054642.1	117	gi 7669537 ref NM_013987.1 Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 2, mRNA	2	parkin isoform 2; parkin [Homo sapiens]	437
3	Parkin3	gi 7669540 ref NP_054643.1	gi 7669540 ref NP_054643.1	118	gi 7669539 ref NM_013988.1 Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA	3	parkin isoform 3; parkin [Homo sapiens]	316
4	P4HA1	gi 190788 gb AAA36535.1	gi 190788 gb AAA36535.1	119	gi 190787 gb M24487.1 HUMPYHBASB Human prolyl 4-hydroxylase alpha subunit mRNA, complete cds, clone PA-15	4	prolyl 4-hydroxylase alpha subunit (EC 1.14.11.2)	534

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
5	P4HA2	gi 4758868 ref NP_004190.1	gi 4758868 ref NP_004190.1	120	gi 4758867 ref NM_004199.1 Homo sapiens procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II (P4HA2), mRNA	5	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide II; prolyl 4-hydroxylase, alpha polypeptide, type 2; prolyl-4-hydroxylase, alpha polypeptide, type II [Homo sapiens]; gi 2439985 gb AAB71339.1 prolyl 4-hydroxyla	535
6	Scribbled	gi 13112035 gb AAH03193.1 AAH03193	gi 13112035 gb AAH03193.1 AAH03193	121	gi 13112034 gb BC003193.1 BC003193 Homo sapiens, Similar to scribbled, clone MGC:936, mRNA, complete cds	6	Similar to scribbled [Homo sapiens]	524
7	KIAA0147	gi 1469876 dbj BAA09768.1	gi 1469876 dbj BAA09768.1	122	gi 1469875 dbj D63481.1 D63481 Human mRNA for KIAA0147 gene, partial cds	7	The KIAA0147 gene product is related to adenylyl cyclase. [Homo sapiens]	1551
8	ERBIN	gi 8923909 ref NP_061165.1	gi 8923909 ref NP_061165.1	123	gi 8923908 ref NM_018695.1 Homo sapiens erbb2-interacting protein ERBIN (LOC55914), mRNA	8	erbb2-interacting protein ERBIN [Homo sapiens]; gi 8572221 gb AAF77048.1 AF263744_1 erbb2-interacting protein ERBIN [Homo sapiens]	1371

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
9	KIAA1225	gi 6330668 dbj BAA86539.1	gi 6330668 dbj BAA86539.1	124	gi 6330667 dbj AB033051.1 AB033051 Homo sapiens mRNA for KIAA1225 protein, partial cds	9	KIAA1225 protein [Homo sapiens]	1271
10	APC10	gi 4836700 gb AAD30527.1	gi 4836700 gb AAD30527.1	125	gi 4836699 gb AF132794.1 AF132794 Homo sapiens anaphase promoting complex subunit 10 mRNA, complete cds	10	anaphase promoting complex subunit 10 [Homo sapiens]	185
11	KIAA1360	gi 7243101 dbj BAA92598.1	gi 7243101 dbj BAA92598.1	126	gi 7243100 dbj AB037781.1 AB037781 Homo sapiens mRNA for KIAA1360 protein, partial cds	11	KIAA1360 protein [Homo sapiens]	796
12	BAB14869	gi 10436614 dbj BAB14869.1	gi 10436614 dbj BAB14869.1	127	gi 10436613 dbj AK024274.1 AK024274 Homo sapiens cDNA FLJ14212 fis, clone NT2RP3003500, weakly similar to SCY1 PROTEIN	12	unnamed protein product [Homo sapiens]	735
13	TRAF4	NP_004286.1	gi 4759252 ref NP_004286.1	128	gi 4759251 ref NM_004295.1	13	TNF receptor-associated factor 4 [Homo sapiens]	470
14	CAP1	AAA68195	gi 695358 gb AAA68195.1	129	>gi 695357 gb L38509.1 HUMCAP1A	14	CD40-associated protein - human	543
15	TRAF2	S56163	gi 10863939 ref NP_066961.1	130	gi 10863938 ref NM_021138.1	15	tumor necrosis factor receptor-associated protein - human	501
16	TRAF3	XP_007256.1	gi 13647953 ref XP_007256.2	131	gi 13647952 ref XM_007256.3	16	TNF receptor-associated factor 3 [Homo sapiens]	640

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
17	DSCR1 L1	gi 12732604 gnl NCBIGenomeProt TR00066904	gi 12732604 gnl NCBIGenomeProt TR00066904	132	gi 12732603 ref XM_004495.2 Homo sapiens Down syndrome critical region gene 1-like 1 (DSCR1L1), mRNA	17	Down syndrome critical region gene 1-like 1 protein [Homo sapiens]	197
18	DSCR1 L2	gi 7305009 ref NP_038469.1	gi 7305009 ref NP_038469.1	133	gi 7305008 ref NM_013441.1 Homo sapiens Down syndrome critical region gene 1-like 2 (DSCR1L2), mRNA	18	Down syndrome critical region gene 1-like 2 protein; Down syndrome candidate region 1-like 2 [Homo sapiens]; gi 6017919 gb AA01684.1 AF176116_1 Down Syndrome candidate region 1-like protein 2 [Homo sapiens]; gi 11422951 gnl NCBIGenomeProt TR00063928 Down	241
19	SAP18	gi 11433775 gnl NCBIGenomeProt TR00069518	gi 11433775 gnl NCBIGenomeProt TR00069518	134	gi 13627633 ref XM_007104.2 Homo sapiens sin3-associated polypeptide, 18kD (SAP18), mRNA	19	sin3 associated polypeptide p18 [Homo sapiens]; gi 5231141 gb AA041090.1 AF153608_1 sin3 associated polypeptide [Homo sapiens]; gi 2108210 gb AA051322.1 sin3 associated polypeptide p18 [Homo sapiens]; gi 6831678 sp O00422 SP18_HUMAN SIN3 ASSOCIATED POLYP	153

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
20	KIAA0957	gi 4589558 dbj BAA76801.1	gi 4589558 dbj BAA76801.1	135	gi 4589557 dbj AB023174.1 AB023174 Homo sapiens mRNA for KIAA0957 protein, complete cds	20	KIAA0957 protein [Homo sapiens]; gi 7662406 ref NP_055757.1 KIAA0957 protein [Homo sapiens]	692
21	PkB	gi 2407613 gb AAC51825.1	gi 2407613 gb AAC51825.1	136	gi 2407612 gb AF017995.1 AF017995 Homo sapiens 3-phosphoinositide dependent protein kinase-1 (PDK1) mRNA, complete cds	21	3-phosphoinositide dependent protein kinase-1 [Homo sapiens]; gi 2505936 emb CAA75341.1 PkB kinase [Homo sapiens]; gi 4505695 ref NP_002604.1 3-phosphoinositide dependent protein kinase-1; PkB kinase [Homo sapiens]	556

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
22	ELOVL1	gi 11427179 gnl NCBIGenomeProt TR00064446	gi 11427179 gnl NCBIGenomeProt TR00064446	137	gi 13638544 ref XM_002040.2 Homo sapiens elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 (ELOVL1), mRNA	22	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1 [Homo sapiens]; gi 8217571 emb CAB92758.1 dJ92O14.4 (CGI-88 protein) [Homo sapiens]; gi 12653671 gb AAH00618.1 AAH00618 elongation of very long chain fatty acids (FEN1/Elo2, S	279

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
23	ELOVL2	gi 11418666 gn NCBI Genome Prot TR00066756	gi 11418666 gn NCBI Genome Prot TR00066756	138	gi 13643290 ref XM_004347.3 Homo sapiens elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (ELOVL2), mRNA	23	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 [Homo sapiens]	324

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
24	TRIM2	gi 13446227 ref NP_056086.1	gi 13446227 ref NP_056086.1	139	gi 13446226 ref NM_015271.1 Homo sapiens tripartite motif protein TRIM2 (KIAA0517), mRNA	24	tripartite motif protein TRIM2; KIAA0517 protein [Homo sapiens]; brain expressed ring finger protein [Homo sapiens]; gi 12407371 gb AAG53474.1 AF220020_1 tripartite motif protein TRIM3 isoform alpha [Homo sapiens]; gi 5453569 ref NP_006449.1 ring finger protein 22; brain expressed ring finger [Homo sapiens]	744
25	ZFP270	gi 12056482 ref NP_004225.2	gi 12056482 ref NP_004225.2	140	gi 12056481 ref NM_004234.3 Homo sapiens zinc finger protein homologous to Zfp93 in mouse (ZFP93), mRNA	25	zinc finger protein 270; zinc finger protein homologous to mouse Zfp93 [Homo sapiens]	738
26	FBL3	gi 5919219 gb AAD56248.1 AF186273_1	gi 5919219 gb AAD56248.1 AF186273_1	141	gi 6456734 gb AF199355.1 AF199355 Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds	26	leucine-rich repeats containing F-box protein FBL3 [Homo sapiens]; SCF ubiquitin-protein ligase complex	423
27	KIAA1150	gi 6330051 dbj BAA86464.1	gi 6330051 dbj BAA86464.1	142	gi 6330050 dbj AB032976.1 AB032976 Homo sapiens mRNA for KIAA1150 protein, partial cds	27	KIAA1150 protein [Homo sapiens] - related to xenopus Mi-2 - complex couples DNA methylation to chromatin remodelling and histone deacetylation	499

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
28	ADSL2	gi 12654919 gb AAH01305.1 AAH01305	gi 12654919 gb AAH01305.1 AAH01305	143	gi 12654918 gb BC001305.1 BC001305 Homo sapiens, clone MGC:5487, mRNA, complete cds	28	Unknown (protein for MGC:5487) [Homo sapiens]; gi 10440045 dbj BAB15632.1 unnamed protein product [Homo sapiens]; gi 13129088 ref NP_076995.1 hypothetical protein MGC5487 [Homo sapiens]	265

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
29	PL6	gi 1209020 gb AAA92281.1	gi 1209020 gb AAA92281.1	144	gi 1209019 gb U09584.1 HSU09584 Human PL6 protein (PL6) mRNA, complete cds	29	PL6 protein; gi 7513245 pir G01430 PL6 protein - human; gi 5902022 ref NP_008955.1 PL6 protein [Homo sapiens]; PL6 protein, unknown function but deleted in small cell lung cancer [Homo sapiens]	351

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
30	SPRY2	gi 5032115 ref NP_005833.1	gi 5032115 ref NP_005833.1	145	gi 5032114 ref NM_005842.1 Homo sapiens sprouty (Drosophila) homolog 2 (SPRY2), mRNA	30	sprouty (Drosophila) homolog 2; sprouty, Drosophila, homolog of, 2 [Homo sapiens]; gi 13124551 sp O43597 SPY2_HUMAN SPROUTY HOMOLOG 2 (SPRY-2); gi 2809400 gb AAC04258.1 Sprouty 2 [Homo sapiens]; gi 11435347 gnl NCBIGenomeProt TR00069619 sprouty Homolog 2 of Drosophila sprouty which is an FGF signaling antagonist involved in determining apical branching of airways	315
31	SPRY3	gi 8979789 emb CAB96768.1	gi 8979789 emb CAB96768.1	146	gi 8979788 emb AJ271735.1 HSA271735 Homo sapiens Xq pseudoautosomal region; segment 1/2	31	sprouty (Drosophila) homolog 3 [Homo sapiens]; gi 13124553 sp O43610 SPY3_HUMAN SPROUTY HOMOLOG 3 (SPRY-3)	288

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
32	SPRY4 A	gi 12655913 gb AAK00652.1 AF227516_1	gi 12655913 gb AAK00652.1 AF227516_1	147	gi 12655912 gb AF227516.1 AF227516 Homo sapiens sprouty-4A mRNA, complete cds	32	sprouty-4A [Homo sapiens]	322
33	SGT1	gi 12654187 gb AAH00911.1 AAH00911	gi 12654187 gb AAH00911.1 AAH00911	148	gi 12654186 gb BC000911.1 BC000911 Homo sapiens, suppressor of G2 allele of SKP1, S. cerevisiae, homolog of, clone MGC:5348, mRNA, complete cds	33	suppressor of G2 allele of SKP1, S. cerevisiae, homolog of [Homo sapiens]; gi 5730041 ref NP_006695.1 suppressor of G2 allele of SKP1, S. cerevisiae, homolog of [Homo sapiens]; gi 4809026 gb AAD30062.1 suppressor of G2 allele of skp1 homolog SGT1 encodes an essential component of the yeast kinetochore assembly pathway and a novel subunit of the SCF ubiquitin ligase complex.	333

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
34	WDR5	gi 6714707 emb CA B66159.1	gi 6714707 emb CAB 66159.1	149	gi 6714706 emb AJ01 1376.1 HSA011376 Homo sapiens mRNA for hypothetical protein (WDR5 gene), partial	34	hypothetical protein [Homo sapiens]; gi 12230771 sp Q9UGP9 WDR5_HUMAN WD-REPEAT PROTEIN 5	362
35	TBLR1	gi 12642596 gb AAK00301.1 AF314544_1	gi 12642596 gb AAK00301.1 AF314544_1	150	gi 12642595 gb AF314 544.1 AF314544 Homo sapiens nuclear receptor co-repressor/HDAC3 complex subunit TBLR1 (TBLR1) mRNA, complete cds	35	nuclear receptor co-repressor/HDAC 3 complex subunit TBLR1 [Homo sapiens]	514
36	BAB15310	gi 10438686 dbj BA B15310.1	gi 10438686 dbj BAB1 5310.1	151	gi 10438685 dbj AK02 5994.1 AK025994 Homo sapiens cDNA: FLJ22341 fis, clone HRC06032	36	(AK025994) unnamed protein product [Homo sapiens]	619

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
37	RPN1	gi 132559 sp P04843 RIB1_HUMAN	gi 132559 sp P04843 RIB1_HUMAN	152	gi 36052 emb Y00281.1 HSRIBIR Human mRNA for ribophorin I	37	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 67 KDA SUBUNIT PRECURSOR (RIBOPHORIN I) (RPN-I); gi 88566 pir A26168 ribophorin I precursor - human; gi 4506675 ref NP_002941.1 ribophorin I [Homo sapiens]; gi 36053 emb CAA68392.1 precursor; Human ribophorins I and II: the primary structure and membrane topology of two highly conserved rough endoplasmic reticulum-specific	607

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
38	KIAA1532	gi 7959331 dbj BAA96056.1	gi 7959331 dbj BAA96056.1	153	gi 7959330 dbj AB040965.1 AB040965 Homo sapiens mRNA for KIAA1532 protein, partial cds	38	KIAA1532 protein [Homo sapiens]	601

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
39	CAC33282	gi 13185197 emb CAC33282.1	gi 13185197 emb CAC33282.1	154	gi 13185196 emb AX083359.1 AX083359 Sequence 51 from Patent WO0112660	39	unnamed protein product [Homo sapiens]	377

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
40	Pinin	gi 4505923 ref NP_002678.1	gi 4505923 ref NP_002678.1	155	gi 4505922 ref NM_002687.1 Homo sapiens pinin, desmosome associated protein (PNN), mRNA	40	pinin, desmosome associated protein [Homo sapiens]; gi 1684847 gb AB48304.1 pinin [Homo sapiens] memA/DRS, a putative mediator of multiprotein complexes, is overexpressed in the metastasizing human melanoma cell lines BLM and MV3	743
41	IGSF4	gi 7230399 gb AAF42983.1 AF138903_1	gi 7230399 gb AAF42983.1 AF138903_1	156	gi 7767238 gb AF132811.1 AF132811 Homo sapiens necln-like protein 2 (NECL2) mRNA, complete cds	41	immunoglobulin superfamily protein beta-like two [Homo sapiens]; gi 7767239 gb AF69029.1 AF132811_1 immunoglobulin superfamily member protein [Homo sapiens]; IGSF4 [Homo sapiens]; gi 7657226 ref NP_055148.1 immunoglobulin superfamily, member 4 [Homo sapiens]	442

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
42	NPHS1	gi 12742020 gnl NCBI Genome Prot TR00071761	gi 12742020 gnl NCBI Genome Prot TR00071761	157	gi 12742019 ref XM_009344.2 Homo sapiens nephrosis 1, congenital, Finnish type (nephrin) (NPHS1), mRNA	42	nephrin [Homo sapiens]; gi 3025699 gb AAC39687.1 nephrin [Homo sapiens]; gi 10441644 gb AAG17141.1 AF190637_1 nephrin [Homo sapiens]; gi 4758822 ref NP_004637.1 nephrin [Homo sapiens]; gi 7513196 pir T37190 nephrin - human	1241
43	SKIP43	gi 7209857 dbj BAA92341.1	gi 7209857 dbj BAA92341.1	158	gi 7209856 dbj AB036830.1 AB036830 Homo sapiens mRNA for 43-kDa form skeletal muscle and kidney enriched inositol phosphatase, complete cds	43	43-kDa form skeletal muscle and kidney enriched inositol phosphatase [Homo sapiens]	372
44	CHD1	gi 3182949 sp O14646 CHD1_HUMAN	gi 3182949 sp O14646 CHD1_HUMAN	159	gi 4557450 ref NM_001272.1 Homo sapiens chromodomain helicase DNA binding protein 3 (CHD3), mRNA	44	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1); gi 2645429 gb AAB87381.1 CHD1 [Homo sapiens]; gi 4557447 ref NP_001261.1 chromodomain helicase DNA binding protein 1 [Homo sapiens]	1709

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
45	FAA	gi 12739036 gnl NCBI Genome Prot TR00070119	gi 12739036 gnl NCBI Genome Prot TR00070119	160	gi 11433018 ref XM_007704.1 Homo sapiens fumarylacetoacetate (FAH), mRNA	45	fumarylacetoacetase [Homo sapiens]; fumarylacetoacetase [Homo sapiens]; gi 119778 sp P16930 FAAA_HUMAN FUMARYLACETOACETASE (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA); gi 182393 gb AA52422.1 fumarylacetoacetate hydrolase; gi 12803409 gb AAH02527.1 AAH02527 fumarylacetoacetate [Homo sapiens]; gi 106043 pir A37926 fumarylacetoacetase (EC 3.7.1.2) human	437
46	CDC14	gi 4502697 ref NP_003663.1	gi 4502697 ref NP_003663.1	161	gi 4502696 ref NM_003672.1 Homo sapiens CDC14 (cell division cycle 14, S. cerevisiae) homolog A (CDC14A), mRNA	46	CDC14 (cell division cycle 14, S. cerevisiae) homolog A; S. cerevisiae CDC14 homolog, gene A [Homo sapiens]; gi 2662417 gb AB88277.1 cdc14 homolog [Homo sapiens]	580

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
47	Cdc14B1	gi 4263740 gb AAD15415.1	gi 4263740 gb AAD15415.1	162	gi 4156157 gb AC006024.1 AC006024 Homo sapiens PAC clone RP5-1166G19 from 7p12-p11.2, complete sequence	47	similar to Cdc14B1 phosphatase; similar to AF064104 (PID:g3136332) [Homo sapiens]	447
48	SDHD	gi 11437805 gnl NCBIGenomeProt TR00068703	gi 11437805 gnl NCBIGenomeProt TR00068703	163	gi 13636608 ref XM_006290.3 Homo sapiens hypothetical gene supported by NM_003002 (LOC82356), mRNA	48	succinate dehydrogenase complex, subunit D precursor [Homo sapiens]; gi 4506865 ref NP_002993.1 succinate dehydrogenase complex, subunit D precursor; succinate dehydrogenase ubiquinone cytochrome B small subunit [Homo sapiens]; gi 2351037 dbj BAA22054.1 cytochrome b small subunit of complex II [Homo sapiens]; gi 5295994 dbj BAA81889.1 small subunit of cytochrome b of succinate dehydrogenase [Homo sapiens]; gi 3913480 sp O14521 DHSD_H	159

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
49	MOI	gi 13449289 ref NP_085124.1	gi 13449289 ref NP_085124.1	164	gi 13449288 ref NM_030621.1 Homo sapiens helicase-moi (KIAA0928), mRNA	49	helicase-moi [Homo sapiens]; gi 5019620 dbj BAA78691.1 helicase-MOI [Homo sapiens]	1924
50	HD1	gi 2498443 sp Q13547 HDA1_HUMAN	gi 2498443 sp Q13547 HDA1_HUMAN	165	gi 13128859 ref NM_004964.2 Homo sapiens histone deacetylase 1 (HDAC1), mRNA	50	HISTONE DEACETYLASE 1 (HD1); gi 13128860 ref NP_004955.2 histone deacetylase 1; reduced potassium dependency, yeast homolog-like 1 [Homo sapiens]; gi 1277084 gb AAC50475.1 histone deacetylase HD1; gi 12653071 gb AAH00301.1 AAH00301 histone deacetylase 1 [Homo sapiens]	482
51	HD2	gi 12732423 gnl NCBIGenomeProt TR00066779	gi 12732423 gnl NCBIGenomeProt TR00066779	166	gi 13643715 ref XM_004370.3 Homo sapiens histone deacetylase 2 (HDAC2), mRNA	51	histone deacetylase 2 [Homo sapiens]	556

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
52	HD3	gi 3334210 sp O15379 HDA3_HUMAN	gi 3334210 sp O15379 HDA3_HUMAN	167	gi 13128861 ref NM_003883.2 Homo sapiens histone deacetylase 3 (HDAC3), mRNA	52	HISTONE DEACETYLASE 3 (HD3) (RPD3-2); gi 12653663 gb AAH00614.1 AAH00614 histone deacetylase 3 [Homo sapiens]; gi 2661172 gb AB88241.1 RPD3-2B [Homo sapiens]; gi 13128862 ref NP_003874.2 histone deacetylase 3 [Homo sapiens]; gi 2789656 gb AAC98927.1 histone deacetylase 3 [Homo sapiens]; gi 3201676 gb AAC26509.1 histone deacetylase 3 [Homo sapiens]	428

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
53	CSK	gi 30256 emb CAA42556.1	gi 30256 emb CAA42556.1	168	gi 30255 emb X59932.1 HSCSRCKIN Human mRNA for C-SRC-kinase	53	c-src-kinase [Homo sapiens]; gi 30315 emb CAA42713.1 put. cytoplasmic tyrosine kinase [Homo sapiens]; gi 729887 sp P41240 CSK_HUMAN TYROSINE-PROTEIN KINASE CSK (C-SRC KINASE) (PROTEIN-TYROSINE KINASE CYL); gi 88519 pir JH0559 protein-tyrosine kinase (EC 2.7.1.112) CSK - human; gi 4758078 ref NP_004374.1 c-src tyrosine kinase [Homo sapiens]; gi 6077093 emb CAB58562.1 protein tyrosine kinase [Homo sapiens]	450

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
54	CTK	gi 1082751 pir A55625	gi 1082751 pir A55625	169	gi 896208 gb S75145.1 H006874S02 Homo sapiens megakaryocyte-associated tyrosine kinase (MATK) gene, exon 2	54	protein-tyrosine kinase (EC 2.7.1.112) matk, short splice form human; gi 13111883 gb AAH03109.1 AAH03109 megakaryocyte-associated tyrosine kinase [Homo sapiens]; gi 557272 emb CAA54493.1 HYL tyrosine kinase [Homo sapiens]; gi 12652729 gb AAH00114.1 AAH00114 megakaryocyte-associated tyrosine kinase [Homo sapiens]; gi 3702304 gb AAC62843.1 MATK_HUMAN; TYROSINE-PROTEIN KINASE CTK; PROTEIN KINASE HYL; HEMATOPOIETI	507
55	IKBKAP	gi 12002688 gb AAG43369.1 AF153419_1	gi 12002688 gb AAG43369.1 AF153419_1	170	gi 13133509 gb AF153419.2 AF153419 Homo sapiens IkappaBkinase complex-associated protein (IKBKAP) mRNA, complete cds	55	IkappaBkinase complex-associated protein [Homo sapiens]	1332
56	MINT	gi 11427712 gnl NCBIGenomeProt TR00064496	gi 11427712 gnl NCBIGenomeProt TR00064496	171	gi 11427711 ref XM_002090.1 Homo sapiens KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA	56	KIAA0929 protein Msx2 interacting nuclear target (MINT) homolog [Homo sapiens]	3371

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
57	Sno-N	gi 68923 pir TVHUSN	gi 68923 pir TVHUSN	172	gi 4506966 ref NM_003036.1 Homo sapiens v-ski avian sarcoma viral oncogene homolog (SKI), mRNA	57	transforming protein sno-N - human; gi 4885599 ref NP_005405.1 SKI-like; SKI-RELATED ONCOGENE SNON; SnoA; SnoN [Homo sapiens]; gi 134594 sp P12757 SNON_HUMAN SKI-RELATED ONCOGENE SNON; gi 36511 emb CAA33289.1 snoN protein (AA 1 - 684) [Homo sapiens]	684

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
58	Cortactin	gi 299626 gb AAB26248.1	gi 299626 gb AAB26248.1	173	gi 4885204 ref NM_005231.1 Homo sapiens ems1 sequence (mammary tumor and squamous cell carcinoma-associated (p80/85 src substrate) (EMS1), mRNA	58	EMS1 gene product [human, Peptide, 550 aa]; gi 2498954 sp Q14247 SRC8_HUMAN SRC SUBSTRATE CORTACTIN (AMPLAXIN) (ONCOGENE EMS1); gi 182087 gb AA58455.1 amplaxin [Homo sapiens]; gi 477079 pir A48063 mammary tumor/squamous cell carcinoma-associated protein EMS1 - human; gi 4885205 ref NP_005222.1 cortactin; oncogene EMS1 [Homo sapiens]; TITLE The product of the EMS1 gene, amplified and overexpressed in	550

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
59	LCKBP1	gi 123557 sp P14317 HS1_HUMAN	gi 123557 sp P14317 HS1_HUMAN	174	gi 32054 emb X16663.1 HSHEAM Human HS1 gene for heamatopoietic lineage cell specific protein	59	HEMATOPOIETIC LINEAGE CELL SPECIFIC PROTEIN (HEMATOPOIETIC CELL-SPECIFIC LYN SUBSTRATE 1) (LCKBP1); gi 106326 pir S07633 hematopoietic lineage cell-specific protein HS1 - human; gi 32055 emb CAA34651.1 haematopoietic lineage cell protein (AA 1-486) [Homo sapiens]; gi 4885405 ref NP_005326.1 hematopoietic cell-specific Lyn substrate 1 [Homo sapiens]; [FUNCTION] SUBSTRATE OF THE ANTIGEN	486
60	ANX7	gi 12803595 gb AAH02632.1 AAH02632	gi 12803595 gb AAH02632.1 AAH02632	175	gi 12803594 gb BC002632.1 BC002632 Homo sapiens, annexin A7, clone MGC:3917, mRNA, complete cds	60	annexin A7 [Homo sapiens]; gi 113966 sp P20073 ANX7_HUMAN ANNEXIN A7 (ANNEXIN VII) (SYNEXIN); gi 338244 gb AA36616.1 synexin; gi 4502111 ref NP_001147.1 annexin VII isoform 1; annexin VII (synexin); synexin [Homo sapiens]	466

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
61	ANX11	gi 8671171 emb CAB94995.1	gi 8671171 emb CAB94995.1	176	gi 8671170 emb AJ278463.1 HSA278463 Homo sapiens mRNA for annexin A11 (ANXA11 gene), isoform a	61	annexin A11 [Homo sapiens]; gi 8671173 emb CAB94996.1 annexin A11 [Homo sapiens]; gi 1082212 pir A53152 annexin XI - human; gi 4557317 ref NP_001148.1 annexin XI; annexin XI (56kD autoantigen) [Homo sapiens]; gi 8671175 emb CAB94997.1 annexin A11 [Homo sapiens]; gi 1703322 sp P50995 ANXB_HUMAN ANNEXIN A11 (ANNEXIN XI) (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50) (56 KDA AUTOANTIGEN); gi 457129 gb AA	505
62	SLC7A6a	XP_007888	gi 13647530 ref XP_007888.3	177	gi 13647529 ref XM_007888.3	62	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	515

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
63	HMT1	gi 12229661 sp Q9NR22 ANM4_HUMAN	gi 9652074 gb AAF91390.1 AF263539_1	178	gi 9652073 gb AF263539.1 AF263539	63	PROTEIN ARGININE N-METHYLTRANSFERASE 4; gi 9652074 gb AAF91390.1 AF263539_1 arginine N-methyltransferase [Homo sapiens]; gi 9789979 ref NP_062828.1 HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 3 [Homo sapiens]	334
64	HRMT1L2	gi 7453576 gb AAF62894.1 AF222689_2	gi 7453576 gb AAF62894.1 AF222689_2	179	gi 7453574 gb AF222689.1 AF222689 Homo sapiens protein arginine N-methyltransferase 1 (HRMT1L2) gene, complete cds, alternatively spliced	64	protein arginine N-methyltransferase 1-variant 3 [Homo sapiens]	347

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
65	ALK6	gi 2055309 dbj BAA19765.1	gi 2055309 dbj BAA19765.1	180	gi 2055308 dbj D89675.1 D89675 Homo sapiens mRNA for bone morphogenetic protein type IB receptor, complete cds	65	bone morphogenetic protein type IB receptor [Homo sapiens]; gi 4502431 ref NP_001194.1 bone morphogenetic protein receptor, type IB; serine/threonine receptor kinase [Homo sapiens]; gi 6226778 sp O00238 BMRB_HUMAN BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE IB PRECURSOR; gi 11435743 gnl NCBIGenomeProt TR00065811 bone morphogenetic protein receptor, type IB [Homo sapiens]; gi 3377789 gb AAC28131.1	502

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
66	ALK3	gi 547778 sp P36894 BMRA_HUMAN	gi 547778 sp P36894 BMRA_HUMAN	181	gi 10862691 ref NM_020327.1 Homo sapiens activin A receptor, type IB (ACVR1B), transcript variant 2, mRNA	66	BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE IA PRECURSOR (SERINE/THREONINE-PROTEIN KINASE RECEPTOR R5) (SKR5) (ACTIVIN RECEPTOR-LIKE KINASE 3) (ALK-3); gi 402187 emb CAA80257.1 ALK-3 [Homo sapiens]; gi 4757854 ref NP_004320.1 bone morphogenetic protein receptor, type IA precursor; activin A receptor, type II-like kinase 3 [Homo sapiens]; gi 2134722 pir I37163 ALK-3 -	532
67	FLJ11209	gi 12743284 gnl NCBIGenomeProt TR00072690	gi 12743284 gnl NCBIGenomeProt TR00072690	182	gi 13631373 ref XM_010273.3 Homo sapiens hypothetical protein FLJ11209 (FLJ11209), mRNA	67	hypothetical protein FLJ11209 [Homo sapiens] - related to chicken 77kD muscle glycoprotein and a neurite-outgrowth-promoting protein, is important for the differentiation and the survival of the spinal motoneurons	395

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
68	dJ622L5.2	gi 7018360 emb CAB75615.1	gi 7018360 emb CAB75615.1	183	gi 6010175 emb AL049795.20 HSDJ622L5 Human DNA sequence from clone RP4-622L5 on chromosome 1p34.2-36.11. Contains the gene for importin alpha 7 (karyopherin), up to six novel genes and the 5' end of the EIF3S2 gene for eukaryotic translation initiation factor 3 beta. Contains ESTs, STSs, >	68	dJ622L5.2 (novel protein) [Homo sapiens]	356
69	FLJ20142	gi 8923143 ref NP_060156.1	gi 8923143 ref NP_060156.1	184	gi 8923142 ref NM_017686.1 Homo sapiens hypothetical protein FLJ20142 (FLJ20142), mRNA	69	hypothetical protein FLJ20142 [Homo sapiens]; gi 7020049 dbj BAA90976.1 unnamed protein product [Homo sapiens]; gi 11426585 gnl NCBIGenomeProt TR00064394 hypothetical protein FLJ20142 [Homo sapiens]	497

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
70	TXN	gi 135773 sp P10599	gi 135773 sp P10599	185	gi 4507744 ref NM_003329.1 Homo sapiens thioredoxin (TXN), mRNA	70	THIOREDOXIN (ATL-DERIVED FACTOR) (ADF) -[FUNCTION] THIOREDOXIN PARTICIPATES IN VARIOUS REDOX REACTIONS THROUGH THE REVERSIBLE OXIDATION OF ITS ACTIVE CENTER DITHIOL, TO A DISULFIDE, & CATALYZES DITHIOL-DISULFIDE EXCHANGE REACTIONS. [FUNCTION] ADF AUGMENTS THE EXPRESSION OF THE INTERLEUKIN-2	105
71	Trio	gi 3644048 gb AAC43042.1	gi 3644048 gb AAC43042.1	186	gi 3644047 gb AF091395.1 AF091395 Homo sapiens Trio isoform mRNA, complete cds	71	Trio isoform [Homo sapiens]; gi 8928460 sp O75962 TRIO_HUMAN TRIPLE FUNCTIONAL DOMAIN PROTEIN (PTPRF INTERACTING PROTEIN)	3038

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
72	Duo	gi 3108195 gb AAC15791.1	gi 3108195 gb AAC15791.1	187	gi 3108194 gb U94190.1 U94190 Homo sapiens Duo mRNA, complete cds	72	Duo [Homo sapiens]; gi 4504335 ref NP_003938.1 huntingtin-associated protein interacting protein [Homo sapiens]; gi 8928133 sp O60229 HAPP_HUMAN HUNTINGTIN-ASSOCIATED PROTEIN-INTERACTING PROTEIN (DUO PROTEIN)	1663
73	CSTF64	gi 12053011 emb CAB66681.1	gi 12053011 emb CAB66681.1	188	gi 12053010 emb AL136747.1 HSM801715 Homo sapiens mRNA; cDNA DKFZp434C1013 (from clone DKFZp434C1013); complete cds	73	cleavage stimulation factor; gi 4557493 ref NP_001316.1 cleavage stimulation factor subunit 2 [Homo sapiens]; gi 461847 sp P33240 CST2_HUMAN CLEAVAGE STIMULATION FACTOR, 64 KDA SUBUNIT (CSTF 64 KDA SUBUNIT) (CF-1 64 KDA SUBUNIT); gi 284047 pir A40220 cleavage stimulation factor 64K chain - human	616

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
74	CSTF2	NP_001316	gi 4557493 ref NP_001316.1	189	gi 4557492 ref NM_001325.1	74	<p>cleavage stimulation factor subunit 2 [Homo sapiens].</p> <p>Summary: CSTF2 is one of three (including CSTF1 and CSTF3) cleavage stimulation factors which combine to form CSTF which is involved in the polyadenylation and 3'end cleavage of pre-mRNAs. CSTF2 contains a ribonucleoprotein-type RNA binding domain. CSTF2 is upregulated during activation of B cells which results in the</p>	577

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
75	CSTF3	gi 11437232 gnl NCBI Genome Prot TR00068618	gi 11437232 gnl NCBI Genome Prot TR00068618	190	gi 13639274 ref XM_006205.2 Homo sapiens cleavage stimulation factor, 3' pre-RNA, subunit 3, 77kD (CSTF3), mRNA	75	cleavage stimulation factor subunit 3 [Homo sapiens]; gi 1092656 prf 2024339A cleavage stimulation factor [Homo sapiens]; gi 632498 gb AA61417.1 cleavage stimulation factor 77kDa subunit; gi 1082704 pir S50852 cleavage stimulation factor 77K chain - human; gi 4557495 ref NP_001317.1 cleavage stimulation factor subunit 3 [Homo sapiens]	717
76	NECL2	gi 7230399 gb AAF42983.1 AF138903_1	gi 7230399 gb AAF42983.1 AF138903_1	191	gi 7767238 gb AF132811.1 AF132811 Homo sapiens nectin-like protein 2 (NECL2) mRNA, complete cds	76	immunoglobulin superfamily protein beta-like two [Homo sapiens]; gi 7767239 gb AA69029.1 AF132811_1 immunoglobulin superfamily member protein [Homo sapiens]; IGSF4 [Homo sapiens]; gi 7657226 ref NP_055148.1 immunoglobulin superfamily, member 4 [Homo sapiens]; nectin-like protein 2	442

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
77	CGI-83	gi 12654127 gb AAH00878.1 AAH00878	gi 12654127 gb AAH00878.1 AAH00878	192	gi 12654126 gb BC000878.1 BC000878 Homo sapiens, CGI-83 protein, clone MGC:4879, mRNA, complete cds	77	CGI-83 protein [Homo sapiens]; gi 11359880 pir T44603 hypothetical protein CGI-83 [imported] - human; gi 4929635 gb AAD34078.1 AF151841_1 CGI-83 protein [Homo sapiens]; gi 7705793 ref NP_057111.1 CGI-83 protein [Homo sapiens]	288
78	SAP145	gi 11739055 gb AAA97461.1	gi 11739055 gb AAA97461.1	193	gi 1173904 gb U41371.1 HSU41371 Human spliceosome associated protein (SAP 145) mRNA, complete cds	78	spliceosome associated protein; gi 2498883 sp Q13435 S145_HUMAN SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150); gi 5803155 ref NP_006833.1 splicing factor 3b, subunit 2, 145kD; spliceosome associated protein 145, SF3b subunit [Homo sapiens]	872

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
79	ZNT1	gi 12382779 gb AA G53405.1	gi 12382779 gb AAG53405.1	194	gi 12382778 gb AF323590.1 AF323590 Homo sapiens zinc transporter 1 (ZNT1) gene, complete cds	79	zinc transporter 1 [Homo sapiens]	507

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
80	RACK1	gi 12653197 gb AAH00366.1 AAH00366	gi 12653197 gb AAH00366.1 AAH00366	195	gi 12653196 gb BC000366.1 BC000366 Homo sapiens, guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1, clone MGC:8325, mRNA, complete cds	80	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 [Homo sapiens]; gi 12652915 gb AAH00214.1 AAH00214 guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 [Homo sapiens]; gi 121027 sp P25388 GBLP_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3 (P205) (RECEPTOR OF ACTIVATED PROTEIN KINASE C 1) (RACK1) (GNB2-RS1); gi 106177 pir B3	317

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
81	HLP2	gi 3023628 sp O00571 DDX3_HUMAN	gi 3023628 sp O00571 DDX3_HUMAN	196	gi 4503294 ref NM_001356.1 Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 (DDX3), mRNA	81	DEAD-BOX PROTEIN 3 (HELICASE-LIKE PROTEIN 2) (HLP2) (DEAD-BOX, X ISOFORM); gi 12743305 gnl NCBIGenomeProt TR00072697 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 [Homo sapiens]; gi 4503295 ref NP_001347.1 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3; DEAD/H box-3 [Homo sapiens]; gi 3523150 gb AAC34298.1 DEAD box RNA helicase DDX3 [Homo sapiens]; gi 2148924 gb AAB95637.1 helicase like protein 2 [Homo sapiens]	662

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
82	HLP3	gi 6014945 sp O15523 DDXY_HUMAN	gi 6014945 sp O15523 DDXY_HUMAN	197	gi 4759303 ref NM_004679.1 Homo sapiens variable charge, Y chromosome (VCY), mRNA	82	DEAD-BOX PROTEIN 3, Y-CHROMOSOMAL; gi 2580556 gb AAC51832.1 dead box, Y isoform [Homo sapiens]; gi 4758126 ref NP_004651.1 DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome; DEAD/H box-3, Y-linked [Homo sapiens]; gi 2580554 gb AAC51831.1 dead box, Y isoform [Homo sapiens]	660
83	RanBP 16	gi 11999174 ref NP_055839.1	gi 11999174 ref NP_055839.1	198	gi 11999173 ref NM_015024.1 Homo sapiens RAN binding protein 16 (RANBP16), mRNA	83	RAN binding protein 16; KIAA0745 protein; RAN binding protein 16 [Homo sapiens]; gi 6650214 gb AAF21771.1 RAN binding protein 16 [Homo sapiens]	1087
84	RanBP 17	gi 12597633 ref NP_075048.1	gi 12597633 ref NP_075048.1	199	gi 12597632 ref NM_022897.1 Homo sapiens RAN binding protein 17 (RANBP17), mRNA	84	RAN binding protein 17 [Homo sapiens]; gi 12004990 gb AAG44255.1 AF222747_1 RanBP17 [Homo sapiens]	1088

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
85	Maxi-K	gi 4504853 ref NP_002238.1	gi 4504853 ref NP_002238.1	200	gi 4504852 ref NM_002247.1 Homo sapiens potassium large conductance calcium-activated channel, subfamily M, alpha member 1 (KCNMA1), mRNA	85	potassium large conductance calcium-activated channel, subfamily M, alpha member 1; Potassium large conductance calcium-activated channel, subfamily M, [Homo sapiens]; gi 606876 gb AAC50353.1 calcium activated potassium channel	1154
86	Cad23	gi 11321508 gb AA G27034.1	gi 11321508 gb AAG27034.1	201	gi 11321507 gb AY010111.1 Homo sapiens cadherin-23 (CDH23) mRNA, partial cds	86	cadherin-23 [Homo sapiens]	2552

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
87	PCGN2	gi 3242598 dbj BAA29023.1	gi 3242598 dbj BAA29023.1	202	gi 3242597 dbj AB015050.1 AB015050 Homo sapiens mRNA for OCTN2, complete cds	87	OCTN2 [Homo sapiens]; gi 4507005 ref NP_003051.1 solute carrier family 22 (organic cation transporter), member 5 [Homo sapiens]; gi 4126718 dbj BAA36712.1 OCTN2 [Homo sapiens]; gi 7513217 pir JW0089 organic cation transporter protein 2 - human; gi 3273741 gb AAC24828.1 organic cation transporter OCTN2 [Homo sapiens]; gi 12731117 gnl NCBIGenomeProt TR00066110 solute carrier family 22 (organic cation	557
88	KIAA0750	gi 3882221 dbj BAA34470.1	gi 3882221 dbj BAA34470.1	203	gi 3882220 dbj AB018293.1 AB018293 Homo sapiens mRNA for KIAA0750 protein, complete cds	88	KIAA0750 protein [Homo sapiens]; gi 7662284 ref NP_055447.1 KIAA0750 gene product [Homo sapiens]	1124

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
89	MAT-I/III	gi 417297 sp Q00266 METL_HUMAN	gi 4557737 ref NP_00420.1	204	gi 4557736 ref NM_00429.1	89	S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) (MAT-I/III); gi 36329 emb CAA4882.1 methionine adenosyltransferase [Homo sapiens]; gi 11429841 gnl NCBIGenomeProt TR00068102 methionine adenosyltransferase I, alpha [Homo sapiens]; gi 4557737 ref NP_000420.1 methionine adenosyltransferase I, alpha [Homo sapiens]; gi 479655 pir S3	395
90	KIAA1121	gi 6329721 dbj BAA86435.1	gi 6329721 dbj BAA86435.1	205	gi 14133238 dbj AB032947.2 AB032947 Homo sapiens mRNA for KIAA1121 protein, partial cds	90	KIAA1121 protein [Homo sapiens]	1207

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
91	KIAA1591	gi 10047257 dbj BA13417.1	gi 10047257 dbj BAB13417.1	206	gi 10047256 dbj AB046811.1 AB046811 Homo sapiens mRNA for KIAA1591 protein, partial cds	91	KIAA1591 protein [Homo sapiens]	1018
92	purH	gi 1709935 sp P31939 PUR9_HUMAN	gi 1709935 sp P31939 PUR9_HUMAN	207	gi 9845513 ref NM_005978.2 Homo sapiens S100 calcium-binding protein A2 (S100A2), mRNA	92	BIFUNCTIONAL PURINE BIOSYNTHESIS PROTEIN PURH [INCLUDES: PHOSPHORIBOSYLAMINOIMIDAZOLECARBOXAMIDE FORMYLTRANSFERASE (AICAR TRANSFORMYLASE); IMP CYCLOHYDROLASE (INOSINICASE) (IMP SYNTHETASE) (ATIC)]; gi 4757802 ref NP_004035.1 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase; AICARFT/IMPC HASE [Homo sapiens]; gi 1263196 gb AA97405.1	591

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
93	NRM29	gi 5639823 gb AAD45885.1 AF143676_1	gi 5639823 gb AAD45885.1 AF143676_1	208	gi 5639822 gb AF143676.1 AF143676 Homo sapiens multispinning nuclear envelope membrane protein nurim (NRM29) mRNA, partial cds	93	multispinning nuclear envelope membrane protein nurim [Homo sapiens]	261
94	TKT	gi 1729976 sp P29401 TKT_HUMAN	gi 1729976 sp P29401 TKT_HUMAN	209	gi 1297296 gb U55017.1 HSU55017 Human transketolase (TKT) mRNA, complete cds	94	TRANSKETOLASE (TK); gi 1297297 gb AA98961.1 transketolase; gi 4507521 ref NP_001055.1 transketolase [Homo sapiens]; gi 11434224 gnl NCBIGenomeProt TR00065516 transketolase [Homo sapiens]	623

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
95	FLJ00010	gi 10440351 dbj BAB15711.1	gi 10440351 dbj BAB15711.1	210	gi 10440350 dbj AK024421.1 AK024421 Homo sapiens mRNA for FLJ00010 protein, partial cds	95	FLJ00010 protein [Homo sapiens]	772
96	prp28	gi 12803125 gb AAH02366.1 AAH02366	gi 12803125 gb AAH02366.1 AAH02366	211	gi 12803124 gb BC002366.1 BC002366 Homo sapiens, prp28, U5 snRNP 100 kd protein, clone MGC:8416, mRNA, complete cds	96	prp28, U5 snRNP 100 kd protein [Homo sapiens]	820
97	KIAA0801	gi 3882323 dbj BAA34521.1	gi 3882323 dbj BAA34521.1	212	gi 3882322 dbj AB018344.1 AB018344 Homo sapiens mRNA for KIAA0801 protein, complete cds	97	KIAA0801 protein [Homo sapiens]; gi 7662318 ref NP_055644.1 KIAA0801 gene product [Homo sapiens]	1032

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
98	FLJ13159	gi 11345478 ref NP_068759.1	gi 11345478 ref NP_068759.1	213	gi 11345477 ref NM_021940.1 Homo sapiens hypothetical protein FLJ13159 (FLJ13159), mRNA	98	hypothetical protein FLJ13159 [Homo sapiens]; gi 10435055 dbj BAB14473.1 unnamed protein product [Homo sapiens]	437
99	CAB70912.	gi 6807591 emb CA B70912.1	gi 6807591 emb CAB 70912.1	214	gi 6807590 emb AL137764.1 HS228H131 Novel human gene mapping to chromosome 1	99	hypothetical protein [Homo sapiens]	409
100	Cdc25C	gi 420023 pir A38874	gi 420023 pir A38874	215	gi 12408659 ref NM_001790.2 Homo sapiens cell division cycle 25C (CDC25C), transcript variant 1, mRNA	100	protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25C - human; gi 180176 gb AA A35666.1 CDC25Hs ORF; gi 266561 sp P30307 MPI3_HUMAN M-PHASE INDUCER PHOSPHATASE 3 (DUAL SPECIFICITY PHOSPHATASE CDC25C); gi 4502707 ref NP_001781.1 cell division cycle 25C protein, isoform a; mitosis inducer CDC25; phosphotyrosine phosphatase; m-phase inducer phosphatase 3; dual specificity phosphatase CDC25C [Homo sapiens]; gi 13169885 em	473

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
101	Cdc25B	gi 11641415 ref NP_068660.1	gi 11641415 ref NP_068660.1	216	gi 11641414 ref NM_021874.1 Homo sapiens cell division cycle 25B (CDC25B), transcript variant 4, mRNA	101	cell division cycle 25B, isoform 4; CDC25B [Homo sapiens]	601
102	Cdc25A	gi 266556 sp P30304 MPI1_HUMAN	gi 266556 sp P30304 MPI1_HUMAN	217	gi 4502704 ref NM_001789.1 Homo sapiens cell division cycle 25A (CDC25A), mRNA	102	M-PHASE INDUCER PHOSPHATASE 1 (DUAL SPECIFICITY PHOSPHATASE CDC25A); gi 180171 gb AA58415.1 putative; gi 105590 pir A41648 protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25A - human; gi 4502705 ref NP_001780.1 cell division cycle 25A; Cdc25A; protein-tyrosine-phosphatase [Homo sapiens]	523
103	MUC2	gi 4505285 ref NP_02448.1	gi 4505285 ref NP_02448.1	218	gi 4505284 ref NM_002457.1 Homo sapiens mucin 2, intestinal/tracheal (MUC2), mRNA	103	mucin 2, intestinal/tracheal [Homo sapiens]; gi 454154 gb AA595295.1 mucin [Homo sapiens]; gi 2506877 sp Q02817 MUC2_HUMAN MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)	5179

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
104	FBN2	gi 1345961 sp P35556 FBN2_HUMAN	gi 1345961 sp P35556 FBN2_HUMAN	219	gi 4755135 ref NM_001999.2 Homo sapiens fibrillin 2 (congenital contractural arachnodactyly) (FBN2), mRNA	104	FIBRILLIN 2 PRECURSOR; gi 437972 gb AA18950.1 fibrillin 2; gi 4503667 ref NP_001990.1 fibrillin 2 [Homo sapiens]	2911

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
105	FBN1	gi 7459676 pir A47221	gi 7459676 pir A47221	220	gi 397553 emb X63556.1 HSFIBMR H.sapiens mRNA for fibrillin	105	fibrillin 1 precursor - human (fragment)	3002
106	SCYLP	gi 3379991 gb AAA36601.1	gi 3379991 gb AAA36601.1	221	gi 337998 gb M63573.1 HUMSCYLP Human secreted cyclophilin-like protein (SCYLP) mRNA, complete cds	106	secreted cyclophilin-like protein; gi 12654579 gb AAH01125.1 AAH01125 peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]; gi 4758950 ref NP_000933.1 peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]; gi 11431876 gnl NCBIGenomeProt TR00070010 peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]	216

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
107	SCYLC	gi 12803685 gb AAH02678.1 AAH02678	gi 12803685 gb AAH02678.1 AAH02678	222	gi 12803684 gb BC002678.1 BC002678 Homo sapiens, peptidylprolyl isomerase C (cyclophilin C), clone MGC:3673, mRNA, complete cds	107	peptidylprolyl isomerase C (cyclophilin C) [Homo sapiens]; gi 1169178 sp P45877 CYPC_HUMAN PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C (PPIASE) (ROTAMASE) (CYCLOPHILIN C); gi 627417 pir A54204 peptidylprolyl isomerase (EC 5.2.1.8) C precursor - human; gi 4505991 ref NP_000934.1 peptidylprolyl isomerase C (cyclophilin C) [Homo sapiens]; gi 547304 gb AA031350.1 cyclophilin C, Cyp-C [human,	212

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
108	FX	gi 13124123 sp Q13630 FCL_HUMAN	gi 13124123 sp Q13630 FCL_HUMAN	223	gi 6598326 ref NM_003313.2 Homo sapiens tissue specific transplantation antigen P35B (TSTA3), mRNA	108	GDP-FUCOSE SYNTHETASE (FX PROTEIN) (RED CELL NADP(H)-BINDING PROTEIN) [INCLUDES: GDP-MANNOSE-4-KETO-6-D EPIMERASE ; GDP-4-KETO-6-L-GALACTOSE REDUCTASE]; gi 12804977 gb AAH01941.1 AAH01941 tissue specific transplantation antigen P35B [Homo sapiens]; gi 1381179 gb AAC50786.1 FX; gi 11422762 gnl NCBIGenomeProt TR00067457 tissue specific transplantation antigen P35B [Homo sapiens]; gi 4507709 ref NP_003304.1	321
109	B3GAT1	gi 12408652 ref NP_061114.1	gi 12408652 ref NP_061114.1	224	gi 12408651 ref NM_018644.1 Homo sapiens beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1), mRNA	109	beta-1,3-glucuronyltransferase 1; glucuronosyltransferase P [Homo sapiens]; gi 8051678 dbj BAA96077.1 glucuronyltransferase [Homo sapiens]	334

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
110	B3GAT3	gi 12736805 gnl NCBI Genome Prot TR00068461	gi 12736805 gnl NCBI Genome Prot TR00068461	225	gi 13646223 ref XM_006048.3 Homo sapiens hypothetical gene supported by NM_012200 (LOC82088), mRNA	110	beta-1,3-glucuronyltransferase 3 [Homo sapiens]; gi 12408654 ref NP_036332.2 beta-1,3-glucuronyltransferase 3; glucuronosyltransferase I; Sqv-8-like protein; galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase [Homo sapiens]	335
111	ManB	gi 2209015 gb AAC51362.1	gi 2209015 gb AAC51362.1	226	gi 2209008 gb U60894.1 HSMANBS10 Human lysosomal alpha-mannosidase (manB) gene, exon 15 and 16	11	lysosomal alpha-mannosidase [Homo sapiens]; gi 3122374 sp O00754 MA2B_HUMAN LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN); gi 10834968 ref NP_000519.1 mannosidase, alpha B, lysosomal [Homo sapiens]	1010

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
112	DRG1	gi 4127988 emb CAA06775.1	gi 4127988 emb CAA06775.1	227	gi 4127987 emb AJ005940.1 HSA005940 Homo sapiens mRNA for GTP-binding protein	112	GTP-binding protein [Homo sapiens]; gi 4758796 ref NP_004138.1 developmentally regulated GTP-binding protein 1; neural precursor cell expressed, developmentally down-regulated 3 [Homo sapiens]; gi 6685390 sp Q9Y295 DRG1_HUMAN DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN 1 (DRG 1); gi 4218945 gb AAD12240.1 developmentally regulated GTP-binding protein [Homo sapiens]	367

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
113	DRG2	gi 4557537 ref NP_001379.1	gi 4557537 ref NP_001379.1	228	gi 4557536 ref NM_001388.1 Homo sapiens developmentally regulated GTP-binding protein 2 (DRG2), mRNA	113	developmentally regulated GTP-binding protein 2 [Homo sapiens]; gi 1706518 sp P55039 DRG2_HUMAN DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN 2 (DRG 2); gi 1082424 pir A55014 GTP-binding protein DRG homolog - human; gi 577779 emb CAA56730.1 GTP-binding protein [Homo sapiens]	364

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
114	TPST-1	gi 3046918 gb AAC13552.1	gi 3046918 gb AAC13552.1	229	gi 3046917 gb AF038009.1 AF038009 Homo sapiens tyrosylprotein sulfotransferase-1 mRNA, complete cds	114	tyrosylprotein sulfotransferase-1 [Homo sapiens]; gi 11420086 gnl NCBIGenomeProt TR00067170 tyrosylprotein sulfotransferase 1 [Homo sapiens]; gi 6686059 sp O60507 TPS1_HUMAN PROTEIN-TYROSINE SULFOTRANSFERASE 1 (TYROSYLPROTEIN SULFOTRANSFERASE-1) (TPST-1); gi 4507665 ref NP_003587.1 tyrosylprotein sulfotransferase 1 [Homo sapiens]	370

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
115	TPST-2	gi 4507667 ref NP_003586.1	gi 4507667 ref NP_003586.1	230	gi 4507666 ref NM_003595.1 Homo sapiens tyrosylprotein sulfotransferase 2 (TPST2), mRNA	115	tyrosylprotein sulfotransferase 2; Tyrosylprotein phosphotransferase 2 [Homo sapiens]; gi 6686027 sp O60704 TPS2_HUMAN PROTEIN-TYROSINE SULFOTRANSFERASE 2 (TYROSYLPROTEIN SULFOTRANSFERASE-2) (TPST-2); gi 6572241 emb CAB62950.1 bK445C9.4 (tyrosylprotein sulfotransferase 2) [Homo sapiens]; gi 3108067 gb AAC34296.1 tyrosylprotein sulfotransferase-2 [Homo sapiens]; gi 12654459 gb AAH01057.1 AA	377

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
116	ABCG1	gi 8051577 ref NP_058198.1	gi 8051577 ref NP_058198.1	233	gi 8051576 ref NM_016818.1 Homo sapiens ATP-binding cassette, sub-family G (WHITE), member 1 (ABCG1), transcript variant 2, mRNA	231	ATP-binding cassette sub-family G member 1 isoform b; ATP-binding cassette 8 (homolog of Drosophila white); ABC transporter 8; white protein homolog (ATP-binding cassette transporter 8) [Homo sapiens]	662

Row	HM Name	HM Acc#	aa gi number	aa SEQ ID NO	na gi number	na SEQ ID NO	HM Description	HM length
117	WHITE 2	gi 11545924 ref NP_071452.1	gi 11545924 ref NP_071452.1	234	gi 11545923 ref NM_022169.1 Homo sapiens putative ABC transporter (WHITE2), mRNA	232	putative ABC transporter [Homo sapiens]; gi 11342541 emb CAC17140.1 putative white family ATP-binding cassette transporter [Homo sapiens]	627

Row	Target type	Category	Motif H	Psört TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
1	SM, AS	Ubiquitin ation	ubiquitin	TM= 0;	tmHMM =0	gi 7296395 gb AAF51683.1 CG10523 gene product [Drosophila melanogaster] /QuerySize=467	467	ubiquitin; 2 (IBR)	Cell Cycle	1.80E-128
2	SM, AS	Ubiquitin ation	ubiquitin	TM= 0;	tmHMM =0	gi 7296395 gb AAF51683.1 CG10523 gene product [Drosophila melanogaster] /QuerySize=467	467		Cell Cycle	6.60E-112
3	SM, AS	Ubiquitin ation	ubiquitin	TM= 0;	tmHMM =0	gi 7296395 gb AAF51683.1 CG10523 gene product [Drosophila melanogaster] /QuerySize=467	467		Cell Cycle	4.20E-102
4	SM, AS	Metabolic -aa	P4-hydrxy	TM= 0;	tmHMM =0	gi 10726381 gb AA G22134.1 CG18749 gene product [Drosophila melanogaster] /QuerySize=454	454	2 (P4-hydrxy_alpha)		3.70E-51

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
5	SM, AS	Metabolic -aa	P4-hydrxy	TM= 0;	tmHMM=0	gi 10726381 gb AA G22134.1 CG18749 gene product [Drosophila melanogaster] /QuerySize=454	454	2 (P4-hydrxy_alpha)		4.10E-44
6	SM, AS	Adapter	14(LRR_ECDa)	TM= 0;	tmHMM=0	gi 7301474 gb AAF 56598.1 CG5462 scrib gene product [Drosophila melanogaster] /QuerySize=430	430	15 (LRR)	Apoptosis	3.40E-175
7	SM, AS	Adapter	12(LRR); 4(PDZ)	TM= 0;	tmHMM=0	gi 7301474 gb AAF 56598.1 CG5462 scrib gene product [Drosophila melanogaster] /QuerySize=430	430		Apoptosis	6.80E-151
8	SM, AS	Adapter	16(LRR); PDZ	TM= 0;	tmHMM=0	gi 7301474 gb AAF 56598.1 CG5462 scrib gene product [Drosophila melanogaster] /QuerySize=430	430		Apoptosis	1.60E-124

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
9	SM, AS	Adapter	12(LRR); PDZ	TM= 0;	tmHMM=0	gi 7301474 gb AAF56598.1 CG5462 scrib gene product [Drosophila melanogaster] /QuerySize=430	430		Apoptosis	3.10E-95
10	SM, AS	Ubiquitination	DOM	TM= 0;	tmHMM=0	gi 7302773 gb AAF57848.1 CG11419 gen	236	None		4.60E-71
11	SM, AS	Pkinase	STKc_cyto	TM= 0;	tmHMM=0	gi 7301728 gb AAF56841.1 CG1951 gene product [Drosophila melanogaster] /QuerySize=834	834	pkinase		2.70E-163
12	SM, AS	Pkinase	STKc_cyto	TM= 0;	tmHMM=0	gi 7301728 gb AAF56841.1 CG1951 gene product [Drosophila melanogaster] /QuerySize=834	834			8.00E-144
13	SM, AS	Adapter - TRAF	RING; 4 (zf-TRAF); MATH			gi 4959432 gb AAD34346.1 AF119794_1 TNF-receptor associated	486	4 (zf-TRAF); MATH		1.00E-112
14	SM, AS	Adapter - TRAF	#N/A			gi 4959432 gb AAD34346.1 AF119794_1 TNF-receptor associated	486			1.00E-36
15	SM, AS	Adapter - TRAF	#N/A			gi 4959432 gb AAD34346.1 AF119794_1 TNF-receptor associated	486			7.00E-34
16	SM, AS	Adapter - TRAF	#N/A			gi 4959432 gb AAD34346.1 AF119794_1 TNF-receptor associated	486			1.00E-31

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
17	SM, AS	RNA-binding	rrm	TM= 0;	tmHMM=0	gi 7300117 gb AAF55285.1 CG6072 nla gene product [Drosophila melanogaster] /QuerySize=291	291	None		5.30E-45
18	SM, AS	RNA-binding	rrm	TM= 0;	tmHMM=0	gi 7300117 gb AAF55285.1 CG6072 nla gene product [Drosophila melanogaster] /QuerySize=291	291			8.50E-43
19	SM, AS	Transcription regulation	clust302	TM= 0;	tmHMM=0	gi 7300116 gb AAF55284.1 CG6046 SAP18 gene product [Drosophila melanogaster] /QuerySize=149	149	None		5.00E-54

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
20	SM, AS	Adapter	8 (ank)	TM= 0;	tmHMM =0	gi 7303699 gb AAF58749.1 CG12342 gene product [Drosophila melanogaster] /QuerySize=920	920	6 (ank)		6.00E-31
21	SM, AS	Pkinase	STKc_cyto	TM= 0;	tmHMM =0	gi 7291915 gb AAF47332.1 CG1210 Pk61C gene product [alt 1] [Drosophila melanogaster] /QuerySize=538	538	STKc_cyto; S_TK_X_cyto	Cell Cycle	2.00E-107

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
22	Ab, SM, AS	Metabolism - Lipid	4 (GNS1_SUR4)	TM=5;TM domain 1: 29 - 45;TM domain 2: 61 - 77;TM domain 3: 113 - 129;TM domain 4: 201 - 217;TM domain 5: 231 - 247;TM domain 6: 281 - 288;TM domain 7: 311 - 318;TM domain 8: 341 - 348;TM domain 9: 371 - 378;TM domain 10: 401 - 408;TM domain 11: 431 - 438;TM domain 12: 461 - 468;TM domain 13: 491 - 498;TM domain 14: 521 - 528;TM domain 15: 551 - 558;TM domain 16: 581 - 588;TM domain 17: 611 - 618;TM domain 18: 641 - 648;TM domain 19: 671 - 678;TM domain 20: 701 - 708;TM domain 21: 731 - 738;TM domain 22: 761 - 768;TM domain 23: 791 - 798;TM domain 24: 821 - 828;TM domain 25: 851 - 858;TM domain 26: 881 - 888;TM domain 27: 911 - 918;TM domain 28: 941 - 948;TM domain 29: 971 - 978;TM domain 30: 1001 - 1008;TM domain 31: 1031 - 1038;TM domain 32: 1061 - 1068;TM domain 33: 1091 - 1098;TM domain 34: 1121 - 1128;TM domain 35: 1151 - 1158;TM domain 36: 1181 - 1188;TM domain 37: 1211 - 1218;TM domain 38: 1241 - 1248;TM domain 39: 1271 - 1278;TM domain 40: 1301 - 1308;TM domain 41: 1331 - 1338;TM domain 42: 1361 - 1368;TM domain 43: 1391 - 1398;TM domain 44: 1421 - 1428;TM domain 45: 1451 - 1458;TM domain 46: 1481 - 1488;TM domain 47: 1511 - 1518;TM domain 48: 1541 - 1548;TM domain 49: 1571 - 1578;TM domain 50: 1601 - 1608;TM domain 51: 1631 - 1638;TM domain 52: 1661 - 1668;TM domain 53: 1691 - 1698;TM domain 54: 1721 - 1728;TM domain 55: 1751 - 1758;TM domain 56: 1781 - 1788;TM domain 57: 1811 - 1818;TM domain 58: 1841 - 1848;TM domain 59: 1871 - 1878;TM domain 60: 1901 - 1908;TM domain 61: 1931 - 1938;TM domain 62: 1961 - 1968;TM domain 63: 1991 - 1998;TM domain 64: 2021 - 2028;TM domain 65: 2051 - 2058;TM domain 66: 2081 - 2088;TM domain 67: 2111 - 2118;TM domain 68: 2141 - 2148;TM domain 69: 2171 - 2178;TM domain 70: 2201 - 2208;TM domain 71: 2231 - 2238;TM domain 72: 2261 - 2268;TM domain 73: 2291 - 2298;TM domain 74: 2321 - 2328;TM domain 75: 2351 - 2358;TM domain 76: 2381 - 2388;TM domain 77: 2411 - 2418;TM domain 78: 2441 - 2448;TM domain 79: 2471 - 2478;TM domain 80: 2501 - 2508;TM domain 81: 2531 - 2538;TM domain 82: 2561 - 2568;TM domain 83: 2591 - 2598;TM domain 84: 2621 - 2628;TM domain 85: 2651 - 2658;TM domain 86: 2681 - 2688;TM domain 87: 2711 - 2718;TM domain 88: 2741 - 2748;TM domain 89: 2771 - 2778;TM domain 90: 2801 - 2808;TM domain 91: 2831 - 2838;TM domain 92: 2861 - 2868;TM domain 93: 2891 - 2898;TM domain 94: 2921 - 2928;TM domain 95: 2951 - 2958;TM domain 96: 2981 - 2988;TM domain 97: 3011 - 3018;TM domain 98: 3041 - 3048;TM domain 99: 3071 - 3078;TM domain 100: 3101 - 3108;TM domain 101: 3131 - 3138;TM domain 102: 3161 - 3168;TM domain 103: 3191 - 3198;TM domain 104: 3221 - 3228;TM domain 105: 3251 - 3258;TM domain 106: 3281 - 3288;TM domain 107: 3311 - 3318;TM domain 108: 3341 - 3348;TM domain 109: 3371 - 3378;TM domain 110: 3401 - 3408;TM domain 111: 3431 - 3438;TM domain 112: 3461 - 3468;TM domain 113: 3491 - 3498;TM domain 114: 3521 - 3528;TM domain 115: 3551 - 3558;TM domain 116: 3581 - 3588;TM domain 117: 3611 - 3618;TM domain 118: 3641 - 3648;TM domain 119: 3671 - 3678;TM domain 120: 3701 - 3708;TM domain 121: 3731 - 3738;TM domain 122: 3761 - 3768;TM domain 123: 3791 - 3798;TM domain 124: 3821 - 3828;TM domain 125: 3851 - 3858;TM domain 126: 3881 - 3888;TM domain 127: 3911 - 3918;TM domain 128: 3941 - 3948;TM domain 129: 3971 - 3978;TM domain 130: 4001 - 4008;TM domain 131: 4031 - 4038;TM domain 132: 4061 - 4068;TM domain 133: 4091 - 4098;TM domain 134: 4121 - 4128;TM domain 135: 4151 - 4158;TM domain 136: 4181 - 4188;TM domain 137: 4211 - 4218;TM domain 138: 4241 - 4248;TM domain 139: 4271 - 4278;TM domain 140: 4301 - 4308;TM domain 141: 4331 - 4338;TM domain 142: 4361 - 4368;TM domain 143: 4391 - 4398;TM domain 144: 4421 - 4428;TM domain 145: 4451 - 4458;TM domain 146: 4481 - 4488;TM domain 147: 4511 - 4518;TM domain 148: 4541 - 4548;TM domain 149: 4571 - 4578;TM domain 150: 4601 - 4608;TM domain 151: 4631 - 4638;TM domain 152: 4661 - 4668;TM domain 153: 4691 - 4698;TM domain 154: 4721 - 4728;TM domain 155: 4751 - 4758;TM domain 156: 4781 - 4788;TM domain 157: 4811 - 4818;TM domain 158: 4841 - 4848;TM domain 159: 4871 - 4878;TM domain 160: 4901 - 4908;TM domain 161: 4931 - 4938;TM domain 162: 4961 - 4968;TM domain 163: 4991 - 4998;TM domain 164: 5021 - 5028;TM domain 165: 5051 - 5058;TM domain 166: 5081 - 5088;TM domain 167: 5111 - 5118;TM domain 168: 5141 - 5148;TM domain 169: 5171 - 5178;TM domain 170: 5201 - 5208;TM domain 171: 5231 - 5238;TM domain 172: 5261 - 5268;TM domain 173: 5291 - 5298;TM domain 174: 5321 - 5328;TM domain 175: 5351 - 5358;TM domain 176: 5381 - 5388;TM domain 177: 5411 - 5418;TM domain 178: 5441 - 5448;TM domain 179: 5471 - 5478;TM domain 180: 5501 - 5508;TM domain 181: 5531 - 5538;TM domain 182: 5561 - 5568;TM domain 183: 5591 - 5598;TM domain 184: 5621 - 5628;TM domain 185: 5651 - 5658;TM domain 186: 5681 - 5688;TM domain 187: 5711 - 5718;TM domain 188: 5741 - 5748;TM domain 189: 5771 - 5778;TM domain 190: 5801 - 5808;TM domain 191: 5831 - 5838;TM domain 192: 5861 - 5868;TM domain 193: 5891 - 5898;TM domain 194: 5921 - 5928;TM domain 195: 5951 - 5958;TM domain 196: 5981 - 5988;TM domain 197: 6011 - 6018;TM domain 198: 6041 - 6048;TM domain 199: 6071 - 6078;TM domain 200: 6101 - 6108;TM domain 201: 6131 - 6138;TM domain 202: 6161 - 6168;TM domain 203: 6191 - 6198;TM domain 204: 6221 - 6228;TM domain 205: 6251 - 6258;TM domain 206: 6281 - 6288;TM domain 207: 6311 - 6318;TM domain 208: 6341 - 6348;TM domain 209: 6371 - 6378;TM domain 210: 6401 - 6408;TM domain 211: 6431 - 6438;TM domain 212: 6461 - 6468;TM domain 213: 6491 - 6498;TM domain 214: 6521 - 6528;TM domain 215: 6551 - 6558;TM domain 216: 6581 - 6588;TM domain 217: 6611 - 6618;TM domain 218: 6641 - 6648;TM domain 219: 6671 - 6678;TM domain 220: 6701 - 6708;TM domain 221: 6731 - 6738;TM domain 222: 6761 - 6768;TM domain 223: 6791 - 6798;TM domain 224: 6821 - 6828;TM domain 225: 6851 - 6858;TM domain 226: 6881 - 6888;TM domain 227: 6911 - 6918;TM domain 228: 6941 - 6948;TM domain 229: 6971 - 6978;TM domain 230: 7001 - 7008;TM domain 231: 7031 - 7038;TM domain 232: 7061 - 7068;TM domain 233: 7091 - 7098;TM domain 234: 7121 - 7128;TM domain 235: 7151 - 7158;TM domain 236: 7181 - 7188;TM domain 237: 7211 - 7218;TM domain 238: 7241 - 7248;TM domain 239: 7271 - 7278;TM domain 240: 7301 - 7308;TM domain 241: 7331 - 7338;TM domain 242: 7361 - 7368;TM domain 243: 7391 - 7398;TM domain 244: 7421 - 7428;TM domain 245: 7451 - 7458;TM domain 246: 7481 - 7488;TM domain 247: 7511 - 7518;TM domain 248: 7541 - 7548;TM domain 249: 7571 - 7578;TM domain 250: 7601 - 7608;TM domain 251: 7631 - 7638;TM domain 252: 7661 - 7668;TM domain 253: 7691 - 7698;TM domain 254: 7721 - 7728;TM domain 255: 7751 - 7758;TM domain 256: 7781 - 7788;TM domain 257: 7811 - 7818;TM domain 258: 7841 - 7848;TM domain 259: 7871 - 7878;TM domain 260: 7901 - 7908;TM domain 261: 7931 - 7938;TM domain 262: 7961 - 7968;TM domain 263: 7991 - 7998;TM domain 264: 8021 - 8028;TM domain 265: 8051 - 8058;TM domain 266: 8081 - 8088;TM domain 267: 8111 - 8118;TM domain 268: 8141 - 8148;TM domain 269: 8171 - 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9318;TM domain 308: 9341 - 9348;TM domain 309: 9371 - 9378;TM domain 310: 9401 - 9408;TM domain 311: 9431 - 9438;TM domain 312: 9461 - 9468;TM domain 313: 9491 - 9498;TM domain 314: 9521 - 9528;TM domain 315: 9551 - 9558;TM domain 316: 9581 - 9588;TM domain 317: 9611 - 9618;TM domain 318: 9641 - 9648;TM domain 319: 9671 - 9678;TM domain 320: 9701 - 9708;TM domain 321: 9731 - 9738;TM domain 322: 9761 - 9768;TM domain 323: 9791 - 9798;TM domain 324: 9821 - 9828;TM domain 325: 9851 - 9858;TM domain 326: 9881 - 9888;TM domain 327: 9911 - 9918;TM domain 328: 9941 - 9948;TM domain 329: 9971 - 9978;TM domain 330: 10001 - 10008;TM domain 331: 10031 - 10038;TM domain 332: 10061 - 10068;TM domain 333: 10091 - 10098;TM domain 334: 10121 - 10128;TM domain 335: 10151 - 10158;TM domain 336: 10181 - 10188;TM domain 337: 10211 - 10218;TM domain 338: 10241 - 10248;TM domain 339: 10271 - 10278;TM domain 340: 10301 - 10308;TM domain 341: 10331 - 10338;TM domain 342: 10361 - 10368;TM domain 343: 10391 - 10398;TM domain 344: 10421 - 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17778;TM domain 590: 17801 - 17808;TM domain 591: 17831 - 17838;TM domain 592: 17861 - 17868;TM domain 593: 17891 - 17898;TM domain 594: 17921 - 17928;TM domain 595: 17951 - 17958;TM domain 596: 17981 - 17988;TM domain 597: 18011 - 18018;TM domain 598: 18041 - 18048;TM domain 599: 18071 - 18078;TM domain 600: 18101 - 18108;TM domain 601: 18131 - 18138;TM domain 602: 18161 - 18168;TM domain 603: 18191 - 18198;TM domain 604: 18221 - 18228;TM domain 605: 18251 - 18258;TM domain 606: 18281 - 18288;TM domain 607: 18311 - 18318;TM domain 608: 18341 - 18348;TM domain 609: 18371 - 18378;TM domain 610: 18401 - 18408;TM domain 611: 18431 - 18438;TM domain 612: 18461 - 18468;TM domain 613: 18491 - 18498;TM domain 614: 18521 - 18528;TM domain 615: 18551 - 18558;TM domain 616: 18581 - 18588;TM domain 617: 18611 - 18618;TM domain 618: 1						

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
23	Ab, SM, AS	Metabolism - Lipid	3 (GNS1_SUR4)	TM=1;TM domain 1: 262 - 278;cytoplasmic - 24%;nuclear - 20%;vesicles - 12%;	tmHMM=7; outside 1 55; TMhelix 56 78; inside 79 89; TMhelix 90 112; outside 113 143; TMhelix 144 163; inside 164 169; TMhelix 170 192; outside 193 206; TMhelix 207 229; inside 230 235; TMhelix	gi 7300877 gb AAF56018.1 CG6921 gene product [Drosophila melanogaster] /QuerySize=321	321			3.90E-48

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
24	AS	Transcription factor	RINGcyto; BBC_Nuclear; Filamin; 6(NHL)	TM= 0;	tmHMM=0	gi 7298552 gb AAF53771.1 brat gen	1090	2 (zf-B_box); 5 NHL		2.90E-44
25	AS	Transcription factor	KRAB; 16 (zf-C2H2)	TM= 0;	tmHMM=0	gi 7298554 gb AAF53772.1 CG17568 gene product [Drosophila melanogaster] /QuerySize=501	501	7 (zf-C2H2)		9.40E-41
26	SM, AS	Ubiquitination	F-box; 5 (LRR)	TM= 0;	tmHMM=0	gi 7303582 gb AAF58635.1 CG9003 gene product [Drosophila melanogaster] /QuerySize=463	463	F-box		4.80E-166
27	SM, AS	DNA methylation	#N/A	TM= 0;	tmHMM=0	gi 7294806 gb AAF50140.1 CG7983 gene product [Drosophila melanogaster] /QuerySize=915	915	None		1.40E-54

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
28	SM, AS	Metabolic	clust16	TM=1;TM domain 1: 63 - 79;cytoplasmic - 24%;e ndoplasmic - 24%;n uclear - 16%;	tmHMM=6; inside 1 33; TMhelix 34 51; outside 52 65; TMhelix 66 88; inside 89 136; TMhelix 137 156; outside 157 160; TMhelix 161 183; inside 184 194; TMhelix 195 217; outside 218 231; TMhelix 232	gi 7294075 gb AAF49430.1 Baldspot gene product CG3971 [Drosophila melanogaster] /QuerySize=312	312	clust16		4.40E-79

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
29	Ab, SM, AS	Ab target - 6 TMD	10 (MPdecase)	TM=4;TM domain 1: 98 - 114;TM domain 2: 133 - 149;TM domain 3: 164 - 180;TM domain 4: 231 - 247;en doplas mic - 36%;pl asma - 20%;m itochon drial - 20%;	tmHMM=6; inside 1 12; TMhelix 13 35; outside 36 97; TMhelix 98 120; inside 121 126; TMhelix 127 149; outside 150 163; TMhelix 164 183; inside 184 189; TMhelix 190 208; outside 209 222; TMhelix	gi 7297120 gb AAF52388.1 CG9536 gene product [Drosophila melanogaster] /QuerySize=449	449			3.20E-70

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PScore
30	AS	Intracellular signalling	#N/A	TM= 0;	tmHMM=0	gi 13124543 sp O44783 CG1921 SPY_DROME PROTEIN SPROUTY (SPRY) /QuerySize=588	588	None		2.80E-48
31	AS	Intracellular signalling	#N/A	TM= 1; TM domain 1: 223 - 239; nuclear - 28%; cytoplasmic - 28%; mitochondrial - 20%;	tmHMM=0	gi 13124543 sp O44783 CG1921 SPY_DROME PROTEIN SPROUTY (SPRY) /QuerySize=588	588			2.90E-44

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
32	AS	Intracellular signalling	#N/A	TM= 1; TM domain 1: 259 - 275; cytoplasmic - 28%; nuclear - 16%; vesicles - 16%;	tmHMM =0	gi 13124543 sp O44783 CG1921 SPY_DROME PROTEIN SPROUTY (SPRY) /QuerySize=588	588			5.90E-41
33	SM, AS	Ubiquitination	3 (TPR)	TM= 0;	tmHMM =0	gi 7299014 gb AAF54216.1 CG9617 gene product [Drosophila melanogaster] /QuerySize=177	177	None		2.20E-45

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
34	SM, AS	Adapter	7 (WD40)	TM= 0;	tmHMM=0	gi 7299015 gb AAF54217.1 CG9615 gene product [Drosophila melanogaster] /QuerySize=319	319	4 (WD40)		4.90E-18
35	SM, AS	Adapter	8 (WD40)	TM= 0;	tmHMM=0	gi 7299015 gb AAF54217.1 CG9615 gene product [Drosophila melanogaster] /QuerySize=319	319			1.20E-16
36	Ab, AS	Ab target - 7 TMD	clust294		tmHMM=7 tmHMM=7; gi_10438686_d bj_BAB15310.1_ TMHM M1.0 inside 1 166 gi_10438686_d bj_BAB15310.1_ TMHM M1.0 TMhelix 167 189 gi_10438686_d bj_BAB15310.1_ TMHM M1.0 outside 190					

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
37	SM, AS	Glycosyltransferase	#N/A	TM=1;TM domain 1: 441 - 457;en doplas mic - 24%;cy toplas mic - 20%;n uclear - 16%;	tmHMM=1; outside 1 439; TMhelix 440 459; inside 460 607;	gi 7297676 gb AAF52928.1 CG5364 gene product [Drosophila melanogaster] /QuerySize=1839	1839			6.10E-126

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
38	Ab, AS	Ab target - 9 TMD	PA; clust264	TM=9;TM domain 1: 184 - 200;T M domain 2: 233 - 249;T M domain 3: 255 - 271;T M domain 4: 307 - 323;T M domain 5: 330 - 346;T M domain 6: 358 - 374;T M domain 7: 423 - 439;T M domain 8: 460 -	tmHMM=9; inside 1 11; TMhelix 12 34; outside 35 181; TMhelix 182 204; inside 205 230; TMhelix 231 253; outside 254 257; TMhelix 258 280; inside 281 306; TMhelix 307 324; outside 325 328;	gi 7301394 gb AAF56521.1 CG17370 gene product [alt 2] [Drosophila melanogaster] /QuerySize=416	416	2 (clust294)	Apoptosis	2.00E-23

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
39	Ab, AS	Ab target - 7 TMD	2 (clust264)	TM= 8;TM domain 1: 32 - 48;TM domain 2: 80 - 96;TM domain 3: 101 - 117;T M domain 4: 162 - 178;T M domain 5: 208 - 224;T M domain 6: 261 - 277;T M domain 7: 295 - 311;T M domain 8: 319 - 335;pla sma -	tmHMM =7; outside 1 31; TMhelix 32 54; inside 55 74; TMhelix 75 97; outside 98 106; TMhelix 107 129; inside 130 209; TMhelix 210 232; outside 233 257; TMhelix 258 277; inside 278 289; TMhelix 290	gi 7301394 gb AAF56521.1 CG17370 gene product [alt 2] [Drosophila melanogaster] /QuerySize=416	416		Apopto sis	6.00E-21

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
40	AS	Cytoskeletal	(a) a serine-rich domain; (b) a glutamine-proline, glutamine-leucine repeat domain; and (c) an acidic domain rich in glutamic acid	TM= 0;	tmHMM=0	gi 7299239 gb AAF54435.1 CG8383 gene product [Drosophila melanogaster] /QuerySize=302	302	None		3.20E-34
41	Ab, AS	Ab target - Ig w 1TMD	3 (IG_ECDa)	TM= 1; TM domain 1: 379 - 395; plasma - 32%; extracellular	tmHMM=1; outside 1 373; TMhelix 374 396; inside 397 442;	gi 7299238 gb AAF54434.1 CG12950 gene product [Drosophila melanogaster] /QuerySize=311	311	2 (IG_like_ECDa)		0.000002

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
42	Ab, AS	Ab target - Ig w 1TMD	8 (IG_ECD a); fn3	TM= 1; TM domain 1: 1059 - 1075; extracellular	tmHMM =1; outside 1 1063; TMhelix 1064 1086; inside 1087 1241;	gi 7299238 gb AAF54434.1 CG12950 gene product [Drosophila melanogaster] /QuerySize=311	311			0.000003
43	SM, AS	Phosphatase	IPPC_cyto	TM= 0;	tmHMM =0	gi 7302845 gb AAF57919.1 CG6805 gene product [Drosophila melanogaster] /QuerySize=356	356			8.10E-52
44	SM, AS	Helicase	2 (chromo); SNF2; helicase_C; SANT_Nuclear	TM= 0;	tmHMM =0	gi 10727422 gb AAF51527.2 CG3660 gene product [Drosophila melanogaster] /QuerySize=2702	2702		Apoptosis	6.70E-112

Row	Target type	Category	Motif H	Sort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
45	SM, AS	Metabolic	FAA_hydro	TM= 0;	tmHMM=0	gi 7292429 gb AAF47833.1 CG14993 gene product [Drosophila melanogaster] /QuerySize=348	348	FAA_hydrolase	Apoptosis	5.10E-150
46	SM, AS	Phosphatase	DSPc	TM= 0;	tmHMM=0	gi 7301043 gb AAF56179.1 CG10371 gene product [Drosophila melanogaster] /QuerySize=193	193	DSPc		0.041118

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
47	SM, AS	Phosphatase	DSPc	TM=1;TM domain 1: 421 - 437;nu clear - 24%;v esicles - 20%;cy toplasmic - 16%;	tmHMM=1; inside 1 414; TMhelix 415 437; outside 438 447;	gi 7301043 gb AAF56179.1 CG10371 gene product [Drosophila melanogaster] /QuerySize=193	193			0.134058
48	SM, AS	Metabolic	Hist_de acetyl	TM=1;TM domain 1: 126 - 142;plasma - 32%;e xtracellular	tmHMM=0	gi 7301044 gb AAF56180.1 CG10219 gene product [Drosophila melanogaster] /QuerySize=181	181	None		4.00E-19

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
49	SM, AS	Helicase	DEAD; helicase_C; PAZ; 3 (Ribonuclease_3); dsrm	TM= 0;	tmHMM=0	gi 7302752 gb AAF57830.1 CG6493 gene product [Drosophila melanogaster] /QuerySize=142	142	DEAD	Apoptosis	0.000044
50	SM, AS	Metabolic	Hist_de acetyl	TM= 0;	tmHMM=0	gi 7292522 gb AAF47924.1 CG7471 Rpd3 gene product [Drosophila melanogaster] /QuerySize=520	520	Hist_de acetyl		3.40E-272
51	SM, AS	Metabolic	Hist_de acetyl	TM= 0;	tmHMM=0	gi 7292522 gb AAF47924.1 CG7471 Rpd3 gene product [Drosophila melanogaster] /QuerySize=520	520			1.10E-270

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
52	SM, AS	Metabolic	#N/A	TM= 0;	tmHMM =0	gi 7292522 gb AAF47924.1 CG7471 Rpd3 gene product [Drosophila melanogaster] /QuerySize=520	520			3.20E-184

Row	Target type	Category	Motif H	Sort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PScore
53	SM, AS	Pkinase	SH3; SH2; PTYKc_cyto	TM= 0;	tmHMM=0	gi 7299480 gb AAF54668.1 CG17309 gene product [Drosophila melanogaster] /QuerySize=819	819	SH2; PTYKc_cyto	Apoptosis	8.90E-154

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
54	SM, AS	Pkinase	SH3; SH2; PTYKc_cyto	TM= 0;	tmHMM=0	gi 7299480 gb AAF54668.1 CG17309 gene product [Drosophila melanogaster] /QuerySize=819	819		Apoptosis	8.90E-125
55	SM, AS	Adapter	#N/A	TM= 0;	tmHMM=0	gi 7299482 gb AAF54670.1 CG10535 gene product [Drosophila melanogaster] /QuerySize=1212	1212	NIDO_E CD		2.10E-159
56	SM, AS	RNA processing	RNA recognition motif	TM= 0;	tmHMM=0	gi 10727421 gb AAF51535.2 CG18497 spen gene product [alt 1] [Drosophila melanogaster] /QuerySize=4969	4969	None	Apoptosis	1.50E-99

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
57	SM, AS	Intracellular signalling	Ski_Sno	TM= 0;	tmHMM=0	gi 7290861 gb AAF46303.1 CG15332 gene product [Drosophila melanogaster] /QuerySize=570	570	None		0.891457

Row	Target type	Category	Motif H	Sort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
58	SM, AS	Adapter	7 (HS1_re p); SH3	TM= 0;	tmHMM=0	gi 7300693 gb AAF55840.1 CG3637 Cortactin gene product [Drosophila melanogaster] /QuerySize=558	558	4 (HS1_re p); SH3		1.80E-122

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
59	SM, AS	Adapter	4 (HS1_re p); SH3	TM= 1; TM domain 1: 420 - 436; nuclear - 24%; cytoplasmic - 20%; vesicles - 16%;	tmHMM=0	gi 7300693 gb AAF55840.1 CG3637 Cortactin gene product [Drosophila melanogaster] /QuerySize=558	558			1.70E-117
60	SM, AS	Adapter	4 (annexin)	TM= 0;	tmHMM=0	gi 12644162 sp P22464 CG5730 ANX9_DROME ANNEXIN IX /QuerySize=323	323	4 (anexin)		8.70E-100

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
61	SM, AS	Adapter	4 (annexin)	TM= 0;	tmHMM=0	gi 12644162 sp P22464 CG5730 ANX9_DROME ANNEXIN IX /QuerySize=323	323			1.70E-99
62	Ab, SM, AS	transport er - aa	clust118			gi 7302046 gb AAF57148.1 CG1607 gene product [Drosophila melanogaster]	518		Apoptosis	9.50E-161

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
63	SM, AS	Metabolic -aa	#N/A	TM= 0;	tmHMM =0	gi 7299276 gb AAF54471.1 CG5358 gene product [Drosophila melanogaster] /QuerySize=529	529	None		1.20E-59
64	SM, AS	Metabolic -aa	#N/A	TM= 0;	tmHMM =0	gi 7299276 gb AAF54471.1 CG5358 gene product [Drosophila melanogaster] /QuerySize=529	529			2.90E-58

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
65	Ab, SM, AS	Pkinase	Activin_r ecp; GS_cyto; pkinase	TM= 1;TM domain 1: 128 - 144;nu clear - 28%;cy toplas mic - 24%;m itochon drial - 24%;	tmHMM =1; outside 1 125; TMhelix 126 148; inside 149 502;	gi 7296958 gb AAF52230.1 CG14026 tkv gene product [Drosophila melanogaster] /QuerySize=545	545	Activin_r ecp; pkinase		1.90E-160

Row	Target type	Category	Motif H	Psor TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
66	Ab, SM, AS	Pkinase	Activin_r ecp; pkinase	TM= 1;TM domain 1: 154 - 170;cyt oplasm ic - 28%;n uclear - 24%;m itochon drial - 24%;	tmHMM =1; outside 1 152; TMhelix 153 175; inside 176 532;	gi 7296958 gb AAF 52230.1 CG14026 tkv gene product [Drosophila melanogaster] /QuerySize=545	545			1.40E-156
67	Ab, AS	Ab target - secreted	#N/A	TM= 0;	tmHMM =0	gi 7301391 gb AAF 56518.1 CG5886 gene product [Drosophila melanogaster] /QuerySize=514	514	None		9.70E-70

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
68	Ab, AS	Ab target - secreted	#N/A	TM= 0;	tmHMM =0	gi 7301391 gb AAF56518.1 CG5886 gene product [Drosophila melanogaster] /QuerySize=514	514			2.50E-69
69	Ab, AS	Ab target - secreted	1A1pp_Nuclear:1S EC14_cyto	TM= 0;	tmHMM =0	gi 10727766 gb AA G22306.1 CG18813 gene product [alt 2] [Drosophila melanogaster] /QuerySize=243	243	SEC14_cyto		1.80E-54

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
70	SM, AS	Metabolic	thioered				106			2.00E-29
71	SM, AS	G protein - GEF	SEC14_cyto; 7 (spectrin); 2 (RhoGEF); 2 (PH); 2 (SH3); 2 (lg); STKc_cyto	TM= 0;	tmHMM=0	gi 10727213 gb AA F47436.2 CG9208 trio gene product [Drosophila melanogaster] /QuerySize=1872	1872	SEC14_cyto; 7 (spectrin); RhoGEF; PH		0.00E+00

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
72	SM, AS	G protein - GEF	SEC14_cyto; 9 (spectrin); RhoGEF; PH	TM= 0;	tmHMM=0	gi 10727213 gb AA F47436.2 CG9208 trio gene product [Drosophila melanogaster] /QuerySize=1872	1872			4.90E-297
73	SM, AS	RNA processing	RRM	TM= 0;	tmHMM=0	gi 7300420 gb AAF 55577.1 CG7697 CstF-64 gene product [Drosophila melanogaster] /QuerySize=398	398	rrm		7.60E-87

Row	Target type	Category	Motif H	Sort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
74	SM, AS	RNA processing	RRM							

Row	Target type	Category	Motif H	Sort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PScore
75	SM, AS	RNA processing	10 (HAT_oter)	TM= 0;	tmHMM=0	gi 135031 sp P25991 CG17170 SUF_DROME SUPPRESSOR OF FORKED PROTEIN /QuerySize=732	732	10 (HAT_oter)		2.50E-159
76	Ab, SM, AS	Ab target - Ig w 1TMD	3 (IG_like_ECDa); 4.1m_cyto	TM= 1; TM domain 1: 379 - 395; plasma - 32%; extracellular	tmHMM=1; outside 1 373; TMhelix 374 396; inside 397 442;	gi 7299772 gb AAF54952.1 CG14372 gene product [Drosophila melanogaster] /QuerySize=349	349			0.000041

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
77	SM, AS	Glycosyl transferase	lactamase_B	TM= 0;	tmHMM=0	gi 7297345 gb AAF52605.1 CG12375 gene product [Drosophila melanogaster] /QuerySize=291	291			2.30E-80
78	SM, AS	RNA processing	SAP; MAM33; SAP	TM= 0;	tmHMM=0	gi 7295859 gb AAF51159.1 CG3605 gene product [Drosophila melanogaster] /QuerySize=733	733			3.00E-245

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
79	Ab, SM, AS	transporter	3 (Cation_efflux)	TM=6;TM domain 1: 12 - 28;TM domain 2: 41 - 57;TM domain 3: 82 - 98;TM domain 4: 114 - 130;TM domain 5: 248 - 264;TM domain 6: 313 - 329;en doplas mic - 36%;pl asma - 20%;m itochon drial - 20%;	tmHMM=6; inside 1 6; TMhelix 7 29; outside 30 43; TMhelix 44 61; inside 62 80; TMhelix 81 98; outside 99 112; TMhelix 113 135; inside 136 248; TMhelix 249 271; outside 272 313; TMhelix 314 336; inside	gi 7296322 gb AAF51612.1 CG5130 gene product [Drosophila melanogaster] /QuerySize=512	512	Cation_efflux		1.70E-24

Row	Target type	Category	Motif H	Sort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PScore
80	SM, AS	Adapter	7 (WD40)	TM= 0;	tmHMM=0	gi 7297305 gb AAF52566.1 CG7111 Rack1 gene product [Drosophila melanogaster] /QuerySize=317	317	7 (WD40)	Apoptosis	2.90E-177

Row	Target type	Category	Motif H	Psor TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
81	SM, AS	Helicase	DEAD; helicase _C	TM= 0;	tmHMM =0	gi 7299061 gb AAF54262.1 CG9748 gene product [Drosophila melanogaster] /QuerySize=797	797	2 (DEAD); helicase_ C		8.10E-232

Row	Target type	Category	Motif H	Sort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
82	SM, AS	Helicase	DEAD; helicase _C	TM= 0;	tmHMM =0	gi 7299061 gb AAF54262.1 CG9748 gene product [Drosophila melanogaster] /QuerySize=797	797			1.40E-226
83	SM, AS	Nuclear transport	#N/A	TM= 0;	tmHMM =0	gi 7293158 gb AAF48542.1 CG9126 gene product [Drosophila melanogaster] /QuerySize=1065	1065			4.60E-171
84	SM, AS	Nuclear transport	#N/A	TM= 0;	tmHMM =0	gi 7293158 gb AAF48542.1 CG9126 gene product [Drosophila melanogaster] /QuerySize=1065	1065			2.80E-156

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
85	Ab, SM, AS	Channel	clust9	TM= 8;TM domain 1: 67 - 83;TM domain 2: 155 - 171;T M domain 3: 195 - 211;T M domain 4: 224 - 240;T M domain 5: 276 - 292;T M domain 6: 344 - 360;T M domain 7: 593 - 609;T M domain 8: 759 - 775;pla	tmHMM =6; outside 1 61; TMhelix 62 84; inside 85 154; TMhelix 155 174; outside 175 188; TMhelix 189 211; inside 212 275; TMhelix 276 298; outside 299 312; TMhelix 313 332; inside 333 338;	gi 7301192 gb AAF56324.1 CG10693 slo gene product [Drosophila melanogaster] /QuerySize=1174	1174			0
86	Ab, SM, AS	Ab target - Cadherin w 1TMD	19 (cadherin)	TM= 1;TM domain 1: 2267 - 2283;cytoplas mic - 24%;n uclear - 20%;v esicles - 16%;	tmHMM =1; outside 1 2265; TMhelix 2266 2288; inside 2289 2552;	gi 10727403 gb AAF51468.2 CG17941 ds gene product [Drosophila melanogaster] /QuerySize=3502	3502			9.20E-210

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
87	Ab, SM, AS	transporter - cation	clust105	TM= 10;TM domain 1: 20 - 36;TM domain 2: 144 - 160;T M domain 3: 193 - 209;T M domain 4: 233 - 249;T M domain 5: 258 - 274;T M domain 6: 340 - 356;T M domain 7: 378 - 394;T M domain 8: 404 - 420;T	tmHMM =12; inside 1 20; TMhelix 21 43; outside 44 141; TMhelix 142 164; inside 165 170; TMhelix 171 190; outside 191 194; TMhelix 195 217; inside 218 228; TMhelix 229 251; outside 252 255;	gi 7300528 gb AAF55681.1 CG17751 gene product [Drosophila melanogaster] /QuerySize=418	418	clust105		5.60E-49
88	SM, AS	Adapter	CH; LIM	TM= 0;	tmHMM =0	gi 7299283 gb AAF54478.1 CG11685 gene product [alt 1] [Drosophila melanogaster] /QuerySize=1194	1194	pyr_redox; LIM		3.10E-214

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
89	SM, AS	Metabolic - aa		TM= 0;	tmHMM =0	gi 7296263 gb AAF51554.1 CG2674 M(2)21AB gene product [alt 2] [Drosophila melanog	427			6.80E-205
90	SM, AS	Adapter	PH	TM= 1;TM domain 1: 1031 - 1047;c ytoplas mic - 20%;n uclear - 20%;v esicles - 16%;	tmHMM =0	gi 10729714 gb AAF45454.2 CG18026 Caps gene product [Drosophila melanogaster] /QuerySize=1518	1518	PH		0

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
91	SM, AS	Adapter	PH	TM= 1; TM domain 1: 844 - 860; cytoplasmic - 20%; nuclear - 16%; vesicles - 16%;	tmHMM = 0	gi 10729714 gb AA F45454.2 CG18026 Caps gene product [Drosophila melanogaster] /QuerySize=1518	1518			0
92	SM, AS	Metabolic -aa	#N/A	TM= 0;	tmHMM = 0	gi 7301227 gb AAF 56358.1 CG11089 gene product [Drosophila melanogaster] /QuerySize=589	589	MGS; AICARF T_IMPC Has		5.90E-290

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
93	SM, AS	Nuclear transport	transketolase	TM= 4;TM domain 1: 58 - 74;TM domain 2: 141 - 157;TM domain 3: 198 - 214;TM domain 4: 217 - 233;en doplas mic - 32%;pl asma - 24%;m itochon drial - 24%;	tmHMM =4; inside 1 4; TMhelix 5 27; outside 28 57; TMhelix 58 80; inside 81 92; TMhelix 93 115; outside 116 134; TMhelix 135 157; inside 158 261;	gi 7300293 gb AAF55455.1 CG7655 gene product [Drosophila melanogaster] /QuerySize=252	252			1.80E-29
94	SM, AS	Metabolic	0	TM= 0;	tmHMM =0	gi 7299065 gb AAF54265.1 CG8036 gene product [Drosophila melanogaster] /QuerySize=625	625	2 (transketolase)		6.30E-257

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
95	Ab, SM, AS	transporter - cation		TM= 10;TM domain 1: 26 - 42;TM domain 2: 56 - 72;TM domain 3: 125 - 141;T M domain 4: 161 - 177;T M domain 5: 197 - 213;T M domain 6: 254 - 270;T M domain 7: 274 - 290;T M domain 8: 316 - 332;T M	tmHMM=7; inside 1 23; TMhelix 24 46; outside 47 49; TMhelix 50 72; inside 73 120; TMhelix 121 143; outside 144 155; TMhelix 156 178; inside 179 190; TMhelix 191 213; outside 214 274; TMhelix 275	gi 7298458 gb AAF53679.1 CG10413 gene product [Drosophila melanogaster] /QuerySize=940	940			1.20E-168
96	SM, AS	Helicase	helicase_C	TM= 0;	tmHMM=0	gi 7298459 gb AAF53680.1 CG10333 gene product [Drosophila melanogaster] /QuerySize=801	801	DEAD; helicase_C; plant_thionins		0
97	SM, AS	Helicase	2 DEAD, helicase_C	TM= 0;	tmHMM=0	gi 7298459 gb AAF53680.1 CG10333 gene product [Drosophila melanogaster] /QuerySize=801	801			6.80E-101

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
98	SM, AS	G protein - GAP	ArfGap	TM= 0;	tmHMM =0	gi 7303978 gb AAF59021.1 CG8243 gene product [Drosophila melanogaster] /QuerySize=517	517	ArfGap		1.40E-57
99	SM, AS	G protein - GAP	ArfGap	TM= 0;	tmHMM =0	gi 7303978 gb AAF59021.1 CG8243 gene product [Drosophila melanogaster] /QuerySize=517	517			1.60E-51
100	SM, AS	Phosphatase	Rhodanese	TM= 0;	tmHMM =0	gi 12644155 sp P20483 CG1395 MPIP_DROME M-PHASE INDUCER PHOSPHATASE (STRING PROTEIN) (CDC25-LIKE PROTEIN) /QuerySize=478	478	Rhodanese		2.20E-56

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
101	SM, AS	Phosphatase	Rhodanese	TM= 0;	tmHMM=0	gi 12644155 sp P20483 CG1395 MPIP_DROME M-PHASE INDUCER PHOSPHATASE (STRING PROTEIN) (CDC25-LIKE PROTEIN) /QuerySize=478	478			2.20E-56
102	SM, AS	Phosphatase	Rhodanese	TM= 0;	tmHMM=0	gi 12644155 sp P20483 CG1395 MPIP_DROME M-PHASE INDUCER PHOSPHATASE (STRING PROTEIN) (CDC25-LIKE PROTEIN) /QuerySize=478	478			6.80E-54
103	Ab, SM, AS	Ab target - secreted	0	TM= 0;	tmHMM=0	gi 7296302 gb AAF51592.1 CG5847 gene product [Drosophila melanogaster] /QuerySize=2283	2283			7.60E-101

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PScore
104	Ab, SM, AS	Ab target - EGF repeat ECM protein	3 EGF,E GF,TB, 2 EGF,E GF,TB, 5 EGF,E GF,TB, 3 EGF,E GF,TB, EGF,TB ,12 EGF,E GF,TB, 2 EGF,E GF,TB, 7 EGF,E GF,TB, 5 EGF,E GF,TB, 7 EGF,ca dherin	TM= 0;	tmHMM =1; inside 1 6; TMhelix 7 26; outside 27 2911;	gi 7295695 gb AAF51000.1 CG15637 gene product [Drosophila melanogaster] /QuerySize=3679	3679	70 (EGF)		2.10E-128

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
105	Ab, SM, AS	Ab target - EGF repeat ECM protein	3 EGF,E GF,TB, 2 EGF,E GF,TB, 5 EGF,E GF,TB, 3 EGF,E GF,TB, EGF,TB ,12 EGF,E GF,TB, 2 EGF,E GF,TB, 7 EGF,E GF,TB, 5 EGF,E GF,TB	TM= 0;	tmHMM =0	gi 7295695 gb AAF51000.1 CG15637 gene product [Drosophila melanogaster] /QuerySize=3679	3679			3.50E-126
106	Ab, SM, AS	isomerase	pro_iso merase	TM= 0;	tmHMM =1; inside 1 10; TMhelix 11 33; outside 34 216;	gi 7291447 gb AAF46873.1 CG2852 gene product [alt 1] [Drosophila melanogaster] /QuerySize=204	204	pro_isom erase		6.90E-91

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
107	Ab, SM, AS	isomerase	pro_isomerase	TM= 0;	tmHMM=1; inside 1 6; TMhelix 7 29; outside 30 212;	gi 7291447 gb AAF46873.1 CG2852 gene product [alt 1] [Drosophila melanogaster] /QuerySize=204	204			2.20E-80

Row	Target type	Category	Motif H	Sort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
108	SM, AS	Glycosyltransferase	#N/A	TM= 0;	tmHMM=0	gi 7291499 gb AAF46924.1 CG3495 gene product [Drosophila melanogaster] /QuerySize=320	320			3.60E-130
109	SM, AS	Glycosyltransferase	#N/A	TM= 0;	tmHMM=1; inside 16; TMhelix 7 24; outside 25 334;	gi 7297540 gb AAF52795.1 CG3881 gene product [Drosophila melanogaster] /QuerySize=442	442	None		4.30E-49

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
110	SM, AS	Glycosyltransferase	Glyco_hydro_38	TM=3;TM domain 1: 8 - 24;TM domain 2: 121 - 137;TM domain 3: 248 - 264;endoplasmic - 32%;mitochondrial - 28%;plasma - 16%;	tmHMM=1; inside 1 6; TMhelix 7 29; outside 30 335;	gi 7297540 gb AAF52795.1 CG3881 gene product [Drosophila melanogaster] /QuerySize=442	442			8.10E-49
111	SM, AS	Glycosyltransferase			tmHMM=0	gi 7297706 gb AAF52958.1 CG6206 BcDNA:GH02419 gene product [Drosophila melanogaster] /QuerySize=1071	1071	Glyco_hydro_38		2.00E-268

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
112	SM, AS	G protein - GTP-binding	GTP1_OBG	TM=1;TM domain 1: 30 - 46;mitochondrial - 40%;cytoplasmic - 16%;endoplasmic - 12%;	tmHMM=0	gi 7303536 gb AAF58591.1 CG8340 128up gene product [Drosophila melanogaster] /QuerySize=367	367	GTP1_OBG		2.40E-210

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
113	SM, AS	G protein - GTP-binding	GTP1_OBG	TM=1;TM domain 1: 135 - 151;cytoplasmic - 24%;endoplasmic - 20%;nuclear - 20%;	tmHMM=0	gi 7303536 gb AAF58591.1 CG8340 128up gene product [Drosophila melanogaster] /QuerySize=367	367			6.50E-140

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
114	SM, AS	Glycosyltransferase	#N/A	TM=1; TM domain 1: 9 - 25; endoplasmic - 28%; cytoplasmic - 20%; nuclear - 20%; - Golgi	tmHMM=0	gi 7292895 gb AAF	442			3.20E-145

Row	Target type	Category	Motif H	Sort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
115	SM, AS	Glycosyltransferase	#N/A	TM= 0;	tmHMM=1; inside 16; TMhelix 7 29; outside 30 377;	gi 7292895 gb AAF	442			4.10E-144

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interaction	PSCORE
116	Ab, SM, AS	transporter - ATP-binding	ABC_tran	TM=5;TM domain 1: 413 - 429;TM domain 2: 442 - 458;TM domain 3: 515 - 531;TM domain 4: 552 - 568;TM domain 5: 637 - 653;plasma - 40%;endonoplasmic - 20%;mitochondrial - 16%;	tmHMM=7; outside 1 405; TMhelix 406 domain 428; inside 429 440; TMhelix 441 463; outside 464 486; TMhelix 487 509; inside 510 515; TMhelix 516 538; outside 539 547; TMhelix 548 570; inside	gi 7296257 gb AAF51548.1 CG3164 gene product [Drosophila melanogaster] /QuerySize=619	619	ABC_tran		6.00E-161

Row	Target type	Category	Motif H	Psort TM	TM HMM	Fly gene Acc	Fly aa	Motif Fly	Interact ion	PSCORE
117	Ab, SM, AS	transporter - ATP-binding	ABC_tran	TM=6;TM domain 1: 378 - 394;TM domain 2: 408 - 424;TM domain 3: 455 - 471;TM domain 4: 489 - 505;TM domain 5: 518 - 534;TM domain 6: 602 - 618;plasma - 48%;e ndoplas mic - 36%;Golgi - 4%;	tmHMM=7; outside 1 371; TMhelix 372 394; inside 395 406; TMhelix 407 429; outside 430 448; TMhelix 449 471; inside 472 483; TMhelix 484 506; outside 507 515; TMhelix 516 536; inside	gi 7296257 gb AAF51548.1 CG3164 gene product [Drosophila melanogaster] /QuerySize=619	619			6.70E-154

Table 2

NA_GI#	SEQ ID NO	Name	Alternate name	breast		colon		kidney		lung		ovary	
10862691	66	BMPR1A	ALK3	0	3	8	30	0	0	0	13	2	7
2055308	65	BMPR1B	ALK6	0	3	6	26	7	19	4	14	2	4
13185196	39	CAC33282		0	3	0	26	0	19	0	14	0	4
4759303	82	DBY	HLP3	2	11	9	26	2	19	3	14	3	4
4503294	81	DDX3	HLP2	1	11	22	30	0	0	7	13	5	7
13631373	67	FLJ11209		0	3	4	30	0	0	1	14	1	7
3108194	72	HAPIP	DUO	0	11	1	30	0	0	7	13	2	7
7453574	64	HRMT1L2		1	3	5	30	0	0	1	13	0	7
7767238	41	IGSF4		1	3	2	25	0	0	0	11	0	3
3882220	88	KIAA0750		4	11	4	30	0	0	1	14	3	7
12742019	42	NPHS1		1	3	3	25	0	0	2	11	1	2
12382778	79	SLC30A1	ZNT1	0	3	4	30	0	0	1	13	1	7
12803124	96	U5-100K	PRP28	1	11	13	30	0	0	11	14	6	7
6010175	68	dJ622L5.2		0	3	3	26	14	19	1	14	0	4
13449288	49	KIAA0928	MOI, LOC112806	0	11	15	30	0	0	11	14	2	7
8051576	231	ABCG1		1	3	9	25	0	0	1	11	1	3
11545923	232	ABCG4	WHITE2	0	3	4	25	0	0	2	11	1	2

WHAT IS CLAIMED IS:

1. A method of identifying a candidate p53 pathway modulating agent, said method comprising the steps of:
 - 5 (a) providing an assay system comprising a purified HM polypeptide or nucleic acid or a functionally active fragment or derivative thereof;
 - (b) contacting the assay system with a test agent under conditions whereby, but for the presence of the test agent, the system provides a reference activity; and
 - (c) detecting a test agent-biased activity of the assay system, wherein a difference
10 between the test agent-biased activity and the reference activity identifies the test agent as a candidate p53 pathway modulating agent.
- 15 2. The method of Claim 1 wherein the assay system comprises cultured cells that express the HM polypeptide.
3. The method of Claim 2 wherein the cultured cells additionally have defective p53 function.
- 20 4. The method of Claim 1 wherein the assay system includes a screening assay comprising a HM polypeptide, and the candidate test agent is a small molecule modulator.
5. The method of Claim 4 wherein the assay is a binding assay.
- 25 6. The method of Claim 1 wherein the assay system is selected from the group consisting of an apoptosis assay system, a cell proliferation assay system, an angiogenesis assay system, and a hypoxic induction assay system.
- 30 7. The method of Claim 1 wherein the assay system includes a binding assay comprising a HM polypeptide and the candidate test agent is an antibody.
8. The method of Claim 1 wherein the assay system includes an expression assay comprising a HM nucleic acid and the candidate test agent is a nucleic acid modulator.

9. The method of claim 8 wherein the nucleic acid modulator is an antisense oligomer.
10. The method of Claim 8 wherein the nucleic acid modulator is a PMO.
- 5 11. The method of Claim 1 additionally comprising:
(d) administering the candidate p53 pathway modulating agent identified in (c) to a model system comprising cells defective in p53 function and, detecting a phenotypic change in the model system that indicates that the p53 function is restored.
- 10 12. The method of Claim 11 wherein the model system is a mouse model with defective p53 function.
13. A method for modulating a p53 pathway of a cell comprising contacting a cell
15 defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid sequence, whereby p53 function is restored.
14. The method of claim 13 wherein the candidate modulator is administered to a vertebrate animal predetermined to have a disease or disorder resulting from a defect in
20 p53 function.
15. The method of Claim 13 wherein the candidate modulator is selected from the group consisting of an antibody and a small molecule.
- 25 16. The method of Claim 1, comprising the additional steps of:
(d) providing a secondary assay system comprising cultured cells or a non-human animal expressing HM ,
(e) contacting the secondary assay system with the test agent of (b) or an agent derived therefrom under conditions whereby, but for the presence of the test agent or agent
30 derived therefrom, the system provides a reference activity; and
(f) detecting an agent-biased activity of the second assay system,
wherein a difference between the agent-biased activity and the reference activity of the second assay system confirms the test agent or agent derived therefrom as a candidate p53 pathway modulating agent,

and wherein the second assay detects an agent-biased change in the p53 pathway.

17. The method of Claim 16 wherein the secondary assay system comprises cultured cells.

5

18. The method of Claim 16 wherein the secondary assay system comprises a non-human animal.

19. The method of Claim 18 wherein the non-human animal mis-expresses a p53 pathway gene.

10

20. A method of modulating p53 pathway in a mammalian cell comprising contacting the cell with an agent that specifically binds a HM polypeptide or nucleic acid.

21. The method of Claim 20 wherein the agent is administered to a mammalian animal predetermined to have a pathology associated with the p53 pathway.

15

22. The method of Claim 20 wherein the agent is a small molecule modulator, a nucleic acid modulator, or an antibody.

20

23. A method for diagnosing a disease in a patient comprising:

(a) obtaining a biological sample from the patient;

(b) contacting the sample with a probe for HM expression;

(c) comparing results from step (b) with a control;

25 (d) determining whether step (c) indicates a likelihood of disease.

25

24. The method of claim 23 wherein said disease is cancer.

25. The method according to claim 24, wherein said cancer is a cancer as shown in Table 2 as having >25% expression level.

30

SEQUENCE LISTING

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<211> 1964
<212> DNA
<213> Homo sapiens

<220>
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<210> 52

<211> 1955

<212> DNA

<213> Homo sapiens

<400> 52

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<211> 2187
 <212> DNA
 <213> Homo sapiens

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 <211> 5924
 <212> DNA
 <213> Homo sapiens

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<213> Homo sapiens

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<211> 1968

<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<211> 3740

<212> DNA

<213> Homo sapiens

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<211> 1312

<212> DNA

<213> Homo sapiens

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<212> DNA

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aaaagaacaa	ggccacagca	caccacttag	ggctgcttaa	ggctcgtctt	gctaagcttc	180
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tggccaagac	aggtgatgct	cgaattggat	ttgttgggtt	tccatctgtg	gggaagtcaa	300
cactgcttag	taacctggca	ggggatatatt	ctgaggtggc	agcctatgaa	ttcactactc	360
tgaccactgt	gcctgggtgct	atcagatata	aaggtgcca	gatccagctc	ctggatctcc	420

caggtatcat	tgaagggtgcc	aaggatggga	aaggtagagg	tcgtcaagtc	attgcagtgg	480
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agataattga	aaatgagctg	gaaggctttg	gcattcgctt	gaacagcaaa	ccccccaaca	600
ttggctttta	gaagaaggac	aaggaggca	ttaatctcac	agccacttgc	ccccagagtg	660
agctggatgc	tgaactgtg	aagagcattc	tggctgaata	caagattcat	aatgccgatg	720
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atgacctatt	ggaaaagatc	tgggactatc	tgaaactagt	gagaatttac	accaaaacca	960
aaggccagtt	accagattac	acatccccag	tgggtgcttc	ttactccagg	accacagtgg	1020
aggattttctg	catgaagatt	cacaaaaatc	ttatcaaaga	atttaaataat	gctctgggtct	1080
ggggtctctc	tgtgaaacac	aatcctcaga	aagtgggtaa	agaccatacg	ttggaggatg	1140
aggatgtcat	tcaaattgtg	aagaagtga	acctttccct	tttcccatct	gccggacgaa	1200
ccacaacagc	gttccccatg	atcaagcacc	ctacccagct	tctttctggt	tttggcagtc	1260
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tgc						1383

<210> 113
 <211> 1880
 <212> DNA
 <213> Homo sapiens

<400> 113
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 cggccagcga ggcagcgtcc tatgagttca ccactctgac gtgtattcct ggggtcattg 360
 aatacaaaagg tgccaacatc cagctcctgg accttcctgg aatcattgaa ggcgcagccc 420
 aaggaaaagg ccgtggccgg caggtgatcg ctgtggcgcg cacggctgac gtcacatca 480
 tgatgctgga tgccaccaag ggagagggtc agagggtctc gctggagaag gagctggagt 540
 ctgtgggcat ccgcctcaac aagcacaagc ctaacatcta cttcaagccc aagaaagggtg 600
 gtggcatctc ctttaactcg acagtacgc tgaccagtg ctcggaaaag ctggtgcagc 660
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 cggacgagtt catcgatgtg atcgtgggca accgggtgta catgccctgc ctgtatgttt 780
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 cctgcccag caaaaaccc caggacctg gctctgcacg cctggggcag ggacttttga 1800
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<210> 114
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 114
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 ctggtgatta gttctgtgac tgtgttttac ctgggccagc atgccatgga atgccatcac 180
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 ttcccctaatg ccaaatttct cctgatgggc cgagatggcc gggcatcagt acattcaatg 660
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 ttccaactac ctgactttct taaagaaaaa ccacagactg agcaagtgga gtagcagaac 1200
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tttttcaaaa taaaagcttt caatgtga 1768

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<210> 115
<211> 1855
<212> DNA
<213> Homo sapiens

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<400> 115
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cctgcctccg gccagcatg cgcctgtcgg tcgggagggt gctgctggca gccggctgcg 240
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tttaatatat gaggctttct ttgattcctc ctgagttcta cctagtttca cagaggaaaa 1800
aaatactctt tgaataaagt gaacagagggc tcatttgttt gtgcctcact ttaca 1855

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<210> 116
<211> 465
<212> PRT
<213> Homo sapiens

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<400> 116
Met Ile Val Phe Val Arg Phe Asn Ser Ser His Gly Phe Pro Val Glu
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Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys
20          25          30

Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys
35          40          45

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Glu Leu Arg Asn Asp Trp Thr Val Gln Asn Cys Asp Leu Asp Gln Gln
 50 55 60
 Ser Ile Val His Ile Val Gln Arg Pro Trp Arg Lys Gly Gln Glu Met
 65 70 75 80
 Asn Ala Thr Gly Gly Asp Asp Pro Arg Asn Ala Ala Gly Gly Cys Glu
 85 90 95
 Arg Glu Pro Gln Ser Leu Thr Arg Val Asp Leu Ser Ser Ser Val Leu
 100 105 110
 Pro Gly Asp Ser Val Gly Leu Ala Val Ile Leu His Thr Asp Ser Arg
 115 120 125
 Lys Asp Ser Pro Pro Ala Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn
 130 135 140
 Ser Phe Tyr Val Tyr Cys Lys Gly Pro Cys Gln Arg Val Gln Pro Gly
 145 150 155 160
 Lys Leu Arg Val Gln Cys Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu
 165 170 175
 Thr Gln Gly Pro Ser Cys Trp Asp Asp Val Leu Ile Pro Asn Arg Met
 180 185 190
 Ser Gly Glu Cys Gln Ser Pro His Cys Pro Gly Thr Ser Ala Glu Phe
 195 200 205
 Phe Phe Lys Cys Gly Ala His Pro Thr Ser Asp Lys Glu Thr Pro Val
 210 215 220
 Ala Leu His Leu Ile Ala Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr
 225 230 235 240
 Cys Thr Asp Val Arg Ser Pro Val Leu Val Phe Gln Cys Asn Ser Arg
 245 250 255
 His Val Ile Cys Leu Asp Cys Phe His Leu Tyr Cys Val Thr Arg Leu
 260 265 270
 Asn Asp Arg Gln Phe Val His Asp Pro Gln Leu Gly Tyr Ser Leu Pro
 275 280 285
 Cys Val Ala Gly Cys Pro Asn Ser Leu Ile Lys Glu Leu His His Phe
 290 295 300
 Arg Ile Leu Gly Glu Glu Gln Tyr Asn Arg Tyr Gln Gln Tyr Gly Ala
 305 310 315 320
 Glu Glu Cys Val Leu Gln Met Gly Gly Val Leu Cys Pro Arg Pro Gly
 325 330 335
 Cys Gly Ala Gly Leu Leu Pro Glu Pro Asp Gln Arg Lys Val Thr Cys
 340 345 350
 Glu Gly Gly Asn Gly Leu Gly Cys Gly Phe Ala Phe Cys Arg Glu Cys
 355 360 365
 Lys Glu Ala Tyr His Glu Gly Glu Cys Ser Ala Val Phe Glu Ala Ser

370 375 380
 Gly Thr Thr Thr Gln Ala Tyr Arg Val Asp Glu Arg Ala Ala Glu Gln
 385 390 395 400
 Ala Arg Trp Glu Ala Ala Ser Lys Glu Thr Ile Lys Lys Thr Thr Lys
 405 410 415
 Pro Cys Pro Arg Cys His Val Pro Val Glu Lys Asn Gly Gly Cys Met
 420 425 430
 His Met Lys Cys Pro Gln Pro Gln Cys Arg Leu Glu Trp Cys Trp Asn
 435 440 445
 Cys Gly Cys Glu Trp Asn Arg Val Cys Met Gly Asp His Trp Phe Asp
 450 455 460
 Val
 465
 <210> 117
 <211> 437
 <212> PRT
 <213> Homo sapiens
 <400> 117
 Met Ile Val Phe Val Arg Phe Asn Ser Ser His Gly Phe Pro Val Glu
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 Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys
 20 25 30
 Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys
 35 40 45
 Glu Leu Arg Asn Asp Trp Thr Val Gln Asn Cys Asp Leu Asp Gln Gln
 50 55 60
 Ser Ile Val His Ile Val Gln Arg Pro Trp Arg Lys Gly Gln Glu Met
 65 70 75 80
 Asn Ala Thr Gly Gly Asp Asp Pro Arg Asn Ala Ala Gly Gly Cys Glu
 85 90 95
 Arg Glu Pro Gln Ser Leu Thr Arg Val Asp Leu Ser Ser Ser Val Leu
 100 105 110
 Pro Gly Asp Ser Val Gly Leu Ala Val Ile Leu His Thr Asp Ser Arg
 115 120 125
 Lys Asp Ser Pro Pro Ala Gly Ser Pro Ala Gly Arg Ser Ile Tyr Asn
 130 135 140
 Ser Phe Tyr Val Tyr Cys Lys Gly Pro Cys Gln Arg Val Gln Pro Gly
 145 150 155 160
 Lys Leu Arg Val Gln Cys Ser Thr Cys Arg Gln Ala Thr Leu Thr Leu
 165 170 175
 Thr Gln Glu Phe Phe Phe Lys Cys Gly Ala His Pro Thr Ser Asp Lys
 180 185 190

Glu Thr Pro Val Ala Leu His Leu Ile Ala Thr Asn Ser Arg Asn Ile
 195 200 205
 Thr Cys Ile Thr Cys Thr Asp Val Arg Ser Pro Val Leu Val Phe Gln
 210 215 220
 Cys Asn Ser Arg His Val Ile Cys Leu Asp Cys Phe His Leu Tyr Cys
 225 230 235 240
 Val Thr Arg Leu Asn Asp Arg Gln Phe Val His Asp Pro Gln Leu Gly
 245 250 255
 Tyr Ser Leu Pro Cys Val Ala Gly Cys Pro Asn Ser Leu Ile Lys Glu
 260 265 270
 Leu His His Phe Arg Ile Leu Gly Glu Glu Gln Tyr Asn Arg Tyr Gln
 275 280 285
 Gln Tyr Gly Ala Glu Glu Cys Val Leu Gln Met Gly Gly Val Leu Cys
 290 295 300
 Pro Arg Pro Gly Cys Gly Ala Gly Leu Leu Pro Glu Pro Asp Gln Arg
 305 310 315 320
 Lys Val Thr Cys Glu Gly Gly Asn Gly Leu Gly Cys Gly Phe Ala Phe
 325 330 335
 Cys Arg Glu Cys Lys Glu Ala Tyr His Glu Gly Glu Cys Ser Ala Val
 340 345 350
 Phe Glu Ala Ser Gly Thr Thr Thr Gln Ala Tyr Arg Val Asp Glu Arg
 355 360 365
 Ala Ala Glu Gln Ala Arg Trp Glu Ala Ala Ser Lys Glu Thr Ile Lys
 370 375 380
 Lys Thr Thr Lys Pro Cys Pro Arg Cys His Val Pro Val Glu Lys Asn
 385 390 395 400
 Gly Gly Cys Met His Met Lys Cys Pro Gln Pro Gln Cys Arg Leu Glu
 405 410 415
 Trp Cys Trp Asn Cys Gly Cys Glu Trp Asn Arg Val Cys Met Gly Asp
 420 425 430
 His Trp Phe Asp Val
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<210> 118
 <211> 316
 <212> PRT
 <213> Homo sapiens

<400> 118
 Met Ile Val Phe Val Arg Phe Asn Ser Ser His Gly Phe Pro Val Glu
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 Val Asp Ser Asp Thr Ser Ile Phe Gln Leu Lys Glu Val Val Ala Lys
 20 25 30
 Arg Gln Gly Val Pro Ala Asp Gln Leu Arg Val Ile Phe Ala Gly Lys
 35 40 45

Glu Leu Arg Asn Asp Trp Thr Val Gln Glu Phe Phe Phe Lys Cys Gly
 50 55 60
 Ala His Pro Thr Ser Asp Lys Glu Thr Pro Val Ala Leu His Leu Ile
 65 70 75 80
 Ala Thr Asn Ser Arg Asn Ile Thr Cys Ile Thr Cys Thr Asp Val Arg
 85 90 95
 Ser Pro Val Leu Val Phe Gln Cys Asn Ser Arg His Val Ile Cys Leu
 100 105 110
 Asp Cys Phe His Leu Tyr Cys Val Thr Arg Leu Asn Asp Arg Gln Phe
 115 120 125
 Val His Asp Pro Gln Leu Gly Tyr Ser Leu Pro Cys Val Ala Gly Cys
 130 135 140
 Pro Asn Ser Leu Ile Lys Glu Leu His His Phe Arg Ile Leu Gly Glu
 145 150 155 160
 Glu Gln Tyr Asn Arg Tyr Gln Gln Tyr Gly Ala Glu Glu Cys Val Leu
 165 170 175
 Gln Met Gly Gly Val Leu Cys Pro Arg Pro Gly Cys Gly Ala Gly Leu
 180 185 190
 Leu Pro Glu Pro Asp Gln Arg Lys Val Thr Cys Glu Gly Gly Asn Gly
 195 200 205
 Leu Gly Cys Gly Phe Ala Phe Cys Arg Glu Cys Lys Glu Ala Tyr His
 210 215 220
 Glu Gly Glu Cys Ser Ala Val Phe Glu Ala Ser Gly Thr Thr Thr Gln
 225 230 235 240
 Ala Tyr Arg Val Asp Glu Arg Ala Ala Glu Gln Ala Arg Trp Glu Ala
 245 250 255
 Ala Ser Lys Glu Thr Ile Lys Lys Thr Thr Lys Pro Cys Pro Arg Cys
 260 265 270
 His Val Pro Val Glu Lys Asn Gly Gly Cys Met His Met Lys Cys Pro
 275 280 285
 Gln Pro Gln Cys Arg Leu Glu Trp Cys Trp Asn Cys Gly Cys Glu Trp
 290 295 300
 Asn Arg Val Cys Met Gly Asp His Trp Phe Asp Val
 305 310 315
 <210> 119
 <211> 534
 <212> PRT
 <213> Homo sapiens
 <400> 119
 Met Ile Trp Tyr Ile Leu Ile Ile Gly Ile Leu Leu Pro Gln Ser Leu
 1 5 10 15
 Ala His Pro Gly Phe Phe Thr Ser Ile Gly Gln Met Thr Asp Leu Ile

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His	Thr	Glu	Lys	Asp	Leu	Val	Thr	Ser	Leu	Lys	Asp	Tyr	Ile	Lys	Ala	
35					40					45						
Glu	Glu	Asp	Lys	Leu	Glu	Gln	Ile	Lys	Lys	Trp	Ala	Glu	Lys	Leu	Asp	
50					55					60						
Arg	Leu	Thr	Ser	Thr	Ala	Thr	Lys	Asp	Pro	Glu	Gly	Phe	Val	Gly	His	
65					70					75					80	
Pro	Val	Asn	Ala	Phe	Lys	Leu	Met	Lys	Arg	Leu	Asn	Thr	Glu	Trp	Ser	
85					90					95						
Glu	Leu	Glu	Asn	Leu	Val	Leu	Lys	Asp	Met	Ser	Asp	Gly	Phe	Ile	Ser	
100					105					110						
Asn	Leu	Thr	Ile	Gln	Arg	Pro	Val	Leu	Ser	Asn	Asp	Glu	Asp	Gln	Val	
115					120					125						
Gly	Ala	Ala	Lys	Ala	Leu	Leu	Arg	Leu	Gln	Asp	Thr	Tyr	Asn	Leu	Asp	
130					135					140						
Thr	Asp	Thr	Ile	Ser	Lys	Gly	Asn	Leu	Pro	Gly	Val	Lys	His	Lys	Ser	
145					150					155					160	
Phe	Leu	Thr	Ala	Glu	Asp	Cys	Phe	Glu	Leu	Gly	Lys	Val	Ala	Tyr	Thr	
165					170					175						
Glu	Ala	Asp	Tyr	Tyr	His	Thr	Glu	Leu	Trp	Met	Glu	Gln	Ala	Leu	Arg	
180					185					190						
Gln	Leu	Asp	Glu	Gly	Glu	Ile	Ser	Thr	Ile	Asp	Lys	Val	Ser	Val	Leu	
195					200					205						
Asp	Tyr	Leu	Ser	Tyr	Ala	Val	Tyr	Gln	Gln	Gly	Asp	Leu	Asp	Lys	Ala	
210					215					220						
Leu	Leu	Leu	Thr	Lys	Lys	Leu	Leu	Glu	Leu	Asp	Pro	Glu	His	Gln	Arg	
225					230					235					240	
Ala	Asn	Gly	Asn	Leu	Lys	Tyr	Phe	Glu	Tyr	Ile	Met	Ala	Lys	Glu	Lys	
245					250					255						
Asp	Val	Asn	Lys	Ser	Ala	Ser	Asp	Asp	Gln	Ser	Asp	Gln	Lys	Thr	Thr	
260					265					270						
Pro	Lys	Lys	Lys	Gly	Val	Ala	Val	Asp	Tyr	Leu	Pro	Glu	Arg	Gln	Lys	
275					280					285						
Tyr	Glu	Met	Leu	Cys	Arg	Gly	Glu	Gly	Ile	Lys	Met	Thr	Pro	Arg	Arg	
290					295					300						
Gln	Lys	Lys	Leu	Phe	Cys	Arg	Tyr	His	Asp	Gly	Asn	Arg	Asn	Pro	Lys	
305					310					315					320	
Phe	Ile	Leu	Ala	Pro	Ala	Lys	Gln	Glu	Asp	Glu	Trp	Asp	Lys	Pro	Arg	
325					330					335						
Ile	Ile	Arg	Phe	His	Asp	Ile	Ile	Ser	Asp	Ala	Glu	Ile	Glu	Ile	Val	
340					345					350						

Lys Asp Leu Ala Lys Pro Arg Leu Arg Arg Ala Thr Ile Ser Asn Pro
 355 360 365
 Ile Thr Gly Asp Leu Glu Thr Val His Tyr Arg Ile Ser Lys Ser Ala
 370 375 380
 Trp Leu Ser Gly Tyr Glu Asn Pro Val Val Ser Arg Ile Asn Met Arg
 385 390 395 400
 Ile Gln Asp Leu Thr Gly Leu Asp Val Ser Thr Ala Glu Glu Leu Gln
 405 410 415
 Val Ala Asn Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe
 420 425 430
 Ala Arg Lys Asp Glu Pro Asp Ala Phe Lys Glu Leu Gly Thr Gly Asn
 435 440 445
 Arg Ile Ala Thr Trp Leu Phe Tyr Met Ser Asp Val Ser Ala Gly Gly
 450 455 460
 Ala Thr Val Phe Pro Glu Val Gly Ala Ser Val Trp Pro Lys Lys Gly
 465 470 475 480
 Thr Ala Val Phe Trp Tyr Asn Leu Phe Ala Ser Gly Glu Gly Asp Tyr
 485 490 495
 Ser Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Asn Lys Trp Val
 500 505 510
 Ser Asn Lys Trp Leu His Glu Arg Gly Gln Glu Phe Arg Arg Pro Cys
 515 520 525
 Thr Leu Ser Glu Leu Glu
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<210> 120
 <211> 535
 <212> PRT
 <213> Homo sapiens

<400> 120
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 35 40 45
 Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser Trp Ala Asn Lys
 50 55 60
 Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp Ala Glu Gly Tyr Leu
 65 70 75 80
 Ala His Pro Val Asn Ala Tyr Lys Leu Val Lys Arg Leu Asn Thr Asp
 85 90 95
 Trp Pro Ala Leu Glu Asp Leu Val Leu Gln Asp Ser Ala Ala Gly Phe
 100 105 110

Ile Ala Asn Leu Ser Val Gln Arg Gln Phe Phe Pro Thr Asp Glu Asp
 115 120 125
 Glu Ile Gly Ala Ala Lys Ala Leu Met Arg Leu Gln Asp Thr Tyr Arg
 130 135 140
 Leu Asp Pro Gly Thr Ile Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr
 145 150 155 160
 Gln Ala Met Leu Ser Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala
 165 170 175
 Tyr Asn Glu Gly Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val
 180 185 190
 Leu Lys Gln Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln
 195 200 205
 Val Leu Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His
 210 215 220
 Arg Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His
 225 230 235 240
 Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu Glu
 245 250 255
 Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu Ala Thr
 260 265 270
 Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro Glu Arg Asp
 275 280 285
 Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys Leu Thr Pro Arg
 290 295 300
 Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His Gly Asn Arg Ala Pro
 305 310 315 320
 Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu Asp Glu Trp Asp Ser Pro
 325 330 335
 His Ile Val Arg Tyr Tyr Asp Val Met Ser Asp Glu Glu Ile Glu Arg
 340 345 350
 Ile Lys Glu Ile Ala Lys Pro Lys Leu Ala Arg Ala Thr Val Arg Asp
 355 360 365
 Pro Lys Thr Gly Val Leu Thr Val Ala Ser Tyr Arg Val Ser Lys Ser
 370 375 380
 Ser Trp Leu Glu Glu Asp Asp Asp Pro Val Val Ala Arg Val Asn Arg
 385 390 395 400
 Arg Met Gln His Ile Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu
 405 410 415
 Gln Val Ala Asn Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp
 420 425 430
 Phe Ser Arg Asn Asp Glu Arg Asp Thr Phe Lys His Leu Gly Thr Gly

435 440 445
 Asn Arg Val Ala Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly
 450 455 460
 Gly Ala Thr Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys
 465 470 475 480
 Gly Thr Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp
 485 490 495
 Tyr Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
 500 505 510
 Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg Pro
 515 520 525
 Cys Gly Ser Thr Glu Val Asp
 530 535
 <210> 121
 <211> 524
 <212> PRT
 <213> Homo sapiens
 <400> 121
 Met Phe His Cys Ile Pro Leu Trp Arg Cys Asn Arg His Val Glu Ser
 1 5 10 15
 Ile Asp Lys Arg His Cys Ser Leu Val Tyr Val Pro Glu Glu Ile Tyr
 20 25 30
 Arg Tyr Ala Arg Ser Leu Glu Glu Leu Leu Leu Asp Ala Asn Gln Leu
 35 40 45
 Arg Glu Leu Pro Glu Gln Phe Phe Gln Leu Val Lys Leu Arg Lys Leu
 50 55 60
 Gly Leu Ser Asp Asn Glu Ile Gln Arg Leu Pro Pro Glu Ile Ala Asn
 65 70 75 80
 Phe Met Gln Leu Val Glu Leu Asp Val Ser Arg Asn Glu Ile Pro Glu
 85 90 95
 Ile Pro Glu Ser Ile Ser Phe Cys Lys Ala Leu Gln Val Ala Asp Phe
 100 105 110
 Ser Gly Asn Pro Leu Thr Arg Leu Pro Glu Ser Phe Pro Glu Leu Gln
 115 120 125
 Asn Leu Thr Cys Leu Ser Val Asn Asp Ile Ser Leu Gln Ser Leu Pro
 130 135 140
 Glu Asn Ile Gly Asn Leu Tyr Asn Leu Ala Ser Leu Glu Leu Arg Glu
 145 150 155 160
 Asn Leu Leu Thr Tyr Leu Pro Asp Ser Leu Thr Gln Leu Arg Arg Leu
 165 170 175
 Glu Glu Leu Asp Leu Gly Asn Asn Glu Ile Tyr Asn Leu Pro Glu Ser
 180 185 190

Ile Gly Ala Leu Leu His Leu Lys Asp Leu Trp Leu Asp Gly Asn Gln
 195 200 205
 Leu Ser Glu Leu Pro Gln Glu Ile Gly Asn Leu Lys Asn Leu Leu Cys
 210 215 220
 Leu Asp Val Ser Glu Asn Arg Leu Glu Arg Leu Pro Glu Glu Ile Ser
 225 230 235 240
 Gly Leu Thr Ser Leu Thr Asp Leu Val Ile Ser Gln Asn Leu Leu Glu
 245 250 255
 Thr Ile Pro Asp Gly Ile Gly Lys Leu Lys Lys Leu Ser Ile Leu Lys
 260 265 270
 Val Asp Gln Asn Arg Leu Thr Gln Leu Pro Glu Ala Val Gly Glu Cys
 275 280 285
 Glu Ser Leu Thr Glu Leu Val Leu Thr Glu Asn Gln Leu Leu Thr Leu
 290 295 300
 Pro Lys Ser Ile Gly Lys Leu Lys Lys Leu Ser Asn Leu Asn Ala Asp
 305 310 315 320
 Arg Asn Lys Leu Val Ser Leu Pro Lys Glu Ile Gly Gly Cys Cys Ser
 325 330 335
 Leu Thr Val Phe Cys Val Arg Asp Asn Arg Leu Thr Arg Ile Pro Ala
 340 345 350
 Glu Val Ser Gln Ala Thr Glu Leu His Val Leu Asp Val Ala Gly Asn
 355 360 365
 Arg Leu Leu His Leu Pro Leu Ser Leu Thr Ala Leu Lys Leu Lys Ala
 370 375 380
 Leu Trp Leu Ser Asp Asn Gln Ser Gln Pro Leu Leu Thr Phe Gln Thr
 385 390 395 400
 Asp Thr Asp Tyr Thr Thr Gly Glu Lys Ile Leu Thr Cys Val Leu Leu
 405 410 415
 Pro Gln Leu Pro Ser Glu Pro Thr Cys Gln Glu Asn Leu Pro Arg Cys
 420 425 430
 Gly Ala Leu Glu Asn Leu Val Asn Asp Val Ser Asp Glu Ala Trp Asn
 435 440 445
 Glu Arg Ala Val Asn Arg Val Ser Ala Ile Arg Phe Val Glu Asp Glu
 450 455 460
 Lys Asp Glu Glu Asp Asn Glu Thr Arg Thr Leu Leu Arg Arg Ala Thr
 465 470 475 480
 Pro His Pro Gly Glu Leu Lys His Met Lys Lys Thr Val Glu Asn Leu
 485 490 495
 Arg Asn Asp Met Asn Ala Ala Lys Gly Leu Asp Ser Asn Lys Asn Glu
 500 505 510
 Val Asn His Ala Ile Asp Arg Val Thr Thr Ser Val
 515 520

<210> 122
 <211> 1551
 <212> PRT
 <213> Homo sapiens

<400> 122

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Ser Asp Asn Glu Ile Gln Arg Leu Pro Pro Glu Val Ala Asn Phe Met
1          5          10          15

Gln Leu Val Glu Leu Asp Val Ser Arg Asn Asp Ile Pro Glu Ile Pro
      20          25          30

Glu Ser Ile Lys Phe Cys Lys Ala Leu Glu Ile Ala Asp Phe Ser Gly
      35          40          45

Asn Pro Leu Ser Arg Leu Pro Asp Gly Phe Thr Gln Leu Arg Ser Leu
      50          55          60

Ala His Leu Ala Leu Asn Asp Val Ser Leu Gln Ala Leu Pro Gly Asp
      65          70          75          80

Val Gly Asn Leu Ala Asn Leu Val Thr Leu Glu Leu Arg Glu Asn Leu
      85          90          95

Leu Lys Ser Leu Pro Ala Ser Leu Ser Phe Leu Val Lys Leu Glu Gln
      100         105         110

Leu Asp Leu Gly Gly Asn Asp Leu Glu Val Leu Pro Asp Thr Leu Gly
      115         120         125

Ala Leu Pro Asn Leu Arg Glu Leu Trp Leu Asp Arg Asn Gln Leu Ser
      130         135         140

Ala Leu Pro Pro Glu Leu Gly Asn Leu Arg Arg Leu Val Cys Leu Asp
      145         150         155         160

Val Ser Glu Asn Arg Leu Glu Glu Leu Pro Ala Glu Leu Gly Gly Leu
      165         170         175

Val Leu Leu Thr Asp Leu Leu Leu Ser Gln Asn Leu Leu Arg Arg Leu
      180         185         190

Pro Asp Gly Ile Gly Gln Leu Lys Gln Leu Ser Ile Leu Lys Val Asp
      195         200         205

Gln Asn Arg Leu Cys Glu Val Thr Glu Ala Ile Gly Asp Cys Glu Asn
      210         215         220

Leu Ser Glu Leu Ile Leu Thr Glu Asn Leu Leu Met Ala Leu Pro Arg
      225         230         235         240

Ser Leu Gly Lys Leu Thr Lys Leu Thr Asn Leu Asn Val Asp Arg Asn
      245         250         255

His Leu Glu Ala Leu Pro Pro Glu Ile Gly Gly Cys Val Ala Leu Ser
      260         265         270

Val Leu Ser Leu Arg Asp Asn Arg Leu Ala Val Leu Pro Pro Glu Leu
      275         280         285

Ala His Thr Thr Glu Leu His Val Leu Asp Val Ala Gly Asn Arg Leu

```

290	295	300
Gln Ser Leu Pro Phe Ala Leu Thr His Leu Asn Leu Lys Ala Leu Trp 305 310 315 320		
Leu Ala Glu Asn Gln Ala Gln Pro Met Leu Arg Phe Gln Thr Glu Asp 325 330 335		
Asp Ala Arg Thr Gly Glu Lys Val Leu Thr Cys Tyr Leu Leu Pro Gln 340 345 350		
Gln Pro Pro Leu Ser Leu Glu Asp Ala Gly Gln Gln Gly Ser Leu Ser 355 360 365		
Glu Thr Trp Ser Asp Ala Pro Pro Ser Arg Val Ser Val Ile Gln Phe 370 375 380		
Leu Glu Ala Pro Ile Gly Asp Glu Asp Ala Glu Glu Ala Ala Ala Glu 385 390 395 400		
Lys Arg Gly Leu Gln Arg Arg Ala Thr Pro His Pro Ser Glu Leu Lys 405 410 415		
Val Met Lys Arg Ser Ile Glu Gly Arg Arg Ser Glu Ala Cys Pro Cys 420 425 430		
Gln Pro Asp Ser Gly Ser Pro Leu Pro Ala Glu Glu Glu Lys Arg Leu 435 440 445		
Ser Ala Glu Ser Gly Leu Ser Glu Asp Ser Arg Pro Ser Ala Ser Thr 450 455 460		
Val Ser Glu Ala Glu Pro Glu Gly Pro Ser Ala Glu Ala Gln Gly Gly 465 470 475 480		
Ser Gln Gln Glu Ala Thr Thr Ala Gly Gly Glu Glu Asp Ala Glu Glu 485 490 495		
Asp Tyr Gln Glu Pro Thr Val His Phe Ala Glu Asp Ala Leu Leu Pro 500 505 510		
Gly Asp Asp Arg Glu Ile Glu Glu Gly Gln Pro Glu Ala Pro Trp Thr 515 520 525		
Leu Pro Gly Gly Arg Gln Arg Leu Ile Arg Lys Asp Thr Pro His Tyr 530 535 540		
Lys Lys His Phe Lys Ile Ser Lys Leu Pro Gln Pro Glu Ala Val Val 545 550 555 560		
Ala Leu Leu Gln Gly Met Gln Pro Asp Gly Glu Gly Pro Val Ala Pro 565 570 575		
Gly Gly Trp His Asn Gly Pro His Ala Pro Trp Ala Pro Arg Ala Gln 580 585 590		
Lys Glu Glu Glu Glu Glu Glu Glu Gly Ser Pro Gln Glu Glu Glu Glu 595 600 605		
Glu Glu Glu Glu Glu Asn Arg Ala Glu Glu Glu Glu Ala Ser Thr Glu 610 615 620		

Glu Glu Asp Lys Glu Gly Ala Val Val Ser Ala Pro Ser Val Lys Gly
 625 630 635 640
 Val Ser Phe Asp Gln Ala Asn Asn Leu Leu Ile Glu Pro Ala Arg Ile
 645 650 655
 Glu Glu Glu Glu Leu Thr Leu Thr Ile Leu Arg Gln Thr Gly Gly Leu
 660 665 670
 Gly Ile Ser Ile Ala Gly Gly Lys Gly Ser Thr Pro Tyr Lys Gly Asp
 675 680 685
 Asp Glu Gly Ile Phe Ile Ser Arg Val Ser Glu Glu Gly Pro Ala Ala
 690 695 700
 Arg Ala Gly Val Arg Val Gly Asp Lys Leu Leu Glu Val Asn Gly Val
 705 710 715 720
 Ala Leu Gln Gly Ala Glu His His Glu Ala Val Glu Ala Leu Arg Gly
 725 730 735
 Ala Gly Thr Ala Val Gln Met Arg Val Trp Arg Glu Arg Met Val Glu
 740 745 750
 Pro Glu Asn Ala Val Thr Ile Thr Pro Leu Arg Pro Glu Asp Asp Tyr
 755 760 765
 Ser Pro Arg Glu Arg Arg Gly Gly Gly Leu Arg Leu Pro Leu Leu Pro
 770 775 780
 Pro Glu Ser Pro Gly Pro Leu Arg Gln Arg His Val Ala Cys Leu Ala
 785 790 795 800
 Arg Ser Glu Arg Gly Leu Gly Phe Ser Ile Ala Gly Gly Lys Gly Ser
 805 810 815
 Thr Pro Tyr Arg Ala Gly Asp Ala Gly Ile Phe Val Ser Arg Ile Ala
 820 825 830
 Glu Gly Gly Ala Ala His Arg Ala Gly Thr Leu Gln Val Gly Asp Arg
 835 840 845
 Val Leu Ser Ile Asn Gly Val Asp Val Thr Glu Ala Arg His Asp His
 850 855 860
 Ala Val Ser Leu Leu Thr Ala Ala Ser Pro Thr Ile Ala Leu Leu Leu
 865 870 875 880
 Glu Arg Glu Ala Gly Gly Pro Leu Pro Pro Ser Pro Leu Pro His Ser
 885 890 895
 Ser Pro Pro Thr Ala Ala Val Ala Thr Thr Ser Ile Thr Thr Ala Thr
 900 905 910
 Pro Gly Val Pro Gly Leu Pro Ser Leu Ala Pro Ser Leu Leu Ala Ala
 915 920 925
 Ala Leu Glu Gly Pro Tyr Pro Val Glu Glu Ile Arg Leu Pro Arg Ala
 930 935 940
 Gly Gly Pro Leu Gly Leu Ser Ile Val Gly Gly Ser Asp His Ser Ser
 945 950 955 960

His Pro Phe Gly Val Gln Glu Pro Gly Val Phe Ile Ser Lys Val Leu
 965 970 975
 Pro Arg Gly Leu Ala Ala Arg Ser Gly Leu Arg Val Gly Asp Arg Ile
 980 985 990
 Leu Ala Val Asn Gly Gln Asp Val Arg Asp Ala Thr His Gln Glu Ala
 995 1000 1005
 Val Ser Ala Leu Leu Arg Pro Cys Leu Glu Leu Ser Leu Leu Val
 1010 1015 1020
 Arg Arg Asp Pro Ala Pro Pro Gly Leu Arg Glu Leu Cys Ile Gln
 1025 1030 1035
 Lys Ala Pro Gly Glu Arg Leu Gly Ile Ser Ile Arg Gly Gly Ala
 1040 1045 1050
 Arg Gly His Ala Gly Asn Pro Arg Asp Pro Thr Asp Glu Gly Ile
 1055 1060 1065
 Phe Ile Ser Lys Val Ser Pro Thr Gly Ala Ala Gly Arg Asp Gly
 1070 1075 1080
 Arg Leu Arg Val Gly Leu Arg Leu Leu Glu Val Asn Gln Gln Ser
 1085 1090 1095
 Leu Leu Gly Leu Thr His Gly Glu Ala Val Gln Leu Leu Arg Ser
 1100 1105 1110
 Val Gly Asp Thr Leu Thr Val Leu Val Cys Asp Gly Phe Glu Ala
 1115 1120 1125
 Ser Thr Asp Ala Ala Leu Glu Val Ser Pro Gly Val Ile Ala Asn
 1130 1135 1140
 Pro Phe Ala Ala Gly Ile Gly His Arg Asn Ser Leu Glu Ser Ile
 1145 1150 1155
 Ser Ser Ile Asp Arg Glu Leu Ser Pro Glu Gly Pro Gly Lys Glu
 1160 1165 1170
 Lys Glu Leu Pro Gly Gln Thr Leu His Trp Gly Pro Glu Ala Thr
 1175 1180 1185
 Glu Ala Ala Gly Arg Gly Leu Gln Pro Leu Lys Leu Asp Tyr Arg
 1190 1195 1200
 Ala Leu Ala Ala Val Pro Ser Ala Gly Ser Val Gln Arg Val Pro
 1205 1210 1215
 Ser Gly Ala Ala Gly Gly Lys Met Ala Glu Ser Pro Cys Ser Pro
 1220 1225 1230
 Ser Gly Gln Gln Pro Pro Ser Pro Pro Ser Pro Asp Glu Leu Pro
 1235 1240 1245
 Ala Asn Val Lys Gln Ala Tyr Arg Ala Phe Ala Ala Val Pro Thr
 1250 1255 1260
 Ser His Pro Pro Glu Asp Ala Pro Ala Gln Pro Pro Thr Pro Gly

1265	1270	1275
Pro Ala Ala Ser Pro Glu Gln	Leu Ser Phe Arg Glu	Arg Gln Lys
1280	1285	1290
Tyr Phe Glu Leu Glu Val Arg	Val Pro Gln Ala Glu	Gly Pro Pro
1295	1300	1305
Lys Arg Val Ser Leu Val Gly	Ala Asp Asp Leu Arg	Lys Met Gln
1310	1315	1320
Glu Glu Glu Ala Arg Lys Leu	Gln Gln Lys Arg Ala	Gln Met Leu
1325	1330	1335
Arg Glu Ala Ala Glu Ala Gly	Ala Glu Ala Arg Leu	Ala Leu Asp
1340	1345	1350
Gly Glu Thr Leu Gly Glu Glu	Glu Gln Glu Asp Glu	Gln Pro Pro
1355	1360	1365
Trp Ala Ser Pro Ser Pro Thr	Ser Arg Gln Ser Pro	Ala Ser Pro
1370	1375	1380
Pro Pro Leu Gly Gly Gly Ala	Pro Val Arg Thr Ala	Lys Ala Glu
1385	1390	1395
Arg Arg His Gln Glu Arg Leu	Arg Val Gln Ser Pro	Glu Pro Pro
1400	1405	1410
Ala Pro Glu Arg Ala Leu Ser	Pro Ala Glu Leu Arg	Ala Leu Glu
1415	1420	1425
Ala Glu Lys Arg Ala Leu Trp	Arg Ala Ala Arg Met	Lys Ser Leu
1430	1435	1440
Glu Gln Asp Ala Leu Arg Ala	Gln Met Val Leu Ser	Arg Ser Gln
1445	1450	1455
Glu Gly Arg Gly Thr Arg Gly	Pro Leu Glu Arg Leu	Ala Glu Ala
1460	1465	1470
Pro Ser Pro Ala Pro Thr Pro	Ser Pro Thr Pro Val	Glu Asp Leu
1475	1480	1485
Gly Pro Gln Thr Ser Thr Ser	Pro Gly Arg Leu Ser	Pro Asp Phe
1490	1495	1500
Ala Glu Glu Leu Arg Ser Leu	Glu Pro Ser Pro Ser	Pro Gly Pro
1505	1510	1515
Gln Arg Arg Met Glu Lys Trp	Leu Trp Cys Phe Trp	Ala Gly Pro
1520	1525	1530
His Pro Ala Leu Trp Ala Leu	Lys Met Trp His Cys	Ala Ala Ala
1535	1540	1545
Ala Ala Pro		
1550		

<210> 123
 <211> 1371
 <212> PRT

<213> Homo sapiens

<400> 123

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Met Thr Thr Lys Arg Ser Leu Phe Val Arg Leu Val Pro Cys Arg Cys
1          5          10          15

Leu Arg Gly Glu Glu Glu Thr Val Thr Thr Leu Asp Tyr Ser His Cys
20          25          30

Ser Leu Glu Gln Val Pro Lys Glu Ile Phe Thr Phe Glu Lys Thr Leu
35          40          45

Glu Glu Leu Tyr Leu Asp Ala Asn Gln Ile Glu Glu Leu Pro Lys Gln
50          55          60

Leu Phe Asn Cys Gln Ser Leu His Lys Leu Ser Leu Pro Asp Asn Asp
65          70          75          80

Leu Thr Thr Leu Pro Ala Ser Ile Ala Asn Leu Ile Asn Leu Arg Glu
85          90          95

Leu Asp Val Ser Lys Asn Gly Ile Gln Glu Phe Pro Glu Asn Ile Lys
100         105         110

Asn Cys Lys Val Leu Thr Ile Val Glu Ala Ser Val Asn Pro Ile Ser
115         120         125

Lys Leu Pro Asp Gly Phe Ser Gln Leu Leu Asn Leu Thr Gln Leu Tyr
130         135         140

Leu Asn Asp Ala Phe Leu Glu Phe Leu Pro Ala Asn Phe Gly Arg Leu
145         150         155         160

Thr Lys Leu Gln Ile Leu Glu Leu Arg Glu Asn Gln Leu Lys Met Leu
165         170         175

Pro Lys Thr Met Asn Arg Leu Thr Gln Leu Glu Arg Leu Asp Leu Gly
180         185         190

Ser Asn Glu Phe Thr Glu Val Pro Glu Val Leu Glu Gln Leu Ser Gly
195         200         205

Leu Lys Glu Phe Trp Met Asp Ala Asn Arg Leu Thr Phe Ile Pro Gly
210         215         220

Phe Ile Gly Ser Leu Lys Gln Leu Thr Tyr Leu Asp Val Ser Lys Asn
225         230         235         240

Asn Ile Glu Met Val Glu Glu Gly Ile Ser Thr Cys Glu Asn Leu Gln
245         250         255

Asp Leu Leu Leu Ser Ser Asn Ser Leu Gln Gln Leu Pro Glu Thr Ile
260         265         270

Gly Ser Leu Lys Asn Ile Thr Thr Leu Lys Ile Asp Glu Asn Gln Leu
275         280         285

Met Tyr Leu Pro Asp Ser Ile Gly Gly Leu Ile Ser Val Glu Glu Leu
290         295         300

Asp Cys Ser Phe Asn Glu Val Glu Ala Leu Pro Ser Ser Ile Gly Gln
305         310         315         320

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Leu Thr Asn Leu Arg Thr Phe Ala Ala Asp His Asn Tyr Leu Gln Gln
 325 330 335
 Leu Pro Pro Glu Ile Gly Ser Trp Lys Asn Ile Thr Val Leu Phe Leu
 340 345 350
 His Ser Asn Lys Leu Glu Thr Leu Pro Glu Glu Met Gly Asp Met Gln
 355 360 365
 Lys Leu Lys Val Ile Asn Leu Ser Asp Asn Arg Leu Lys Asn Leu Pro
 370 375 380
 Phe Ser Phe Thr Lys Leu Gln Gln Leu Thr Ala Met Trp Leu Ser Asp
 385 390 395 400
 Asn Gln Ser Lys Pro Leu Ile Pro Leu Gln Lys Glu Thr Asp Ser Glu
 405 410 415
 Thr Gln Lys Met Val Leu Thr Asn Tyr Met Phe Pro Gln Gln Pro Arg
 420 425 430
 Thr Glu Asp Val Met Phe Ile Ser Asp Asn Glu Ser Phe Asn Pro Ser
 435 440 445
 Leu Trp Glu Glu Gln Arg Lys Gln Arg Ala Gln Val Ala Phe Glu Cys
 450 455 460
 Asp Glu Asp Lys Asp Glu Arg Glu Ala Pro Pro Arg Glu Gly Asn Leu
 465 470 475 480
 Lys Arg Tyr Pro Thr Pro Tyr Pro Asp Glu Leu Lys Asn Met Val Lys
 485 490 495
 Thr Val Gln Thr Ile Val His Arg Leu Lys Asp Glu Glu Thr Asn Glu
 500 505 510
 Asp Ser Gly Arg Asp Leu Lys Pro His Glu Asp Gln Gln Asp Ile Asn
 515 520 525
 Lys Asp Val Gly Val Lys Thr Ser Glu Ser Thr Thr Thr Val Lys Ser
 530 535 540
 Lys Val Asp Glu Arg Glu Lys Tyr Met Ile Gly Asn Ser Val Gln Lys
 545 550 555 560
 Ile Ser Glu Pro Glu Ala Glu Ile Ser Pro Gly Ser Leu Pro Val Thr
 565 570 575
 Ala Asn Met Lys Ala Ser Glu Asn Leu Lys His Ile Val Asn His Asp
 580 585 590
 Asp Val Phe Glu Glu Ser Glu Glu Leu Ser Ser Asp Glu Glu Met Lys
 595 600 605
 Met Ala Glu Met Arg Pro Pro Leu Ile Glu Thr Ser Ile Asn Gln Pro
 610 615 620
 Lys Val Val Ala Leu Ser Asn Asn Lys Lys Asp Asp Thr Lys Glu Thr
 625 630 635 640
 Asp Ser Leu Ser Asp Glu Val Thr His Asn Ser Asn Gln Asn Asn Ser

645					650					655					
Asn	Cys	Ser	Ser	Pro	Ser	Arg	Met	Ser	Asp	Ser	Val	Ser	Leu	Asn	Thr
			660					665					670		
Asp	Ser	Ser	Gln	Asp	Thr	Ser	Leu	Cys	Ser	Pro	Val	Lys	Gln	Thr	His
			675				680					685			
Ile	Asp	Ile	Asn	Ser	Lys	Ile	Arg	Gln	Glu	Asp	Glu	Asn	Phe	Asn	Ser
			690				695					700			
Leu	Leu	Gln	Asn	Gly	Asp	Ile	Leu	Asn	Ser	Ser	Thr	Glu	Glu	Lys	Phe
				710								715			720
Lys	Ala	His	Asp	Lys	Lys	Asp	Phe	Asn	Leu	Pro	Glu	Tyr	Asp	Leu	Asn
				725					730					735	
Val	Glu	Glu	Arg	Leu	Val	Leu	Ile	Glu	Lys	Ser	Val	Asp	Ser	Thr	Ala
				740				745						750	
Thr	Ala	Asp	Asp	Thr	His	Lys	Leu	Asp	His	Ile	Asn	Met	Asn	Leu	Asn
				755				760					765		
Lys	Leu	Ile	Thr	Asn	Asp	Thr	Phe	Gln	Pro	Glu	Ile	Met	Glu	Arg	Ser
				770				775				780			
Lys	Thr	Gln	Asp	Ile	Val	Leu	Gly	Thr	Ser	Phe	Leu	Ser	Ile	Asn	Ser
				785					790			795			800
Lys	Glu	Glu	Thr	Glu	His	Leu	Glu	Asn	Gly	Asn	Lys	Tyr	Pro	Asn	Leu
				805					810					815	
Glu	Ser	Val	Asn	Lys	Val	Asn	Gly	His	Ser	Glu	Glu	Thr	Ser	Gln	Ser
				820				825						830	
Pro	Asn	Arg	Thr	Glu	Pro	His	Asp	Ser	Asp	Cys	Ser	Val	Asp	Leu	Gly
				835				840					845		
Ile	Ser	Lys	Ser	Thr	Glu	Asp	Leu	Ser	Pro	Gln	Lys	Ser	Gly	Pro	Val
				850				855					860		
Gly	Ser	Val	Val	Lys	Ser	His	Ser	Ile	Thr	Asn	Met	Glu	Ile	Gly	Gly
				865					870			875			880
Leu	Lys	Ile	Tyr	Asp	Ile	Leu	Ser	Asp	Asn	Gly	Pro	Gln	Gln	Pro	Ser
				885					890					895	
Thr	Thr	Val	Lys	Ile	Thr	Ser	Ala	Val	Asp	Gly	Lys	Asn	Ile	Val	Arg
				900				905					910		
Ser	Lys	Ser	Ala	Thr	Leu	Leu	Tyr	Asp	Gln	Pro	Leu	Gln	Val	Phe	Thr
				915				920					925		
Gly	Ser	Ser	Ser	Ser	Ser	Asp	Leu	Ile	Ser	Gly	Thr	Lys	Ala	Ile	Phe
				930				935					940		
Lys	Phe	Asp	Ser	Asn	His	Asn	Pro	Glu	Glu	Pro	Asn	Ile	Ile	Arg	Gly
				945					950			955			960
Pro	Thr	Ser	Gly	Pro	Gln	Ser	Ala	Pro	Gln	Ile	Tyr	Gly	Pro	Pro	Gln
				965					970					975	

Tyr Asn Ile Gln Tyr Ser Ser Ser Ala Ala Val Lys Asp Thr Leu Trp
 980 985 990
 His Ser Lys Gln Asn Pro Gln Ile Asp His Ala Ser Phe Pro Pro Gln
 995 1000 1005
 Leu Leu Pro Arg Ser Glu Ser Thr Glu Asn Gln Ser Tyr Ala Lys
 1010 1015 1020
 His Ser Ala Asn Met Asn Phe Ser Asn His Asn Asn Val Arg Ala
 1025 1030 1035
 Asn Thr Ala Tyr His Leu His Gln Arg Leu Gly Pro Ala Arg His
 1040 1045 1050
 Gly Glu Met Trp Ala Ile Ser Pro Asn Asp Arg Leu Ile Pro Ala
 1055 1060 1065
 Val Thr Arg Ser Thr Ile Gln Arg Gln Ser Ser Val Ser Ser Thr
 1070 1075 1080
 Ala Ser Val Asn Leu Gly Asp Pro Gly Ser Thr Arg Arg Ala Gln
 1085 1090 1095
 Ile Pro Glu Gly Asp Tyr Leu Ser Tyr Arg Glu Phe His Ser Ala
 1100 1105 1110
 Gly Arg Thr Pro Pro Met Met Pro Gly Ser Gln Arg Pro Leu Ser
 1115 1120 1125
 Ala Arg Thr Tyr Ser Ile Asp Gly Pro Asn Ala Ser Arg Pro Gln
 1130 1135 1140
 Ser Ala Arg Pro Ser Ile Asn Glu Ile Pro Glu Arg Thr Met Ser
 1145 1150 1155
 Val Ser Asp Phe Asn Tyr Ser Arg Thr Ser Pro Ser Lys Arg Pro
 1160 1165 1170
 Asn Ala Arg Val Gly Ser Glu His Ser Leu Leu Asp Pro Pro Gly
 1175 1180 1185
 Lys Ser Lys Val Pro Arg Asp Trp Arg Glu Gln Val Leu Arg His
 1190 1195 1200
 Ile Glu Ala Lys Lys Leu Glu Lys Met Pro Leu Ser Asn Gly Gln
 1205 1210 1215
 Met Gly Gln Pro Leu Arg Pro Gln Ala Asn Tyr Ser Gln Ile His
 1220 1225 1230
 His Pro Pro Gln Ala Ser Val Ala Arg His Pro Ser Arg Glu Gln
 1235 1240 1245
 Leu Ile Asp Tyr Leu Met Leu Lys Val Ala His Gln Pro Pro Tyr
 1250 1255 1260
 Thr Gln Pro His Cys Ser Pro Arg Gln Gly His Glu Leu Ala Lys
 1265 1270 1275
 Gln Glu Ile Arg Val Arg Val Glu Lys Asp Pro Glu Leu Gly Phe
 1280 1285 1290

Ser Ile Ser Gly Gly Val Gly Gly Arg Gly Asn Pro Phe Arg Pro
 1295 1300 1305
 Asp Asp Asp Gly Ile Phe Val Thr Arg Val Gln Pro Glu Gly Pro
 1310 1315 1320
 Ala Ser Lys Leu Leu Gln Pro Gly Asp Lys Ile Ile Gln Ala Asn
 1325 1330 1335
 Gly Tyr Ser Phe Ile Asn Ile Glu His Gly Gln Ala Val Ser Leu
 1340 1345 1350
 Leu Lys Thr Phe Gln Asn Thr Val Glu Leu Ile Ile Val Arg Glu
 1355 1360 1365
 Val Ser Ser
 1370
 <210> 124
 <211> 1271
 <212> PRT
 <213> Homo sapiens
 <400> 124
 Arg Pro Thr Arg Pro Glu Phe Pro Glu Asn Ile Lys Asn Cys Lys Val
 1 5 10 15
 Leu Thr Ile Val Glu Ala Ser Val Asn Pro Ile Ser Lys Leu Pro Asp
 20 25 30
 Gly Phe Ser Gln Leu Leu Asn Leu Thr Gln Leu Tyr Leu Asn Asp Ala
 35 40 45
 Phe Leu Glu Phe Leu Pro Ala Asn Phe Gly Arg Leu Thr Lys Leu Gln
 50 55 60
 Ile Leu Glu Leu Arg Glu Asn Gln Leu Lys Met Leu Pro Lys Thr Met
 65 70 75 80
 Asn Arg Leu Thr Gln Leu Glu Arg Leu Asp Leu Gly Ser Asn Glu Phe
 85 90 95
 Thr Glu Val Pro Glu Val Leu Glu Gln Leu Ser Gly Leu Lys Glu Phe
 100 105 110
 Trp Met Asp Ala Asn Arg Leu Thr Phe Ile Pro Gly Phe Ile Gly Ser
 115 120 125
 Leu Lys Gln Leu Thr Tyr Leu Asp Val Ser Lys Asn Asn Ile Glu Met
 130 135 140
 Val Glu Glu Gly Ile Ser Thr Cys Glu Asn Leu Gln Asp Leu Leu Leu
 145 150 155 160
 Ser Ser Asn Ser Leu Gln Gln Leu Pro Glu Thr Ile Gly Ser Leu Lys
 165 170 175
 Asn Ile Thr Thr Leu Lys Ile Asp Glu Asn Gln Leu Met Tyr Leu Pro
 180 185 190
 Asp Ser Ile Gly Gly Leu Ile Ser Val Glu Glu Leu Asp Cys Ser Phe

195	200	205
Asn Glu Val Glu Ala Leu Pro Ser Ser Ile Gly Gln Leu Thr Asn Leu 210 215 220		
Arg Thr Phe Ala Ala Asp His Asn Tyr Leu Gln Gln Leu Pro Pro Glu 225 230 240		
Ile Gly Ser Trp Lys Asn Ile Thr Val Leu Phe Leu His Ser Asn Lys 245 250 255		
Leu Glu Thr Leu Pro Glu Glu Met Gly Asp Met Gln Lys Leu Lys Val 260 265 270		
Ile Asn Leu Ser Asp Asn Arg Leu Lys Asn Leu Pro Phe Ser Phe Thr 275 280 285		
Lys Leu Gln Gln Leu Thr Ala Met Trp Leu Ser Asp Asn Gln Ser Lys 290 295 300		
Pro Leu Ile Pro Leu Gln Lys Glu Thr Asp Ser Glu Thr Gln Lys Met 305 310 315 320		
Val Leu Thr Asn Tyr Met Phe Pro Gln Gln Pro Arg Thr Glu Asp Val 325 330 335		
Met Phe Ile Ser Asp Asn Glu Ser Phe Asn Pro Ser Leu Trp Glu Glu 340 345 350		
Gln Arg Lys Gln Arg Ala Gln Val Ala Phe Glu Cys Asp Glu Asp Lys 355 360 365		
Asp Glu Arg Glu Ala Pro Pro Arg Glu Gly Asn Leu Lys Arg Tyr Pro 370 375 380		
Thr Pro Tyr Pro Asp Glu Leu Lys Asn Met Val Lys Thr Val Gln Thr 385 390 395 400		
Ile Val His Arg Leu Lys Asp Glu Glu Thr Asn Glu Asp Ser Gly Arg 405 410 415		
Asp Leu Lys Pro His Glu Asp Gln Gln Asp Ile Asn Lys Asp Val Gly 420 425 430		
Val Lys Thr Ser Glu Ser Thr Thr Thr Val Lys Ser Lys Val Asp Glu 435 440 445		
Arg Glu Lys Tyr Met Ile Gly Asn Ser Val Gln Lys Ile Ser Glu Pro 450 455 460		
Glu Ala Glu Ile Ser Pro Gly Ser Leu Pro Val Thr Ala Asn Met Lys 465 470 475 480		
Ala Ser Glu Asn Leu Lys His Ile Val Asn His Asp Asp Val Phe Glu 485 490 495		
Glu Ser Glu Glu Leu Ser Ser Asp Glu Glu Met Lys Met Ala Glu Met 500 505 510		
Arg Pro Pro Leu Ile Glu Thr Ser Ile Asn Gln Pro Lys Val Val Ala 515 520 525		

Leu Ser Asn Asn Lys Lys Asp Asp Thr Lys Glu Thr Asp Ser Leu Ser
 530 535 540
 Asp Glu Val Thr His Asn Ser Asn Gln Asn Asn Ser Asn Cys Ser Ser
 545 550 555 560
 Pro Ser Arg Met Ser Asp Ser Val Ser Leu Asn Thr Asp Ser Ser Gln
 565 570 575
 Asp Thr Ser Leu Cys Ser Pro Val Lys Gln Thr His Ile Asp Ile Asn
 580 585 590
 Ser Lys Ile Arg Gln Glu Asp Glu Asn Phe Asn Ser Leu Leu Gln Asn
 595 600 605
 Gly Asp Ile Leu Asn Ser Ser Thr Glu Glu Lys Phe Lys Ala His Asp
 610 615 620
 Lys Lys Asp Phe Asn Leu Pro Glu Tyr Asp Leu Asn Val Glu Glu Arg
 625 630 635 640
 Leu Val Leu Ile Glu Lys Ser Val Asp Ser Thr Ala Thr Ala Asp Asp
 645 650 655
 Thr His Lys Leu Asp His Ile Asn Met Asn Leu Asn Lys Leu Ile Thr
 660 665 670
 Asn Asp Thr Phe Gln Pro Glu Ile Met Glu Arg Ser Lys Thr Gln Asp
 675 680 685
 Ile Val Leu Gly Thr Ser Phe Leu Ser Ile Asn Ser Lys Glu Glu Thr
 690 695 700
 Glu His Leu Glu Asn Gly Asn Lys Tyr Pro Asn Leu Glu Ser Val Asn
 705 710 715 720
 Lys Val Asn Gly His Ser Glu Glu Thr Ser Gln Ser Pro Asn Arg Thr
 725 730 735
 Glu Pro His Asp Ser Asp Cys Ser Val Asp Leu Gly Ile Ser Lys Ser
 740 745 750
 Thr Glu Asp Leu Ser Pro Gln Lys Ser Gly Pro Val Gly Ser Val Val
 755 760 765
 Lys Ser His Ser Ile Thr Asn Met Glu Ile Gly Gly Leu Lys Ile Tyr
 770 775 780
 Asp Ile Leu Ser Asp Asn Gly Pro Gln Gln Pro Ser Thr Thr Val Lys
 785 790 795 800
 Ile Thr Ser Ala Val Asp Gly Lys Asn Ile Val Arg Ser Lys Ser Ala
 805 810 815
 Thr Leu Leu Tyr Asp Gln Pro Leu Gln Val Phe Thr Gly Ser Ser Ser
 820 825 830
 Ser Ser Asp Leu Ile Ser Gly Thr Lys Ala Ile Phe Lys Phe Asp Ser
 835 840 845
 Asn His Asn Pro Glu Glu Pro Asn Ile Ile Arg Gly Pro Thr Ser Gly
 850 855 860

Pro Gln Ser Ala Pro Gln Ile Tyr Gly Pro Pro Gln Tyr Asn Ile Gln
 865 870 875 880
 Tyr Ser Ser Ser Ala Ala Val Lys Asp Thr Leu Trp His Ser Lys Gln
 885 890 895
 Asn Pro Gln Ile Asp His Ala Ser Phe Pro Pro Gln Leu Leu Pro Arg
 900 905 910
 Ser Glu Ser Thr Glu Asn Gln Ser Tyr Ala Lys His Ser Ala Asn Met
 915 920 925
 Asn Phe Ser Asn His Asn Asn Val Arg Ala Asn Thr Ala Tyr His Leu
 930 935 940
 His Gln Arg Leu Gly Pro Ala Arg His Gly Glu Met Trp Ala Ile Ser
 945 950 955 960
 Pro Asn Asp Arg Leu Ile Pro Ala Val Thr Arg Ser Thr Ile Gln Arg
 965 970 975
 Gln Ser Ser Val Ser Ser Thr Ala Ser Val Asn Leu Gly Asp Pro Gly
 980 985 990
 Ser Thr Arg Arg Ala Gln Ile Pro Glu Gly Asp Tyr Leu Ser Tyr Arg
 995 1000 1005
 Glu Phe His Ser Ala Gly Arg Thr Pro Pro Met Met Pro Gly Ser
 1010 1015 1020
 Gln Arg Pro Leu Ser Ala Arg Thr Tyr Ser Ile Asp Gly Pro Asn
 1025 1030 1035
 Ala Ser Arg Pro Gln Ser Ala Arg Pro Ser Ile Asn Glu Ile Pro
 1040 1045 1050
 Glu Arg Thr Met Ser Val Ser Asp Phe Asn Tyr Ser Arg Thr Ser
 1055 1060 1065
 Pro Ser Lys Arg Pro Asn Ala Arg Val Gly Ser Glu His Ser Leu
 1070 1075 1080
 Leu Asp Pro Pro Gly Lys Ser Lys Val Pro Arg Asp Trp Arg Glu
 1085 1090 1095
 Gln Val Leu Arg His Ile Glu Ala Lys Lys Leu Glu Lys Met Pro
 1100 1105 1110
 Leu Ser Asn Gly Gln Met Gly Gln Pro Leu Arg Pro Gln Ala Asn
 1115 1120 1125
 Tyr Ser Gln Ile His His Pro Pro Gln Ala Ser Val Ala Arg His
 1130 1135 1140
 Pro Ser Arg Glu Gln Leu Ile Asp Tyr Leu Met Leu Lys Val Ala
 1145 1150 1155
 His Gln Pro Pro Tyr Thr Gln Pro His Cys Ser Pro Arg Gln Gly
 1160 1165 1170
 His Glu Leu Ala Lys Gln Glu Ile Arg Val Arg Val Glu Lys Asp

1175	1180	1185
Pro Glu Leu Gly Phe Ser Ile Ser Gly Gly Val Gly Gly Arg Gly		
1190	1195	1200
Asn Pro Phe Arg Pro Asp Asp Asp Gly Ile Phe Val Thr Arg Val		
1205	1210	1215
Gln Pro Glu Gly Pro Ala Ser Lys Leu Leu Gln Pro Gly Asp Lys		
1220	1225	1230
Ile Ile Gln Ala Asn Gly Tyr Ser Phe Ile Asn Ile Glu His Gly		
1235	1240	1245
Gln Ala Val Ser Leu Leu Lys Thr Phe Gln Asn Thr Val Glu Leu		
1250	1255	1260
Ile Ile Val Arg Glu Val Ser Ser		
1265	1270	

<210> 125
 <211> 185
 <212> PRT
 <213> Homo sapiens

<400> 125
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 20 25 30
 Leu Ser Ser Cys Lys Pro Gly Phe Gly Val Asp Gln Leu Arg Asp Asp
 35 40 45
 Asn Leu Glu Thr Tyr Trp Gln Ser Asp Gly Ser Gln Pro His Leu Val
 50 55 60
 Asn Ile Gln Phe Arg Arg Lys Thr Thr Val Lys Thr Leu Cys Ile Tyr
 65 70 75 80
 Ala Asp Tyr Lys Ser Asp Glu Ser Tyr Thr Pro Ser Lys Ile Ser Val
 85 90 95
 Arg Val Gly Asn Asn Phe His Asn Leu Gln Glu Ile Arg Gln Leu Glu
 100 105 110
 Leu Val Glu Pro Ser Gly Trp Ile His Val Pro Leu Thr Asp Asn His
 115 120 125
 Lys Lys Pro Thr Arg Thr Phe Met Ile Gln Ile Ala Val Leu Ala Asn
 130 135 140
 His Gln Asn Gly Arg Asp Thr His Met Arg Gln Ile Lys Ile Tyr Thr
 145 150 155 160
 Pro Val Glu Glu Ser Ser Ile Gly Lys Phe Pro Arg Cys Thr Thr Ile
 165 170 175
 Asp Phe Met Met Tyr Arg Ser Ile Arg
 180 185

<210> 126
 <211> 796
 <212> PRT
 <213> Homo sapiens

<400> 126
 Ser Leu Met Ser Gly Asp Ile Gly Asp Tyr Lys Leu Tyr Asp Val Glu
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 Thr Lys Tyr Gly Leu Leu Gln Val Ser Glu Gly Leu Ser Phe Leu His
 20 25 30
 Ser Ser Val Lys Met Val His Gly Asn Ile Thr Pro Glu Asn Ile Ile
 35 40 45
 Leu Asn Lys Ser Gly Ala Trp Lys Ile Met Gly Phe Asp Phe Cys Val
 50 55 60
 Ser Ser Thr Asn Pro Ser Glu Gln Glu Pro Lys Phe Pro Cys Lys Glu
 65 70 75 80
 Trp Asp Pro Asn Leu Pro Ser Leu Cys Leu Pro Asn Pro Glu Tyr Leu
 85 90 95
 Ala Pro Glu Tyr Ile Leu Ser Val Ser Cys Glu Thr Ala Ser Asp Met
 100 105 110
 Tyr Ser Leu Gly Thr Val Met Tyr Ala Val Phe Asn Lys Gly Lys Pro
 115 120 125
 Ile Phe Glu Val Asn Lys Gln Asp Ile Tyr Lys Ser Phe Ser Arg Gln
 130 135 140
 Leu Asp Gln Leu Ser Arg Leu Gly Ser Ser Ser Leu Thr Asn Ile Pro
 145 150 155 160
 Glu Glu Val Arg Glu His Val Lys Leu Leu Leu Asn Val Thr Pro Thr
 165 170 175
 Val Arg Pro Asp Ala Asp Gln Met Thr Lys Ile Pro Phe Phe Asp Asp
 180 185 190
 Val Gly Ala Val Thr Leu Gln Tyr Phe Asp Thr Leu Phe Gln Arg Asp
 195 200 205
 Asn Leu Gln Lys Ser Gln Phe Phe Lys Gly Leu Pro Lys Val Leu Pro
 210 215 220
 Lys Leu Pro Lys Arg Val Ile Val Gln Arg Ile Leu Pro Cys Leu Thr
 225 230 235 240
 Ser Glu Phe Val Asn Pro Asp Met Val Pro Phe Val Leu Pro Asn Val
 245 250 255
 Leu Leu Ile Ala Glu Glu Cys Thr Lys Glu Glu Tyr Val Lys Leu Ile
 260 265 270
 Leu Pro Glu Leu Gly Pro Val Phe Lys Gln Gln Glu Pro Ile Gln Ala
 275 280 285
 Ser Asn Met Ile Leu Leu Ile Phe Leu Gln Lys Met Asp Leu Leu Leu
 290 295 300

Thr Lys Thr Pro Pro Asp Glu Ile Lys Asn Ser Val Leu Pro Met Val
 305 310 315 320
 Tyr Arg Ala Leu Glu Ala Pro Ser Ile Gln Ile Gln Glu Leu Cys Leu
 325 330 335
 Asn Ile Ile Pro Thr Phe Ala Asn Leu Ile Asp Tyr Pro Ser Met Lys
 340 345 350
 Asn Ala Leu Ile Pro Arg Ile Lys Asn Ala Cys Leu Gln Thr Ser Ser
 355 360 365
 Leu Ala Val Arg Val Asn Ser Leu Val Cys Leu Gly Lys Ile Leu Glu
 370 375 380
 Tyr Leu Asp Lys Trp Phe Val Leu Asp Asp Ile Leu Pro Phe Leu Gln
 385 390 395 400
 Gln Ile Pro Ser Lys Glu Pro Ala Val Leu Met Gly Ile Leu Gly Ile
 405 410 415
 Tyr Lys Cys Thr Phe Thr His Lys Lys Leu Gly Ile Thr Lys Glu Gln
 420 425 430
 Leu Ala Gly Lys Val Leu Pro His Leu Ile Pro Leu Ser Ile Glu Asn
 435 440 445
 Asn Leu Asn Leu Asn Gln Phe Asn Ser Phe Ile Ser Val Ile Lys Glu
 450 455 460
 Met Leu Asn Arg Leu Glu Ser Glu His Lys Thr Lys Leu Glu Gln Leu
 465 470 475 480
 His Ile Met Gln Glu Gln Gln Lys Ser Leu Asp Ile Gly Asn Gln Met
 485 490 495
 Asn Val Ser Glu Glu Met Lys Val Thr Asn Ile Gly Asn Gln Gln Ile
 500 505 510
 Asp Lys Val Phe Asn Asn Ile Gly Ala Asp Leu Leu Thr Gly Ser Glu
 515 520 525
 Ser Glu Asn Lys Glu Asp Gly Leu Gln Asn Lys His Lys Arg Ala Ser
 530 535 540
 Leu Thr Leu Glu Glu Lys Gln Lys Leu Ala Lys Glu Gln Glu Gln Ala
 545 550 555 560
 Gln Lys Leu Lys Ser Gln Gln Pro Leu Lys Pro Gln Val His Thr Pro
 565 570 575
 Val Ala Thr Val Lys Gln Thr Lys Asp Leu Thr Asp Thr Leu Met Asp
 580 585 590
 Asn Met Ser Ser Leu Thr Ser Leu Ser Val Ser Thr Pro Lys Ser Ser
 595 600 605
 Ala Ser Ser Thr Phe Thr Ser Val Pro Ser Met Gly Ile Gly Met Met
 610 615 620
 Phe Ser Thr Pro Thr Asp Asn Thr Lys Arg Asn Leu Thr Asn Gly Leu

625	630	635	640
Asn Ala Asn Met Gly Phe Gln Thr Ser Gly Phe Asn Met Pro Val Asn			
645		650	655
Thr Asn Gln Asn Phe Tyr Ser Ser Pro Ser Thr Val Gly Val Thr Lys			
660		665	670
Met Thr Leu Gly Thr Pro Pro Thr Leu Pro Asn Phe Asn Ala Leu Ser			
675		680	685
Val Pro Pro Ala Gly Ala Lys Gln Thr Gln Gln Arg Pro Thr Asp Met			
690		695	700
Ser Ala Leu Asn Asn Leu Phe Gly Pro Gln Lys Pro Lys Val Ser Met			
705	710	715	720
Asn Gln Leu Ser Gln Gln Lys Pro Asn Gln Trp Leu Asn Gln Phe Val			
725		730	735
Pro Pro Gln Gly Ser Pro Thr Met Gly Ser Ser Val Met Gly Thr Gln			
740		745	750
Met Asn Val Ile Gly Gln Ser Ala Phe Gly Met Gln Gly Asn Pro Phe			
755	760		765
Phe Asn Pro Gln Asn Phe Ala Gln Pro Pro Thr Thr Met Thr Asn Ser			
770	775		780
Ser Ser Ala Ser Asn Asp Leu Lys Asp Leu Phe Gly			
785	790		795
<210> 127			
<211> 735			
<212> PRT			
<213> Homo sapiens			
<400> 127			
Met Gly Phe Asp Phe Cys Val Ser Ser Thr Asn Pro Ser Glu Gln Glu			
1	5	10	15
Pro Lys Phe Pro Cys Lys Glu Trp Asp Pro Asn Leu Pro Ser Leu Cys			
20	25		30
Leu Pro Asn Pro Glu Tyr Leu Ala Pro Glu Tyr Ile Leu Ser Val Ser			
35	40		45
Cys Glu Thr Ala Ser Asp Met Tyr Ser Leu Gly Thr Val Met Tyr Ala			
50	55	60	
Val Phe Asn Lys Gly Lys Pro Ile Phe Glu Val Asn Lys Gln Asp Ile			
65	70	75	80
Tyr Lys Ser Phe Ser Arg Gln Leu Asp Gln Leu Ser Arg Leu Gly Ser			
85	90		95
Ser Ser Leu Thr Asn Ile Pro Glu Glu Val Arg Glu His Val Lys Leu			
100	105		110
Leu Leu Asn Val Thr Pro Thr Val Arg Pro Asp Ala Asp Gln Met Thr			
115	120		125

Lys Ile Pro Phe Phe Asp Asp Val Gly Ala Val Thr Leu Gln Tyr Phe
 130 135 140
 Asp Thr Leu Phe Gln Arg Asp Asn Leu Gln Lys Ser Gln Phe Phe Lys
 145 150 155 160
 Gly Leu Leu Lys Val Leu Pro Lys Leu Pro Lys Arg Val Ile Val Gln
 165 170 175
 Arg Ile Leu Pro Cys Leu Thr Ser Glu Phe Val Asn Pro Asp Met Val
 180 185 190
 Pro Phe Val Leu Pro Asn Val Leu Leu Ile Ala Glu Glu Cys Thr Lys
 195 200 205
 Glu Glu Tyr Val Lys Leu Ile Leu Pro Glu Leu Gly Pro Val Phe Lys
 210 215 220
 Gln Gln Glu Pro Ile Gln Ile Leu Leu Ile Phe Leu Gln Lys Met Asp
 225 230 235 240
 Leu Leu Leu Thr Arg Thr Pro Pro Asp Glu Ile Lys Asn Ser Val Leu
 245 250 255
 Pro Met Val Tyr Arg Ala Leu Glu Ala Pro Ser Ile Gln Ile Gln Glu
 260 265 270
 Leu Cys Leu Asn Ile Ile Pro Thr Phe Ala Asn Leu Ile Asp Tyr Pro
 275 280 285
 Ser Met Lys Asn Ala Leu Ile Pro Arg Ile Lys Asn Ala Cys Leu Gln
 290 295 300
 Thr Ser Ser Leu Ala Val Arg Val Asn Ser Leu Val Cys Leu Gly Lys
 305 310 315 320
 Ile Leu Glu Tyr Leu Asp Lys Trp Phe Val Leu Asp Asp Ile Leu Pro
 325 330 335
 Phe Leu Gln Gln Ile Pro Ser Lys Glu Pro Ala Val Leu Met Gly Ile
 340 345 350
 Leu Gly Ile Tyr Lys Cys Thr Phe Thr His Lys Lys Leu Gly Ile Thr
 355 360 365
 Lys Glu Gln Leu Ala Gly Lys Val Leu Pro His Leu Ile Pro Leu Ser
 370 375 380
 Ile Glu Asn Asn Leu Asn Leu Asn Gln Phe Asn Ser Phe Ile Ser Val
 385 390 395 400
 Ile Lys Glu Met Leu Asn Arg Leu Glu Ser Glu His Lys Thr Lys Leu
 405 410 415
 Glu Gln Leu His Ile Met Gln Glu Gln Gln Lys Ser Leu Asp Ile Gly
 420 425 430
 Asn Arg Met Asn Val Ser Glu Glu Met Lys Val Thr Asn Ile Gly Asn
 435 440 445
 Gln Gln Ile Asp Lys Val Phe Asn Asn Ile Gly Ala Asp Leu Leu Thr
 450 455 460

Gly Ser Glu Ser Glu Asn Lys Glu Asp Gly Leu Gln Asn Lys His Lys
 465 470 475 480
 Arg Ala Ser Leu Thr Leu Glu Glu Lys Gln Lys Leu Ala Lys Glu Gln
 485 490 495
 Glu Gln Ala Gln Lys Leu Lys Ser Gln Gln Pro Leu Lys Pro Gln Val
 500 505 510
 His Thr Pro Val Ala Thr Val Lys Gln Thr Lys Asp Leu Thr Asp Thr
 515 520 525
 Leu Met Asp Asn Met Ser Ser Leu Thr Ser Leu Ser Val Ser Thr Pro
 530 535 540
 Lys Ser Ser Ala Ser Ser Thr Phe Thr Ser Val Pro Ser Met Gly Ile
 545 550 555 560
 Gly Met Met Phe Ser Thr Pro Thr Asp Asn Thr Lys Arg Asn Leu Thr
 565 570 575
 Asn Gly Leu Asn Ala Asn Met Gly Phe Gln Thr Ser Gly Phe Asn Met
 580 585 590
 Pro Val Asn Thr Asn Gln Asn Phe Tyr Ser Ser Pro Ser Thr Val Gly
 595 600 605
 Val Thr Lys Met Thr Leu Gly Thr Pro Pro Thr Leu Pro Asn Phe Asn
 610 615 620
 Ala Leu Ser Val Pro Pro Ala Gly Ala Lys Gln Thr Gln Gln Arg Pro
 625 630 635 640
 Thr Asp Met Ser Ala Leu Asn Asn Leu Phe Gly Pro Gln Lys Pro Lys
 645 650 655
 Val Ser Met Asn Gln Leu Ser Gln Gln Lys Pro Asn Gln Trp Leu Asn
 660 665 670
 Gln Phe Val Pro Pro Gln Gly Ser Pro Thr Met Gly Ser Ser Val Met
 675 680 685
 Gly Thr Gln Met Asn Val Ile Gly Gln Ser Ala Phe Gly Met Gln Gly
 690 695 700
 Asn Pro Phe Phe Asn Pro Gln Asn Phe Ala Gln Pro Pro Thr Thr Met
 705 710 715 720
 Thr Asn Ser Ser Ser Ala Ser Asn Asp Leu Lys Asp Leu Phe Gly
 725 730 735
 <210> 128
 <211> 470
 <212> PRT
 <213> Homo sapiens
 <400> 128
 Met Pro Gly Phe Asp Tyr Lys Phe Leu Glu Lys Pro Lys Arg Arg Leu
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 Leu Cys Pro Leu Cys Gly Lys Pro Met Arg Glu Pro Val Gln Val Ser

20										25										30																																		
Thr	Cys	Gly	His	Arg	Phe	Cys	Asp	Thr	Cys	Leu	Gln	Glu	Phe	Leu	Ser																																							
		35					40					45																																										
Glu	Gly	Val	Phe	Lys	Cys	Pro	Glu	Asp	Gln	Leu	Pro	Leu	Asp	Tyr	Ala																																							
		50				55					60																																											
Lys	Ile	Tyr	Pro	Asp	Pro	Glu	Leu	Glu	Val	Gln	Val	Leu	Gly	Leu	Pro																																							
		65			70					75					80																																							
Ile	Arg	Cys	Ile	His	Ser	Glu	Glu	Gly	Cys	Arg	Trp	Ser	Gly	Pro	Leu																																							
				85				90						95																																								
Arg	His	Leu	Gln	Gly	His	Leu	Asn	Thr	Cys	Ser	Phe	Asn	Val	Ile	Pro																																							
			100					105					110																																									
Cys	Pro	Asn	Arg	Cys	Pro	Met	Lys	Leu	Ser	Arg	Arg	Asp	Leu	Pro	Ala																																							
		115					120					125																																										
His	Leu	Gln	His	Asp	Cys	Pro	Lys	Arg	Arg	Leu	Lys	Cys	Glu	Phe	Cys																																							
		130				135					140																																											
Gly	Cys	Asp	Phe	Ser	Gly	Glu	Ala	Tyr	Glu	Ser	His	Glu	Gly	Met	Cys																																							
		145			150				155					160																																								
Pro	Gln	Glu	Ser	Val	Tyr	Cys	Glu	Asn	Lys	Cys	Gly	Ala	Arg	Met	Met																																							
				165				170						175																																								
Arg	Gly	Leu	Leu	Ala	Gln	His	Ala	Thr	Ser	Glu	Cys	Pro	Lys	Arg	Thr																																							
			180					185					190																																									
Gln	Pro	Cys	Thr	Tyr	Cys	Thr	Lys	Glu	Phe	Val	Phe	Asp	Thr	Ile	Gln																																							
		195					200					205																																										
Ser	His	Gln	Tyr	Gln	Cys	Pro	Arg	Leu	Pro	Val	Ala	Cys	Pro	Asn	Gln																																							
		210				215					220																																											
Cys	Gly	Val	Gly	Thr	Val	Ala	Arg	Glu	Asp	Leu	Pro	Gly	His	Leu	Lys																																							
		225			230				235					240																																								
Asp	Ser	Cys	Asn	Thr	Ala	Leu	Val	Leu	Cys	Pro	Phe	Lys	Asp	Ser	Gly																																							
				245				250					255																																									
Cys	Lys	His	Arg	Cys	Pro	Lys	Leu	Ala	Met	Ala	Arg	His	Val	Glu	Glu																																							
			260				265					270																																										
Ser	Val	Lys	Pro	His	Leu	Ala	Met	Met	Cys	Ala	Leu	Val	Ser	Arg	Gln																																							
		275				280					285																																											
Arg	Gln	Glu	Leu	Gln	Glu	Leu	Arg	Arg	Glu	Leu	Glu	Glu	Leu	Ser	Val																																							
		290				295					300																																											
Gly	Ser	Asp	Gly	Val	Leu	Ile	Trp	Lys	Ile	Gly	Ser	Tyr	Gly	Arg	Arg																																							
		305			310				315					320																																								
Leu	Gln	Glu	Ala	Lys	Ala	Lys	Pro	Asn	Leu	Glu	Cys	Phe	Ser	Pro	Ala																																							
				325				330						335																																								
Phe	Tyr	Thr	His	Lys	Tyr	Gly	Tyr	Lys	Leu	Gln	Val	Ser	Ala	Phe	Leu																																							
			340					345					350																																									

Asn Gly Asn Gly Ser Gly Glu Gly Thr His Leu Ser Leu Tyr Ile Arg
 355 360 365
 Val Leu Pro Gly Ala Phe Asp Asn Leu Leu Glu Trp Pro Phe Ala Arg
 370 375 380
 Arg Val Thr Phe Ser Leu Leu Asp Gln Ser Asp Pro Gly Leu Ala Lys
 385 390 395 400
 Pro Gln His Val Thr Glu Thr Phe His Pro Asp Pro Asn Trp Lys Asn
 405 410 415
 Phe Gln Lys Pro Gly Thr Trp Arg Gly Ser Leu Asp Glu Ser Ser Leu
 420 425 430
 Gly Phe Gly Tyr Pro Lys Phe Ile Ser His Gln Asp Ile Arg Lys Arg
 435 440 445
 Asn Tyr Val Arg Asp Asp Ala Val Phe Ile Arg Ala Ala Val Glu Leu
 450 455 460
 Pro Arg Lys Ile Leu Ser
 465 470
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 <211> 543
 <212> PRT
 <213> Homo sapiens
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 Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
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 Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
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 Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
 35 40 45
 Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
 50 55 60
 Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
 65 70 75 80
 Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
 85 90 95
 Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
 100 105 110
 Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
 115 120 125
 Thr Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu
 130 135 140
 Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys
 145 150 155 160
 Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr
 165 170 175

Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His
 180 185 190
 Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys
 195 200 205
 Ser Val Gln Thr Leu Leu Arg Ser Glu Gly Thr Asn Gln Gln Ile Lys
 210 215 220
 Ala His Glu Ala Ser Ser Ala Val Gln His Val Asn Leu Leu Lys Glu
 225 230 235 240
 Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu Leu Gln Asn Glu Ser
 245 250 255
 Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His Asn Gln Ile Cys Ser
 260 265 270
 Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met Leu Arg Asn Asn Glu
 275 280 285
 Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp Ser Gln Ala Glu Lys
 290 295 300
 Leu Lys Glu Leu Asp Lys Glu Ile Arg Ser Phe Arg Gln Asn Trp Glu
 305 310 315 320
 Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser Leu Gln Asn Arg Val
 325 330 335
 Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly Gln Val Ala Arg Asn
 340 345 350
 Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His Asp Gln Met Leu Ser
 355 360 365
 Val His Asp Ile Arg Leu Ala Asp Met Asp Leu Arg Phe Gln Val Leu
 370 375 380
 Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp Lys Ile Arg Asp Tyr
 385 390 395 400
 Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys Thr Leu Ser Leu Tyr
 405 410 415
 Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr Lys Met Cys Ala Arg
 420 425 430
 Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly Thr His Leu Ser Leu
 435 440 445
 Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu Pro Trp Pro
 450 455 460
 Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp Gln Gly Ser Ser Arg
 465 470 475 480
 Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser Ser Ser Phe
 485 490 495
 Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys Pro Val Phe

500 505 510
 Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys Asp Asp Thr
 515 520 525
 Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp Leu Pro Asp Pro
 530 535 540
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 <211> 501
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 <213> Homo sapiens
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 Met Ala Ala Ala Ser Val Thr Pro Pro Gly Ser Leu Glu Leu Leu Gln
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 Pro Gly Phe Ser Lys Thr Leu Leu Gly Thr Lys Leu Glu Ala Lys Tyr
 20 25 30
 Leu Cys Ser Ala Cys Arg Asn Val Leu Arg Arg Pro Phe Gln Ala Gln
 35 40 45
 Cys Gly His Arg Tyr Cys Ser Phe Cys Leu Ala Ser Ile Leu Ser Ser
 50 55 60
 Gly Pro Gln Asn Cys Ala Ala Cys Val His Glu Gly Ile Tyr Glu Glu
 65 70 75 80
 Gly Ile Ser Ile Leu Glu Ser Ser Ser Ala Phe Pro Asp Asn Ala Ala
 85 90 95
 Arg Arg Glu Val Glu Ser Leu Pro Ala Val Cys Pro Ser Asp Gly Cys
 100 105 110
 Thr Trp Lys Gly Thr Leu Lys Glu Tyr Glu Ser Cys His Glu Gly Arg
 115 120 125
 Cys Pro Leu Met Leu Thr Glu Cys Pro Ala Cys Lys Gly Leu Val Arg
 130 135 140
 Leu Gly Glu Lys Glu Arg His Leu Glu His Glu Cys Pro Glu Arg Ser
 145 150 155 160
 Leu Ser Cys Arg His Cys Arg Ala Pro Cys Cys Gly Ala Asp Val Lys
 165 170 175
 Ala His His Glu Val Cys Pro Lys Phe Pro Leu Thr Cys Asp Gly Cys
 180 185 190
 Gly Lys Lys Lys Ile Pro Arg Glu Lys Phe Gln Asp His Val Lys Thr
 195 200 205
 Cys Gly Lys Cys Arg Val Pro Cys Arg Phe His Ala Ile Gly Cys Leu
 210 215 220
 Glu Thr Val Glu Gly Glu Lys Gln Gln Glu His Glu Val Gln Trp Leu
 225 230 235 240
 Arg Glu His Leu Ala Met Leu Leu Ser Ser Val Leu Glu Ala Lys Pro
 245 250 255

Leu Leu Gly Asp Gln Ser His Ala Gly Ser Glu Leu Leu Gln Arg Cys
 260 265 270
 Glu Ser Leu Glu Lys Lys Thr Ala Thr Phe Glu Asn Ile Val Cys Val
 275 280 285
 Leu Asn Arg Glu Val Glu Arg Val Ala Met Thr Ala Glu Ala Cys Ser
 290 295 300
 Arg Gln His Arg Leu Asp Gln Asp Lys Ile Glu Ala Leu Ser Ser Lys
 305 310 315 320
 Val Gln Gln Leu Glu Arg Ser Ile Gly Leu Lys Asp Leu Ala Met Ala
 325 330 335
 Asp Leu Glu Gln Lys Val Arg Pro Phe Gln Ala Gln Cys Gly His Arg
 340 345 350
 Tyr Cys Ser Phe Cys Leu Ala Ser Ile Leu Arg Lys Leu Gln Glu Ala
 355 360 365
 Val Ala Gly Arg Ile Pro Ala Ile Phe Ser Pro Ala Phe Tyr Thr Ser
 370 375 380
 Arg Tyr Gly Tyr Lys Met Cys Leu Arg Ile Tyr Leu Asn Gly Asp Gly
 385 390 395 400
 Thr Gly Arg Gly Thr His Leu Ser Leu Phe Phe Val Val Met Lys Gly
 405 410 415
 Pro Asn Asp Ala Leu Leu Arg Trp Pro Phe Asn Gln Lys Val Thr Leu
 420 425 430
 Met Leu Leu Asp Gln Asn Asn Arg Glu His Val Ile Asp Ala Phe Arg
 435 440 445
 Pro Asp Val Thr Ser Ser Ser Phe Gln Arg Pro Val Asn Asp Met Asn
 450 455 460
 Ile Ala Ser Gly Cys Pro Leu Phe Cys Pro Val Ser Lys Met Glu Ala
 465 470 475 480
 Lys Asn Ser Tyr Val Arg Asp Asp Ala Ile Phe Ile Lys Ala Ile Val
 485 490 495
 Asp Leu Thr Gly Leu
 500

<210> 131
 <211> 568
 <212> PRT
 <213> Homo sapiens

<400> 131
 Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
 1 5 10 15
 Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
 20 25 30
 Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
 35 40 45

Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
 50 55 60
 Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
 65 70 75 80
 Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
 85 90 95
 Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
 100 105 110
 Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
 115 120 125
 Met Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu
 130 135 140
 Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys
 145 150 155 160
 Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr
 165 170 175
 Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His
 180 185 190
 Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys
 195 200 205
 Ser Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu
 210 215 220
 Cys Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val
 225 230 235 240
 Phe Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala
 245 250 255
 Val Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys
 260 265 270
 Lys Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile
 275 280 285
 Gln Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg
 290 295 300
 Gln Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln
 305 310 315 320
 Arg Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu
 325 330 335
 Ile Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser
 340 345 350
 Ser Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp
 355 360 365
 Lys Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln

370 375 380
 Leu Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala
 385 390 395 400
 Asp Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly
 405 410 415
 Val Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala
 420 425 430
 Val Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly
 435 440 445
 Tyr Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly
 450 455 460
 Met Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly
 465 470 475 480
 Glu Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu
 485 490 495
 Met Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe
 500 505 510
 Lys Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met
 515 520 525
 Asn Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu
 530 535 540
 Asn Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val
 545 550 555 560
 Asp Thr Ser Asp Leu Pro Asp Pro
 565

 <210> 132
 <211> 197
 <212> PRT
 <213> Homo sapiens

 <400> 132
 Met Pro Ala Pro Ser Met Asp Cys Asp Val Ser Thr Leu Val Ala Cys
 1 5 10 15
 Val Val Asp Val Glu Val Phe Thr Asn Gln Glu Val Lys Glu Lys Phe
 20 25 30
 Glu Gly Leu Phe Arg Thr Tyr Asp Asp Cys Val Thr Phe Gln Leu Phe
 35 40 45
 Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Asn Pro Lys Ser Ala
 50 55 60
 Ala Arg Ala Arg Ile Glu Leu His Glu Thr Gln Phe Arg Gly Lys Lys
 65 70 75 80
 Leu Lys Leu Tyr Phe Ala Gln Val Gln Thr Pro Glu Thr Asp Gly Asp
 85 90 95

Lys Leu His Leu Ala Pro Pro Gln Pro Ala Lys Gln Phe Leu Ile Ser
 100 105 110
 Pro Pro Ser Ser Pro Pro Val Gly Trp Gln Pro Ile Asn Asp Ala Thr
 115 120 125
 Pro Val Leu Asn Tyr Asp Leu Leu Tyr Ala Val Ala Lys Leu Gly Pro
 130 135 140
 Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser Thr Pro Ser Val
 145 150 155 160
 Val Val His Val Cys Asp Ser Asp Ile Glu Glu Glu Glu Asp Pro Lys
 165 170 175
 Thr Ser Pro Lys Pro Lys Ile Ile Gln Thr Arg Arg Pro Gly Leu Pro
 180 185 190
 Pro Ser Val Ser Asn
 195
 <210> 133
 <211> 241
 <212> PRT
 <213> Homo sapiens
 <400> 133
 Met Leu Arg Asp Thr Met Lys Ser Trp Asn Asp Ser Gln Ser Asp Leu
 1 5 10 15
 Cys Ser Thr Asp Gln Glu Glu Glu Glu Glu Met Ile Phe Gly Glu Asn
 20 25 30
 Glu Asp Asp Leu Asp Glu Met Met Asp Leu Ser Asp Leu Pro Thr Ser
 35 40 45
 Leu Phe Ala Cys Ser Val His Glu Ala Val Phe Glu Ala Arg Glu Gln
 50 55 60
 Lys Glu Arg Phe Glu Ala Leu Phe Thr Ile Tyr Asp Asp Gln Val Thr
 65 70 75 80
 Phe Gln Leu Phe Lys Ser Phe Arg Arg Val Arg Ile Asn Phe Ser Lys
 85 90 95
 Pro Glu Ala Ala Ala Arg Ala Arg Ile Glu Leu His Glu Thr Asp Phe
 100 105 110
 Asn Gly Gln Lys Leu Lys Leu Tyr Phe Ala Gln Val Gln Met Ser Gly
 115 120 125
 Glu Val Arg Asp Lys Ser Tyr Leu Leu Pro Pro Gln Pro Val Lys Gln
 130 135 140
 Phe Leu Ile Ser Pro Pro Ala Ser Pro Pro Val Gly Trp Lys Gln Ser
 145 150 155 160
 Glu Asp Ala Met Pro Val Ile Asn Tyr Asp Leu Leu Cys Ala Val Ser
 165 170 175
 Lys Leu Gly Pro Gly Glu Lys Tyr Glu Leu His Ala Gly Thr Glu Ser
 180 185 190

Thr Pro Ser Val Val Val His Val Cys Glu Ser Glu Thr Glu Glu Glu
195 200 205

Glu Glu Thr Lys Asn Pro Lys Gln Lys Ile Ala Gln Thr Arg Arg Pro
210 215 220

Asp Pro Pro Thr Ala Ala Leu Asn Glu Pro Gln Thr Phe Asp Cys Ala
225 230 235 240

Leu

<210> 134

<211> 153

<212> PRT

<213> Homo sapiens

<400> 134

Met Ala Val Glu Ser Arg Val Thr Gln Glu Glu Ile Lys Lys Glu Pro
1 5 10 15

Glu Lys Pro Ile Asp Arg Glu Lys Thr Cys Pro Leu Leu Leu Arg Val
20 25 30

Phe Thr Thr Asn Asn Gly Arg His His Arg Met Asp Glu Phe Ser Arg
35 40 45

Gly Asn Val Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met Asp Ala
50 55 60

Thr Leu Lys Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro Glu Ala
65 70 75 80

Arg Lys Lys Gly Thr His Phe Asn Phe Ala Ile Val Phe Thr Asp Val
85 90 95

Lys Arg Pro Gly Tyr Arg Val Lys Glu Ile Gly Ser Thr Met Ser Gly
100 105 110

Arg Lys Gly Thr Asp Asp Ser Met Thr Leu Gln Ser Gln Lys Phe Gln
115 120 125

Ile Gly Asp Tyr Leu Asp Ile Ala Ile Thr Pro Pro Asn Arg Ala Pro
130 135 140

Pro Pro Ser Gly Arg Met Arg Pro Tyr
145 150

<210> 135

<211> 692

<212> PRT

<213> Homo sapiens

<400> 135

Met Ser Gln Gln Asp Ala Val Ala Ala Leu Ser Glu Arg Leu Leu Val
1 5 10 15

Ala Ala Tyr Lys Gly Gln Thr Glu Asn Val Val Gln Leu Ile Asn Lys
20 25 30

Gly Ala Arg Val Ala Val Thr Lys His Gly Arg Thr Pro Leu His Leu

35	40	45
Ala Ala Asn Lys Gly His Leu Pro Val Val Gln Ile Leu Leu Lys Ala 50 55 60		
Gly Cys Asp Leu Asp Val Gln Asp Asp Gly Asp Gln Thr Ala Leu His 65 70 75 80		
Arg Ala Thr Val Val Gly Asn Thr Glu Ile Ile Ala Ala Leu Ile His 85 90 95		
Glu Gly Cys Ala Leu Asp Arg Gln Asp Lys Asp Gly Asn Thr Ala Leu 100 105 110		
His Glu Ala Ser Trp His Gly Phe Ser Gln Ser Ala Lys Leu Leu Val 115 120 125		
Lys Ala Gly Ala Asn Val Leu Ala Lys Asn Lys Ala Gly Asn Thr Ala 130 135 140		
Leu His Leu Ala Cys Gln Asn Ser His Ser Gln Ser Thr Arg Val Leu 145 150 155 160		
Leu Leu Ala Gly Ser Arg Ala Asp Leu Lys Asn Asn Ala Gly Asp Thr 165 170 175		
Cys Leu His Val Ala Ala Arg Tyr Asn His Leu Ser Ile Ile Arg Leu 180 185 190		
Leu Leu Thr Ala Phe Cys Ser Val His Glu Lys Asn Gln Ala Gly Asp 195 200 205		
Thr Ala Leu His Val Ala Ala Ala Leu Asn His Lys Lys Val Ala Lys 210 215 220		
Ile Leu Leu Glu Ala Gly Ala Asp Thr Thr Ile Val Asn Asn Ala Gly 225 230 235 240		
Gln Thr Pro Leu Glu Thr Ala Arg Tyr His Asn Asn Pro Glu Val Ala 245 250 255		
Leu Leu Leu Thr Lys Ala Pro Gln Gly Ser Val Ser Ala Gly Asp Thr 260 265 270		
Pro Ser Ser Glu Gln Ala Val Ala Arg Lys Glu Glu Ala Arg Glu Glu 275 280 285		
Phe Leu Ser Ala Ser Pro Glu Pro Arg Ala Lys Asp Asp Arg Arg Arg 290 295 300		
Lys Ser Arg Pro Lys Val Ser Ala Phe Ser Asp Pro Thr Pro Pro Ala 305 310 315 320		
Asp Gln Gln Pro Gly His Gln Lys Asn Leu His Ala His Asn His Pro 325 330 335		
Lys Lys Arg Asn Arg His Arg Cys Ser Ser Pro Pro Pro Pro His Glu 340 345 350		
Phe Arg Ala Tyr Gln Leu Tyr Thr Leu Tyr Arg Gly Lys Asp Gly Lys 355 360 365		

Val Met Gln Ala Pro Ile Asn Gly Cys Arg Cys Glu Pro Leu Ile Asn
 370 375 380
 Lys Leu Glu Asn Gln Leu Glu Ala Thr Val Glu Glu Ile Lys Ala Glu
 385 390 395 400
 Leu Gly Ser Val Gln Asp Lys Met Asn Thr Lys Leu Gly Gln Met Glu
 405 410 415
 Asn Lys Thr Gln His Gln Met Arg Val Leu Asp Lys Leu Met Val Glu
 420 425 430
 Arg Leu Ser Ala Glu Arg Thr Glu Cys Leu Asn Arg Leu Gln Gln His
 435 440 445
 Ser Asp Thr Glu Lys His Glu Gly Glu Lys Arg Gln Ile Ser Leu Val
 450 455 460
 Asp Glu Leu Lys Thr Trp Cys Met Leu Lys Ile Gln Asn Leu Glu Gln
 465 470 475 480
 Lys Leu Ser Gly Asp Ser Arg Ala Cys Arg Ala Lys Ser Thr Pro Ser
 485 490 495
 Thr Cys Glu Ser Ser Thr Gly Val Asp Gln Leu Val Val Thr Ala Gly
 500 505 510
 Pro Ala Ala Ala Ser Asp Ser Ser Pro Pro Val Val Arg Pro Lys Glu
 515 520 525
 Lys Ala Leu Asn Ser Thr Ala Thr Gln Arg Leu Gln Gln Glu Leu Ser
 530 535 540
 Ser Ser Asp Cys Thr Gly Ser Arg Leu Arg Asn Val Lys Val Gln Thr
 545 550 555 560
 Ala Leu Leu Pro Met Asn Glu Ala Ala Arg Ser Asp Gln Gln Ala Gly
 565 570 575
 Pro Cys Val Asn Arg Gly Thr Gln Thr Lys Lys Ser Gly Lys Ser Gly
 580 585 590
 Pro Thr Arg His Arg Ala Gln Gln Pro Ala Ala Ser Ser Thr Cys Gly
 595 600 605
 Gln Pro Pro Pro Ala Thr Gly Ser Glu Gln Thr Gly Pro His Ile Arg
 610 615 620
 Asp Thr Ser Gln Ala Leu Glu Leu Thr Gln Tyr Phe Phe Glu Ala Val
 625 630 635 640
 Ser Thr Gln Met Glu Lys Trp Tyr Glu Arg Lys Ile Glu Glu Ala Arg
 645 650 655
 Ser Gln Ala Asn Gln Lys Ala Gln Gln Asp Lys Ala Thr Leu Lys Glu
 660 665 670
 His Ile Lys Ser Leu Glu Glu Glu Leu Ala Lys Leu Arg Thr Arg Val
 675 680 685
 Gln Lys Glu Asn
 690

<210> 136
 <211> 556
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Ala Arg Thr Thr Ser Gln Leu Tyr Asp Ala Val Pro Ile Gln Ser
 1 5 10 15
 Ser Val Val Leu Cys Ser Cys Pro Ser Pro Ser Met Val Arg Thr Gln
 20 25 30
 Thr Glu Ser Ser Thr Pro Pro Gly Ile Pro Gly Gly Ser Arg Gln Gly
 35 40 45
 Pro Ala Met Asp Gly Thr Ala Ala Glu Pro Arg Pro Gly Ala Gly Ser
 50 55 60
 Leu Gln His Ala Gln Pro Pro Pro Gln Pro Arg Lys Lys Arg Pro Glu
 65 70 75 80
 Asp Phe Lys Phe Gly Lys Ile Leu Gly Glu Gly Ser Phe Ser Thr Val
 85 90 95
 Val Leu Ala Arg Glu Leu Ala Thr Ser Arg Glu Tyr Ala Ile Lys Ile
 100 105 110
 Leu Glu Lys Arg His Ile Ile Lys Glu Asn Lys Val Pro Tyr Val Thr
 115 120 125
 Arg Glu Arg Asp Val Met Ser Arg Leu Asp His Pro Phe Phe Val Lys
 130 135 140
 Leu Tyr Phe Thr Phe Gln Asp Asp Glu Lys Leu Tyr Phe Gly Leu Ser
 145 150 155 160
 Tyr Ala Lys Asn Gly Glu Leu Leu Lys Tyr Ile Arg Lys Ile Gly Ser
 165 170 175
 Phe Asp Glu Thr Cys Thr Arg Phe Tyr Thr Ala Glu Ile Val Ser Ala
 180 185 190
 Leu Glu Tyr Leu His Gly Lys Gly Ile Ile His Arg Asp Leu Lys Pro
 195 200 205
 Glu Asn Ile Leu Leu Asn Glu Asp Met His Ile Gln Ile Thr Asp Phe
 210 215 220
 Gly Thr Ala Lys Val Leu Ser Pro Glu Ser Lys Gln Ala Arg Ala Asn
 225 230 235 240
 Ser Phe Val Gly Thr Ala Gln Tyr Val Ser Pro Glu Leu Leu Thr Glu
 245 250 255
 Lys Ser Ala Cys Lys Ser Ser Asp Leu Trp Ala Leu Gly Cys Ile Ile
 260 265 270
 Tyr Gln Leu Val Ala Gly Leu Pro Pro Phe Arg Ala Gly Asn Glu Tyr
 275 280 285
 Leu Ile Phe Gln Lys Ile Ile Lys Leu Glu Tyr Asp Phe Pro Glu Lys

290		295		300
Phe Phe Pro Lys Ala Arg Asp Leu Val Glu Lys Leu Leu Val Leu Asp				
305		310		315 320
Ala Thr Lys Arg Leu Gly Cys Glu Glu Met Glu Gly Tyr Gly Pro Leu				
	325		330	335
Lys Ala His Pro Phe Phe Glu Ser Val Thr Trp Glu Asn Leu His Gln				
	340		345	350
Gln Thr Pro Pro Lys Leu Thr Ala Tyr Leu Pro Ala Met Ser Glu Asp				
	355		360	365
Asp Glu Asp Cys Tyr Gly Asn Tyr Asp Asn Leu Leu Ser Gln Phe Gly				
	370		375	380
Cys Met Gln Val Ser Ser Ser Ser Ser Ser His Ser Leu Ser Ala Ser				
	385		390	395 400
Asp Thr Gly Leu Pro Gln Arg Ser Gly Ser Asn Ile Glu Gln Tyr Ile				
	405		410	415
His Asp Leu Asp Ser Asn Ser Phe Glu Leu Asp Leu Gln Phe Ser Glu				
	420		425	430
Asp Glu Lys Arg Leu Leu Leu Glu Lys Gln Ala Gly Gly Asn Pro Trp				
	435		440	445
His Gln Phe Val Glu Asn Asn Leu Ile Leu Lys Met Gly Pro Val Asp				
	450		455	460
Lys Arg Lys Gly Leu Phe Ala Arg Arg Arg Gln Leu Leu Leu Thr Glu				
	465		470	475 480
Gly Pro His Leu Tyr Tyr Val Asp Pro Val Asn Lys Val Leu Lys Gly				
	485		490	495
Glu Ile Pro Trp Ser Gln Glu Leu Arg Pro Glu Ala Lys Asn Phe Lys				
	500		505	510
Thr Phe Phe Val His Thr Pro Asn Arg Thr Tyr Tyr Leu Met Asp Pro				
	515		520	525
Ser Gly Asn Ala His Lys Trp Cys Arg Lys Ile Gln Glu Val Trp Arg				
	530		535	540
Gln Arg Tyr Gln Ser His Pro Asp Ala Ala Val Gln				
	545		550	555
<210> 137				
<211> 279				
<212> PRT				
<213> Homo sapiens				
<400> 137				
Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp				
1	5		10	15
Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr				
	20		25	30

Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg
 35 40 45
 Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val
 50 55 60
 Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe
 65 70 75 80
 Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val
 85 90 95
 Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp
 100 105 110
 Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe
 115 120 125
 Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His
 130 135 140
 His Ser Val Leu Pro Trp Ser Trp Trp Trp Gly Val Lys Ile Ala Pro
 145 150 155 160
 Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val
 165 170 175
 Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln
 180 185 190
 Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln
 195 200 205
 Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser
 210 215 220
 Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly
 225 230 235 240
 Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr
 245 250 255
 Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly
 260 265 270
 Ile Ala Lys Val Lys Ala Asn
 275

<210> 138
 <211> 324
 <212> PRT
 <213> Homo sapiens

<400> 138

Asp Ser Ala Gly Gln Arg Asp Pro Ala Thr Leu Asp Ser Ala Ser Pro
 1 5 10 15
 Pro Ala Arg Val Ala Ala Pro Gln Pro Leu Arg Ile Met Glu His Leu
 20 25 30
 Lys Ala Phe Asp Asp Glu Ile Asn Ala Phe Leu Asp Asn Met Phe Gly
 35 40 45

Pro Arg Asp Ser Arg Val Arg Gly Trp Phe Met Leu Asp Ser Tyr Leu
 50 55 60
 Pro Thr Phe Phe Leu Thr Val Met Tyr Leu Leu Ser Ile Trp Leu Gly
 65 70 75 80
 Asn Lys Tyr Met Lys Asn Arg Pro Ala Leu Ser Leu Arg Gly Ile Leu
 85 90 95
 Thr Leu Tyr Asn Leu Gly Ile Thr Leu Leu Ser Ala Tyr Met Leu Ala
 100 105 110
 Glu Leu Ile Leu Ser Thr Trp Glu Gly Gly Tyr Asn Leu Gln Cys Gln
 115 120 125
 Asp Leu Thr Ser Ala Gly Glu Ala Asp Ile Arg Val Ala Lys Val Leu
 130 135 140
 Trp Trp Tyr Tyr Phe Ser Lys Ser Val Glu Phe Leu Asp Thr Ile Phe
 145 150 155 160
 Phe Val Leu Arg Lys Lys Thr Ser Gln Ile Thr Phe Leu His Val Tyr
 165 170 175
 His His Ala Ser Met Phe Asn Ile Trp Trp Cys Val Leu Asn Trp Ile
 180 185 190
 Pro Cys Gly Gln Ser Phe Phe Gly Pro Thr Leu Asn Ser Phe Ile His
 195 200 205
 Ile Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Val Phe Pro Ser Met His
 210 215 220
 Lys Tyr Leu Trp Trp Lys Lys Tyr Leu Thr Gln Ala Gln Leu Val Gln
 225 230 235 240
 Phe Val Leu Thr Ile Thr His Thr Met Ser Ala Val Val Lys Pro Cys
 245 250 255
 Gly Phe Pro Phe Gly Cys Leu Ile Phe Gln Ser Ser Tyr Met Leu Thr
 260 265 270
 Leu Val Ile Leu Phe Leu Asn Phe Tyr Gln Gln Thr Tyr Arg Lys Lys
 275 280 285
 Pro Met Lys Lys Asp Met Gln Glu Pro Pro Ala Gly Lys Glu Val Lys
 290 295 300
 Asn Gly Phe Ser Lys Ala Tyr Phe Thr Ala Ala Asn Gly Val Met Asn
 305 310 315 320
 Lys Lys Ala Gln

<210> 139

<211> 744

<212> PRT

<213> Homo sapiens

<400> 139

Met Ala Ser Glu Gly Thr Asn Ile Pro Ser Pro Val Val Arg Gln Ile

1	5	10	15
Asp Lys Gln Phe Leu Ile Cys Ser Ile Cys Leu Glu Arg Tyr Lys Asn	20	25	30
Pro Lys Val Leu Pro Cys Leu His Thr Phe Cys Glu Arg Cys Leu Gln	35	40	45
Asn Tyr Ile Pro Ala His Ser Leu Thr Leu Ser Cys Pro Val Cys Arg	50	55	60
Gln Thr Ser Ile Leu Pro Glu Lys Gly Val Ala Ala Leu Gln Asn Asn	65	70	75
Phe Phe Ile Thr Asn Leu Met Asp Val Leu Gln Arg Thr Pro Gly Ser	85	90	95
Asn Ala Glu Glu Ser Ser Ile Leu Glu Thr Val Thr Ala Val Ala Ala	100	105	110
Gly Lys Pro Leu Ser Cys Pro Asn His Asp Gly Asn Val Met Glu Phe	115	120	125
Tyr Cys Gln Ser Cys Glu Thr Ala Met Cys Arg Glu Cys Thr Glu Gly	130	135	140
Glu His Ala Glu His Pro Thr Val Pro Leu Lys Asp Val Val Glu Gln	145	150	155
His Lys Ala Ser Leu Gln Val Gln Leu Asp Ala Val Asn Lys Arg Leu	165	170	175
Pro Glu Ile Asp Ser Ala Leu Gln Phe Ile Ser Glu Ile Ile His Gln	180	185	190
Leu Thr Asn Gln Lys Ala Ser Ile Val Asp Asp Ile His Ser Thr Phe	195	200	205
Asp Glu Leu Gln Lys Thr Leu Asn Val Arg Lys Ser Val Leu Leu Met	210	215	220
Glu Leu Glu Val Asn Tyr Gly Leu Lys His Lys Val Leu Gln Ser Gln	225	230	235
Leu Asp Thr Leu Leu Gln Gly Gln Glu Ser Ile Lys Ser Cys Ser Asn	245	250	255
Phe Thr Ala Gln Ala Leu Asn His Gly Thr Glu Thr Glu Val Leu Leu	260	265	270
Val Lys Lys Gln Met Ser Glu Lys Leu Asn Glu Leu Ala Asp Gln Asp	275	280	285
Phe Pro Leu His Pro Arg Glu Asn Asp Gln Leu Asp Phe Ile Val Glu	290	295	300
Thr Glu Gly Leu Lys Lys Ser Ile His Asn Leu Gly Thr Ile Leu Thr	305	310	315
Thr Asn Ala Val Ala Ser Glu Thr Val Ala Thr Gly Glu Gly Leu Arg	325	330	335

Gln Thr Ile Ile Gly Gln Pro Met Ser Val Thr Ile Thr Thr Lys Asp
 340 345 350
 Lys Asp Gly Glu Leu Cys Lys Thr Gly Asn Ala Tyr Leu Thr Ala Glu
 355 360 365
 Leu Ser Thr Pro Asp Gly Ser Val Ala Asp Gly Glu Ile Leu Asp Asn
 370 375 380
 Lys Asn Gly Thr Tyr Glu Phe Leu Tyr Thr Val Gln Lys Glu Gly Asp
 385 390 395 400
 Phe Thr Leu Ser Leu Arg Leu Tyr Asp Gln His Ile Arg Gly Ser Pro
 405 410 415
 Phe Lys Leu Lys Val Ile Arg Ser Ala Asp Val Ser Pro Thr Thr Glu
 420 425 430
 Gly Val Lys Arg Arg Val Lys Ser Pro Gly Ser Gly His Val Lys Gln
 435 440 445
 Lys Ala Val Lys Arg Pro Ala Ser Met Tyr Ser Thr Gly Lys Arg Lys
 450 455 460
 Glu Asn Pro Ile Glu Asp Asp Leu Ile Phe Arg Val Gly Thr Lys Gly
 465 470 475 480
 Arg Asn Lys Gly Glu Phe Thr Asn Leu Gln Gly Val Ala Ala Ser Thr
 485 490 495
 Asn Gly Lys Ile Leu Ile Ala Asp Ser Asn Asn Gln Cys Val Gln Ile
 500 505 510
 Phe Ser Asn Asp Gly Gln Phe Lys Ser Arg Phe Gly Ile Arg Gly Arg
 515 520 525
 Ser Pro Gly Gln Leu Gln Arg Pro Thr Gly Val Ala Val His Pro Ser
 530 535 540
 Gly Asp Ile Ile Ile Ala Asp Tyr Asp Asn Lys Trp Val Ser Ile Phe
 545 550 555 560
 Ser Ser Asp Gly Lys Phe Lys Thr Lys Ile Gly Ser Gly Lys Leu Met
 565 570 575
 Gly Pro Lys Gly Val Ser Val Asp Arg Asn Gly His Ile Ile Val Val
 580 585 590
 Asp Asn Lys Ala Cys Cys Val Phe Ile Phe Gln Pro Asn Gly Lys Ile
 595 600 605
 Val Thr Arg Phe Gly Ser Arg Gly Asn Gly Asp Arg Gln Phe Ala Gly
 610 615 620
 Pro His Phe Ala Ala Val Asn Ser Asn Asn Glu Ile Ile Ile Thr Asp
 625 630 635 640
 Phe His Asn His Ser Val Lys Val Phe Asn Gln Glu Gly Glu Phe Met
 645 650 655
 Leu Lys Phe Gly Ser Asn Gly Glu Gly Asn Gly Gln Phe Asn Ala Pro
 660 665 670

Thr Gly Val Ala Val Asp Ser Asn Gly Asn Ile Ile Val Ala Asp Trp
 675 680 685
 Gly Asn Ser Arg Ile Gln Val Phe Asp Gly Ser Gly Ser Phe Leu Ser
 690 695 700
 Tyr Ile Asn Thr Ser Ala Asp Pro Leu Tyr Gly Pro Gln Gly Leu Ala
 705 710 715 720
 Leu Thr Ser Asp Gly His Val Val Val Ala Asp Ser Gly Asn His Cys
 725 730 735
 Phe Lys Val Tyr Arg Tyr Leu Gln
 740
 <210> 140
 <211> 744
 <212> PRT
 <213> Homo sapiens
 <400> 140
 Met Ala Ser Glu Gly Thr Asn Ile Pro Ser Pro Val Val Arg Gln Ile
 1 5 10 15
 Asp Lys Gln Phe Leu Ile Cys Ser Ile Cys Leu Glu Arg Tyr Lys Asn
 20 25 30
 Pro Lys Val Leu Pro Cys Leu His Thr Phe Cys Glu Arg Cys Leu Gln
 35 40 45
 Asn Tyr Ile Pro Ala His Ser Leu Thr Leu Ser Cys Pro Val Cys Arg
 50 55 60
 Gln Thr Ser Ile Leu Pro Glu Lys Gly Val Ala Ala Leu Gln Asn Asn
 65 70 75 80
 Phe Phe Ile Thr Asn Leu Met Asp Val Leu Gln Arg Thr Pro Gly Ser
 85 90 95
 Asn Ala Glu Glu Ser Ser Ile Leu Glu Thr Val Thr Ala Val Ala Ala
 100 105 110
 Gly Lys Pro Leu Ser Cys Pro Asn His Asp Gly Asn Val Met Glu Phe
 115 120 125
 Tyr Cys Gln Ser Cys Glu Thr Ala Met Cys Arg Glu Cys Thr Glu Gly
 130 135 140
 Glu His Ala Glu His Pro Thr Val Pro Leu Lys Asp Val Val Glu Gln
 145 150 155 160
 His Lys Ala Ser Leu Gln Val Gln Leu Asp Ala Val Asn Lys Arg Leu
 165 170 175
 Pro Glu Ile Asp Ser Ala Leu Gln Phe Ile Ser Glu Ile Ile His Gln
 180 185 190
 Leu Thr Asn Gln Lys Ala Ser Ile Val Asp Asp Ile His Ser Thr Phe
 195 200 205
 Asp Glu Leu Gln Lys Thr Leu Asn Val Arg Lys Ser Val Leu Leu Met

210					215					220					
Glu	Leu	Glu	Val	Asn	Tyr	Gly	Leu	Lys	His	Lys	Val	Leu	Gln	Ser	Gln
225					230					235					240
Leu	Asp	Thr	Leu	Leu	Gln	Gly	Gln	Glu	Ser	Ile	Lys	Ser	Cys	Ser	Asn
				245					250					255	
Phe	Thr	Ala	Gln	Ala	Leu	Asn	His	Gly	Thr	Glu	Thr	Glu	Val	Leu	Leu
			260					265					270		
Val	Lys	Lys	Gln	Met	Ser	Glu	Lys	Leu	Asn	Glu	Leu	Ala	Asp	Gln	Asp
		275					280					285			
Phe	Pro	Leu	His	Pro	Arg	Glu	Asn	Asp	Gln	Leu	Asp	Phe	Ile	Val	Glu
	290					295					300				
Thr	Glu	Gly	Leu	Lys	Lys	Ser	Ile	His	Asn	Leu	Gly	Thr	Ile	Leu	Thr
305					310					315					320
Thr	Asn	Ala	Val	Ala	Ser	Glu	Thr	Val	Ala	Thr	Gly	Glu	Gly	Leu	Arg
				325					330					335	
Gln	Thr	Ile	Ile	Gly	Gln	Pro	Met	Ser	Val	Thr	Ile	Thr	Thr	Lys	Asp
			340					345					350		
Lys	Asp	Gly	Glu	Leu	Cys	Lys	Thr	Gly	Asn	Ala	Tyr	Leu	Thr	Ala	Glu
		355					360					365			
Leu	Ser	Thr	Pro	Asp	Gly	Ser	Val	Ala	Asp	Gly	Glu	Ile	Leu	Asp	Asn
	370					375					380				
Lys	Asn	Gly	Thr	Tyr	Glu	Phe	Leu	Tyr	Thr	Val	Gln	Lys	Glu	Gly	Asp
385					390					395					400
Phe	Thr	Leu	Ser	Leu	Arg	Leu	Tyr	Asp	Gln	His	Ile	Arg	Gly	Ser	Pro
				405					410					415	
Phe	Lys	Leu	Lys	Val	Ile	Arg	Ser	Ala	Asp	Val	Ser	Pro	Thr	Thr	Glu
			420					425					430		
Gly	Val	Lys	Arg	Arg	Val	Lys	Ser	Pro	Gly	Ser	Gly	His	Val	Lys	Gln
		435					440					445			
Lys	Ala	Val	Lys	Arg	Pro	Ala	Ser	Met	Tyr	Ser	Thr	Gly	Lys	Arg	Lys
	450					455					460				
Glu	Asn	Pro	Ile	Glu	Asp	Asp	Leu	Ile	Phe	Arg	Val	Gly	Thr	Lys	Gly
465					470				475						480
Arg	Asn	Lys	Gly	Glu	Phe	Thr	Asn	Leu	Gln	Gly	Val	Ala	Ala	Ser	Thr
				485					490					495	
Asn	Gly	Lys	Ile	Leu	Ile	Ala	Asp	Ser	Asn	Asn	Gln	Cys	Val	Gln	Ile
			500					505					510		
Phe	Ser	Asn	Asp	Gly	Gln	Phe	Lys	Ser	Arg	Phe	Gly	Ile	Arg	Gly	Arg
		515					520					525			
Ser	Pro	Gly	Gln	Leu	Gln	Arg	Pro	Thr	Gly	Val	Ala	Val	His	Pro	Ser
	530					535					540				

Gly Asp Ile Ile Ile Ala Asp Tyr Asp Asn Lys Trp Val Ser Ile Phe
 545 550 555 560
 Ser Ser Asp Gly Lys Phe Lys Thr Lys Ile Gly Ser Gly Lys Leu Met
 565 570 575
 Gly Pro Lys Gly Val Ser Val Asp Arg Asn Gly His Ile Ile Val Val
 580 585 590
 Asp Asn Lys Ala Cys Cys Val Phe Ile Phe Gln Pro Asn Gly Lys Ile
 595 600 605
 Val Thr Arg Phe Gly Ser Arg Gly Asn Gly Asp Arg Gln Phe Ala Gly
 610 615 620
 Pro His Phe Ala Ala Val Asn Ser Asn Asn Glu Ile Ile Ile Thr Asp
 625 630 635 640
 Phe His Asn His Ser Val Lys Val Phe Asn Gln Glu Gly Glu Phe Met
 645 650 655
 Leu Lys Phe Gly Ser Asn Gly Glu Gly Asn Gly Gln Phe Asn Ala Pro
 660 665 670
 Thr Gly Val Ala Val Asp Ser Asn Gly Asn Ile Ile Val Ala Asp Trp
 675 680 685
 Gly Asn Ser Arg Ile Gln Val Phe Asp Gly Ser Gly Ser Phe Leu Ser
 690 695 700
 Tyr Ile Asn Thr Ser Ala Asp Pro Leu Tyr Gly Pro Gln Gly Leu Ala
 705 710 715 720
 Leu Thr Ser Asp Gly His Val Val Val Ala Asp Ser Gly Asn His Cys
 725 730 735
 Phe Lys Val Tyr Arg Tyr Leu Gln
 740

<210> 141
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 141
 Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro
 1 5 10 15
 Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu
 20 25 30
 Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala Leu Asp
 35 40 45
 Gly Ser Asn Trp Gln Arg Ile Asp Leu Phe Asn Phe Gln Thr Asp Val
 50 55 60
 Glu Gly Arg Val Val Glu Asn Ile Ser Lys Arg Cys Gly Gly Phe Leu
 65 70 75 80
 Arg Lys Leu Ser Leu Arg Gly Cys Ile Gly Val Gly Asp Ser Ser Leu
 85 90 95

Lys Thr Phe Ala Gln Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn
 100 105 110
 Gly Cys Thr Lys Ile Thr Asp Ser Thr Cys Tyr Ser Leu Ser Arg Phe
 115 120 125
 Cys Ser Lys Leu Lys His Leu Asp Leu Thr Ser Cys Val Ser Ile Thr
 130 135 140
 Asn Ser Ser Leu Lys Gly Ile Ser Glu Gly Cys Arg Asn Leu Glu Tyr
 145 150 155 160
 Leu Asn Leu Ser Trp Cys Asp Gln Ile Thr Lys Asp Gly Ile Glu Ala
 165 170 175
 Leu Val Arg Gly Cys Arg Gly Leu Lys Ala Leu Leu Leu Arg Gly Cys
 180 185 190
 Thr Gln Leu Glu Asp Glu Ala Leu Lys His Ile Gln Asn Tyr Cys His
 195 200 205
 Glu Leu Val Ser Leu Asn Leu Gln Ser Cys Ser Arg Ile Thr Asp Glu
 210 215 220
 Gly Val Val Gln Ile Cys Arg Gly Cys His Arg Leu Gln Ala Leu Cys
 225 230 235 240
 Leu Ser Gly Cys Ser Asn Leu Thr Asp Ala Ser Leu Thr Ala Leu Gly
 245 250 255
 Leu Asn Cys Pro Arg Leu Gln Ile Leu Glu Ala Ala Arg Cys Ser His
 260 265 270
 Leu Thr Asp Ala Gly Phe Thr Leu Leu Ala Arg Asn Cys His Glu Leu
 275 280 285
 Glu Lys Met Asp Leu Glu Glu Cys Ile Leu Ile Thr Asp Ser Thr Leu
 290 295 300
 Ile Gln Leu Ser Ile His Cys Pro Lys Leu Gln Ala Leu Ser Leu Ser
 305 310 315 320
 His Cys Glu Leu Ile Thr Asp Asp Gly Ile Leu His Leu Ser Asn Ser
 325 330 335
 Thr Cys Gly His Glu Arg Leu Arg Val Leu Glu Leu Asp Asn Cys Leu
 340 345 350
 Leu Ile Thr Asp Val Ala Leu Glu His Leu Glu Asn Cys Arg Gly Leu
 355 360 365
 Glu Arg Leu Glu Leu Tyr Asp Cys Gln Gln Val Thr Arg Ala Gly Ile
 370 375 380
 Lys Arg Met Arg Ala Gln Leu Pro His Val Lys Val His Ala Tyr Phe
 385 390 395 400
 Ala Pro Val Thr Pro Pro Thr Ala Val Ala Gly Ser Gly Gln Arg Leu
 405 410 415
 Cys Arg Cys Cys Val Ile Leu

420

<210> 142

<211> 499

<212> PRT

<213> Homo sapiens

<400> 142

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Pro Gly Lys Glu Asn Ile Asn Asp Glu Pro Val Asp Met Ser Ala Arg
1          5          10          15

Arg Ser Glu Pro Glu Arg Gly Arg Leu Thr Pro Ser Pro Asp Ile Ile
          20          25          30

Val Leu Ser Asp Asn Glu Ala Ser Ser Pro Arg Ser Ser Ser Arg Met
          35          40          45

Glu Glu Arg Leu Lys Ala Ala Asn Leu Glu Met Phe Lys Gly Lys Gly
50          55          60

Ile Glu Glu Arg Gln Gln Leu Ile Lys Gln Leu Arg Asp Glu Leu Arg
65          70          75          80

Leu Glu Glu Ala Arg Leu Val Leu Leu Lys Lys Leu Arg Gln Ser Gln
          85          90          95

Leu Gln Lys Glu Asn Val Val Gln Lys Thr Pro Val Val Gln Asn Ala
          100          105          110

Ala Ser Ile Val Gln Pro Ser Pro Ala His Val Gly Gln Gln Gly Leu
          115          120          125

Ser Lys Leu Pro Ser Arg Pro Gly Ala Gln Gly Val Glu Pro Gln Asn
          130          135          140

Leu Arg Thr Leu Gln Gly His Ser Val Ile Arg Ser Ala Thr Asn Thr
          145          150          155          160

Thr Leu Pro His Met Leu Met Ser Gln Arg Val Ile Ala Pro Asn Pro
          165          170          175

Ala Gln Leu Gln Gly Gln Arg Gly Pro Pro Lys Pro Gly Leu Val Arg
          180          185          190

Thr Thr Thr Pro Asn Met Asn Pro Ala Ile Asn Tyr Gln Pro Gln Ser
          195          200          205

Ser Ser Ser Val Pro Cys Gln Arg Thr Thr Ser Ser Ala Ile Tyr Met
          210          215          220

Asn Leu Ala Ser His Ile Gln Pro Gly Thr Val Asn Arg Val Ser Ser
          225          230          235          240

Pro Leu Pro Ser Pro Ser Ala Met Thr Asp Ala Ala Asn Ser Gln Ala
          245          250          255

Ala Ala Lys Leu Ala Leu Arg Lys Gln Leu Glu Lys Thr Leu Leu Glu
          260          265          270

Ile Pro Pro Pro Lys Pro Pro Ala Pro Leu Leu His Phe Leu Pro Ser
          275          280          285

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Ala Ala Asn Ser Glu Phe Ile Tyr Met Val Gly Leu Glu Glu Val Val
 290 295 300
 Gln Ser Val Ile Asp Ser Gln Gly Lys Ser Cys Ala Ser Leu Leu Arg
 305 310 315 320
 Val Glu Pro Phe Val Cys Ala Gln Cys Arg Thr Asp Phe Thr Pro His
 325 330 335
 Trp Lys Gln Glu Lys Asn Gly Lys Ile Leu Cys Glu Gln Cys Met Thr
 340 345 350
 Ser Asn Gln Lys Lys Ala Leu Lys Ala Glu His Thr Asn Arg Leu Lys
 355 360 365
 Asn Ala Phe Val Lys Ala Leu Gln Gln Glu Gln Glu Ile Glu Gln Arg
 370 375 380
 Leu Gln Gln Gln Ala Ala Leu Ser Pro Thr Thr Ala Pro Ala Val Ser
 385 390 395 400
 Ser Val Ser Lys Gln Glu Thr Ile Met Arg His His Thr Leu Arg Gln
 405 410 415
 Ala Pro Gln Pro Gln Ser Ser Leu Gln Arg Gly Ile Pro Thr Ser Ala
 420 425 430
 Arg Ser Met Leu Ser Asn Phe Ala Gln Ala Pro Gln Leu Ser Val Pro
 435 440 445
 Gly Gly Leu Leu Gly Met Pro Gly Val Asn Ile Ala Tyr Leu Asn Thr
 450 455 460
 Gly Ile Gly Gly His Lys Gly Pro Ser Leu Ala Asp Arg Gln Arg Glu
 465 470 475 480
 Tyr Leu Leu Asp Met Ile Pro Pro Arg Ser Ile Ser Gln Ser Ile Ser
 485 490 495
 Gly Gln Lys

<210> 143
 <211> 265
 <212> PRT
 <213> Homo sapiens

<400> 143
 Met Asn Met Ser Val Leu Thr Leu Gln Glu Tyr Glu Phe Glu Lys Gln
 1 5 10 15
 Phe Asn Glu Asn Glu Ala Ile Gln Trp Met Gln Glu Asn Trp Lys Lys
 20 25 30
 Ser Phe Leu Phe Ser Ala Leu Tyr Ala Ala Phe Ile Phe Gly Gly Arg
 35 40 45
 His Leu Met Asn Lys Arg Ala Lys Phe Glu Leu Arg Lys Pro Leu Val
 50 55 60
 Leu Trp Ser Leu Thr Leu Ala Val Phe Ser Ile Phe Gly Ala Leu Arg
 65 70 75 80

Thr Gly Ala Tyr Met Val Tyr Ile Leu Met Thr Lys Gly Leu Lys Gln
 85 90 95
 Ser Val Cys Asp Gln Gly Phe Tyr Asn Gly Pro Val Ser Lys Phe Trp
 100 105 110
 Ala Tyr Ala Phe Val Leu Ser Lys Ala Pro Glu Leu Gly Asp Thr Ile
 115 120 125
 Phe Ile Ile Leu Arg Lys Gln Lys Leu Ile Phe Leu His Trp Tyr His
 130 135 140
 His Ile Thr Val Leu Leu Tyr Ser Trp Tyr Ser Tyr Lys Asp Met Val
 145 150 155 160
 Ala Gly Gly Gly Trp Phe Met Thr Met Asn Tyr Gly Val His Ala Val
 165 170 175
 Met Tyr Ser Tyr Tyr Ala Leu Arg Ala Ala Gly Phe Arg Val Ser Arg
 180 185 190
 Lys Phe Ala Met Phe Ile Thr Leu Ser Gln Ile Thr Gln Met Leu Met
 195 200 205
 Gly Cys Val Val Asn Tyr Leu Val Phe Cys Trp Met Gln His Asp Gln
 210 215 220
 Cys His Ser His Phe Gln Asn Ile Phe Trp Ser Ser Leu Met Tyr Leu
 225 230 235 240
 Ser Tyr Leu Val Leu Phe Cys His Phe Phe Phe Glu Ala Tyr Ile Gly
 245 250 255
 Lys Met Arg Lys Thr Thr Lys Ala Glu
 260 265
 <210> 144
 <211> 351
 <212> PRT
 <213> Homo sapiens
 <400> 144
 Met Gln Arg Ala Leu Pro Gly Ala Arg Gln His Leu Gly Ala Ile Leu
 1 5 10 15
 Ala Ser Ala Ser Val Val Val Lys Ala Leu Cys Ala Ala Val Leu Phe
 20 25 30
 Leu Tyr Leu Leu Ser Phe Ala Val Asp Thr Gly Cys Leu Ala Val Thr
 35 40 45
 Pro Gly Tyr Leu Phe Pro Pro Asn Phe Trp Ile Trp Thr Leu Ala Thr
 50 55 60
 His Gly Leu Met Glu Gln His Val Trp Asp Val Ala Ile Ser Leu Thr
 65 70 75 80
 Thr Val Val Val Ala Gly Arg Leu Leu Glu Pro Leu Trp Gly Ala Leu
 85 90 95
 Glu Leu Leu Ile Phe Phe Ser Val Val Asn Val Ser Val Gly Leu Leu

100					105					110					
Gly	Ala	Phe	Ala	Tyr	Leu	Leu	Thr	Tyr	Met	Ala	Ser	Phe	Asn	Leu	Val
		115					120					125			
Tyr	Leu	Phe	Thr	Val	Arg	Ile	His	Gly	Ala	Leu	Gly	Phe	Leu	Gly	Gly
	130					135					140				
Val	Leu	Val	Ala	Leu	Lys	Gln	Thr	Met	Gly	Asp	Cys	Val	Val	Leu	Arg
145						150					155				160
Val	Pro	Gln	Val	Arg	Val	Ser	Val	Met	Pro	Met	Leu	Leu	Leu	Ala	Leu
				165					170					175	
Leu	Leu	Leu	Leu	Arg	Leu	Ala	Thr	Leu	Leu	Gln	Ser	Pro	Ala	Leu	Ala
			180					185					190		
Ser	Tyr	Gly	Phe	Gly	Leu	Leu	Ser	Ser	Trp	Val	Tyr	Leu	Arg	Phe	Tyr
	195						200					205			
Gln	Arg	His	Ser	Arg	Gly	Arg	Gly	Asp	Met	Ala	Asp	His	Phe	Ala	Phe
	210					215					220				
Ala	Thr	Phe	Phe	Pro	Glu	Ile	Leu	Gln	Pro	Val	Val	Gly	Leu	Leu	Ala
225						230					235				240
Asn	Leu	Val	His	Ser	Leu	Leu	Val	Lys	Val	Lys	Ile	Cys	Gln	Lys	Thr
				245					250					255	
Val	Lys	Arg	Tyr	Asp	Val	Gly	Ala	Pro	Ser	Ser	Ile	Thr	Ile	Ser	Leu
			260					265					270		
Pro	Gly	Thr	Asp	Pro	Gln	Asp	Ala	Glu	Arg	Arg	Arg	Gln	Leu	Ala	Leu
		275					280					285			
Lys	Ala	Leu	Asn	Glu	Arg	Leu	Lys	Arg	Val	Glu	Asp	Gln	Ser	Ile	Trp
	290					295					300				
Pro	Ser	Met	Asp	Asp	Asp	Glu	Glu	Glu	Ser	Gly	Ala	Lys	Val	Asp	Ser
305						310					315				320
Pro	Leu	Pro	Ser	Asp	Lys	Ala	Pro	Thr	Pro	Pro	Gly	Lys	Gly	Ala	Ala
				325					330					335	
Pro	Glu	Ser	Ser	Leu	Ile	Thr	Phe	Glu	Ala	Ala	Pro	Pro	Thr	Leu	
			340					345					350		
<210> 145															
<211> 315															
<212> PRT															
<213> Homo sapiens															
<400> 145															
Met	Glu	Ala	Arg	Ala	Gln	Ser	Gly	Asn	Gly	Ser	Gln	Pro	Leu	Leu	Gln
1				5					10					15	
Thr	Pro	Arg	Asp	Gly	Gly	Arg	Gln	Arg	Gly	Glu	Pro	Asp	Pro	Arg	Asp
			20				25					30			
Ala	Leu	Thr	Gln	Gln	Val	His	Val	Leu	Ser	Leu	Asp	Gln	Ile	Arg	Ala
		35					40					45			

Ile Arg Asn Thr Asn Glu Tyr Thr Glu Gly Pro Thr Val Val Pro Arg
 50 55 60
 Pro Gly Leu Lys Pro Ala Pro Arg Pro Ser Thr Gln His Lys His Glu
 65 70 75 80
 Arg Leu His Gly Leu Pro Glu His Arg Gln Pro Pro Arg Leu Gln His
 85 90 95
 Ser Gln Val His Ser Ser Ala Arg Ala Pro Leu Ser Arg Ser Ile Ser
 100 105 110
 Thr Val Ser Ser Gly Ser Arg Ser Ser Thr Arg Thr Ser Thr Ser Ser
 115 120 125
 Ser Ser Ser Glu Gln Arg Leu Leu Gly Ser Ser Phe Ser Ser Gly Pro
 130 135 140
 Val Ala Asp Gly Ile Ile Arg Val Gln Pro Lys Ser Glu Leu Lys Pro
 145 150 155 160
 Gly Glu Leu Lys Pro Leu Ser Lys Glu Asp Leu Gly Leu His Ala Tyr
 165 170 175
 Arg Cys Glu Asp Cys Gly Lys Cys Lys Cys Lys Glu Cys Thr Tyr Pro
 180 185 190
 Arg Pro Leu Pro Ser Asp Trp Ile Cys Asp Lys Gln Cys Leu Cys Ser
 195 200 205
 Ala Gln Asn Val Ile Asp Tyr Gly Thr Cys Val Cys Cys Val Lys Gly
 210 215 220
 Leu Phe Tyr His Cys Ser Asn Asp Asp Glu Asp Asn Cys Ala Asp Asn
 225 230 235 240
 Pro Cys Ser Cys Ser Gln Ser His Cys Cys Thr Arg Trp Ser Ala Met
 245 250 255
 Gly Val Met Ser Leu Phe Leu Pro Cys Leu Trp Cys Tyr Leu Pro Ala
 260 265 270
 Lys Gly Cys Leu Lys Leu Cys Gln Gly Cys Tyr Asp Arg Val Asn Arg
 275 280 285
 Pro Gly Cys Arg Cys Lys Asn Ser Asn Thr Val Cys Cys Lys Val Pro
 290 295 300
 Thr Val Pro Pro Arg Asn Phe Glu Lys Pro Thr
 305 310 315
 <210> 146
 <211> 288
 <212> PRT
 <213> Homo sapiens
 <400> 146
 Met Asp Ala Ala Val Thr Asp Asp Phe Gln Gln Ile Leu Pro Ile Glu
 1 5 10 15
 Gln Leu Arg Ser Thr His Ala Ser Asn Asp Tyr Val Glu Arg Pro Pro
 20 25 30

Ala Pro Cys Lys Gln Ala Leu Ser Ser Pro Ser Leu Ile Val Gln Thr
 35 40 45
 His Lys Ser Asp Trp Ser Leu Ala Thr Met Pro Thr Ser Leu Pro Arg
 50 55 60
 Ser Leu Ser Gln Cys His Gln Leu Gln Pro Leu Pro Gln His Leu Ser
 65 70 75 80
 Gln Ser Ser Ile Ala Ser Ser Met Ser His Ser Thr Thr Ala Ser Asp
 85 90 95
 Gln Arg Leu Leu Ala Ser Ile Thr Pro Ser Pro Ser Gly Gln Ser Ile
 100 105 110
 Ile Arg Thr Gln Pro Gly Ala Gly Val His Pro Lys Ala Asp Gly Ala
 115 120 125
 Leu Lys Gly Glu Ala Glu Gln Ser Ala Gly His Pro Ser Glu His Leu
 130 135 140
 Phe Ile Cys Glu Glu Cys Gly Arg Cys Lys Cys Val Pro Cys Thr Ala
 145 150 155 160
 Ala Arg Pro Leu Pro Ser Cys Trp Leu Cys Asn Gln Arg Cys Leu Cys
 165 170 175
 Ser Ala Glu Ser Leu Leu Asp Tyr Gly Thr Cys Leu Cys Cys Val Lys
 180 185 190
 Gly Leu Phe Tyr His Cys Ser Thr Asp Asp Glu Asp Asn Cys Ala Asp
 195 200 205
 Glu Pro Cys Ser Cys Gly Pro Ser Ser Cys Phe Val Arg Trp Ala Ala
 210 215 220
 Met Ser Leu Ile Ser Leu Phe Leu Pro Cys Leu Cys Cys Tyr Leu Pro
 225 230 235 240
 Thr Arg Gly Cys Leu His Leu Cys Gln Gln Gly Tyr Asp Ser Leu Arg
 245 250 255
 Arg Pro Gly Cys Arg Cys Lys Arg His Thr Asn Thr Val Cys Arg Lys
 260 265 270
 Ile Ser Ser Gly Ser Ala Pro Phe Pro Lys Ala Gln Glu Lys Ser Val
 275 280 285
 <210> 147
 <211> 322
 <212> PRT
 <213> Homo sapiens
 <400> 147
 Met Leu Ser Pro Leu Pro Thr Gly Pro Leu Glu Ala Cys Phe Ser Val
 1 5 10 15
 Gln Ser Arg Thr Ser Ser Pro Met Glu Pro Pro Ile Pro Gln Ser Ala
 20 25 30
 Pro Leu Thr Pro Asn Ser Val Met Val Gln Pro Leu Leu Asp Ser Arg

35					40					45					
Met	Ser	His	Ser	Arg	Leu	Gln	His	Pro	Leu	Thr	Ile	Leu	Pro	Ile	Asp
50						55					60				
Gln	Val	Lys	Thr	Ser	His	Val	Glu	Asn	Asp	Tyr	Ile	Asp	Asn	Pro	Ser
65					70					75					80
Leu	Ala	Leu	Thr	Thr	Gly	Pro	Lys	Arg	Thr	Arg	Gly	Gly	Ala	Pro	Glu
					85					90				95	
Leu	Ala	Pro	Thr	Pro	Ala	Arg	Cys	Asp	Gln	Asp	Val	Thr	His	His	Trp
			100					105					110		
Ile	Ser	Phe	Ser	Gly	Arg	Pro	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ser	Thr
		115					120					125			
Ser	Ser	Asp	Gln	Arg	Leu	Leu	Asp	His	Met	Ala	Pro	Pro	Pro	Val	Ala
		130				135					140				
Asp	Gln	Ala	Ser	Pro	Arg	Ala	Val	Arg	Ile	Gln	Pro	Lys	Val	Val	His
145					150					155					160
Cys	Gln	Pro	Leu	Asp	Leu	Lys	Gly	Pro	Ala	Val	Pro	Pro	Glu	Leu	Asp
					165				170					175	
Lys	His	Phe	Leu	Leu	Cys	Glu	Ala	Cys	Gly	Lys	Cys	Lys	Cys	Lys	Glu
			180					185					190		
Cys	Ala	Ser	Pro	Arg	Thr	Leu	Pro	Ser	Cys	Trp	Val	Cys	Asn	Gln	Glu
		195					200					205			
Cys	Leu	Cys	Ser	Ala	Gln	Thr	Leu	Val	Asn	Tyr	Gly	Thr	Cys	Met	Cys
		210				215					220				
Leu	Val	Gln	Gly	Ile	Phe	Tyr	His	Cys	Thr	Asn	Glu	Asp	Asp	Glu	Gly
225					230					235					240
Ser	Cys	Ala	Asp	His	Pro	Cys	Ser	Cys	Ser	Arg	Ser	Asn	Cys	Cys	Ala
				245					250					255	
Arg	Trp	Ser	Phe	Met	Gly	Ala	Leu	Ser	Val	Val	Leu	Pro	Cys	Leu	Leu
			260					265					270		
Cys	Tyr	Leu	Pro	Ala	Thr	Gly	Cys	Val	Lys	Leu	Ala	Gln	Arg	Gly	Tyr
		275					280					285			
Asp	Arg	Leu	Arg	Arg	Pro	Gly	Cys	Arg	Cys	Lys	His	Thr	Asn	Ser	Val
		290				295					300				
Ile	Cys	Lys	Ala	Ala	Ser	Gly	Asp	Ala	Lys	Thr	Ser	Arg	Pro	Asp	Lys
305					310					315					320
Pro	Phe														

<210> 148
 <211> 333
 <212> PRT
 <213> Homo sapiens
 <400> 148

Met Ala Ala Ala Ala Ala Gly Thr Ala Thr Ser Gln Arg Phe Phe Gln
 1 5 10 15
 Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln Ala Ala Leu Glu
 20 25 30
 Glu Leu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp Ala Gln Tyr Tyr
 35 40 45
 Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn Tyr Cys Val Ala
 50 55 60
 Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro Asn Asn Ser Thr
 65 70 75 80
 Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu Lys Asn Tyr Ala
 85 90 95
 Ala Ala Leu Glu Thr Phe Thr Glu Gly Gln Lys Leu Asp Ser Ala Asp
 100 105 110
 Ala Asn Phe Ser Val Trp Ile Lys Arg Cys Gln Glu Ala Gln Asn Gly
 115 120 125
 Ser Glu Ser Glu Val Trp Thr His Gln Ser Lys Ile Lys Tyr Asp Trp
 130 135 140
 Tyr Gln Thr Glu Ser Gln Val Val Ile Thr Leu Met Ile Lys Asn Val
 145 150 155 160
 Gln Lys Asn Asp Val Asn Val Glu Phe Ser Glu Lys Glu Leu Ser Ala
 165 170 175
 Leu Val Lys Leu Pro Ser Gly Glu Asp Tyr Asn Leu Lys Leu Glu Leu
 180 185 190
 Leu His Pro Ile Ile Pro Glu Gln Ser Thr Phe Lys Val Leu Ser Thr
 195 200 205
 Lys Ile Glu Ile Lys Leu Lys Lys Pro Glu Ala Val Arg Trp Glu Lys
 210 215 220
 Leu Glu Gly Gln Gly Asp Val Pro Thr Pro Lys Gln Phe Val Ala Asp
 225 230 235 240
 Val Lys Asn Leu Tyr Pro Ser Ser Ser Pro Tyr Thr Arg Asn Trp Asp
 245 250 255
 Lys Leu Val Gly Glu Ile Lys Glu Glu Glu Lys Asn Glu Lys Leu Glu
 260 265 270
 Gly Asp Ala Ala Leu Asn Arg Leu Phe Gln Gln Ile Tyr Ser Asp Gly
 275 280 285
 Ser Asp Glu Val Lys Arg Ala Met Asn Lys Ser Phe Met Glu Ser Gly
 290 295 300
 Gly Thr Val Leu Ser Thr Asn Trp Ser Asp Val Gly Lys Arg Lys Val
 305 310 315 320
 Glu Ile Asn Pro Pro Asp Asp Met Glu Trp Lys Lys Tyr
 325 330

<210> 149
 <211> 362
 <212> PRT
 <213> Homo sapiens

<400> 149

Ser Leu Phe Cys Ile Ser Leu Asn Arg Leu Pro Leu Ser Pro Gly Pro
 1 5 10 15
 Ser Thr Leu Val Ser Cys Ala Ala Ser Val Arg Ala Met Ala Thr Glu
 20 25 30
 Glu Lys Lys Pro Glu Thr Glu Ala Ala Arg Ala Gln Pro Thr Pro Ser
 35 40 45
 Ser Ser Ala Thr Gln Ser Lys Pro Thr Pro Val Lys Pro Asn Tyr Ala
 50 55 60
 Leu Lys Phe Thr Leu Ala Gly His Thr Lys Ala Val Ser Ser Val Lys
 65 70 75 80
 Phe Ser Pro Asn Gly Glu Trp Leu Ala Ser Ser Ser Ala Asp Lys Leu
 85 90 95
 Ile Lys Ile Trp Gly Ala Tyr Asp Gly Lys Phe Glu Lys Thr Ile Ser
 100 105 110
 Gly His Lys Leu Gly Ile Ser Asp Val Ala Trp Ser Ser Asp Ser Asn
 115 120 125
 Leu Leu Val Ser Ala Ser Asp Asp Lys Thr Leu Lys Ile Trp Asp Val
 130 135 140
 Ser Ser Gly Lys Cys Leu Lys Thr Leu Lys Gly His Ser Asn Tyr Val
 145 150 155 160
 Phe Cys Cys Asn Phe Asn Pro Gln Ser Asn Leu Ile Val Ser Gly Ser
 165 170 175
 Phe Asp Glu Ser Val Arg Ile Trp Asp Val Lys Thr Gly Lys Cys Leu
 180 185 190
 Lys Thr Leu Pro Ala His Ser Asp Pro Val Ser Ala Val His Phe Asn
 195 200 205
 Arg Asp Gly Ser Leu Ile Val Ser Ser Ser Tyr Asp Gly Leu Cys Arg
 210 215 220
 Ile Trp Asp Thr Ala Ser Gly Gln Cys Leu Lys Thr Leu Ile Asp Asp
 225 230 235 240
 Asp Asn Pro Pro Val Ser Phe Val Lys Phe Ser Pro Asn Gly Lys Tyr
 245 250 255
 Ile Leu Ala Ala Thr Leu Asp Asn Thr Leu Lys Leu Trp Asp Tyr Ser
 260 265 270
 Lys Gly Lys Cys Leu Lys Thr Tyr Thr Gly His Lys Asn Glu Lys Tyr
 275 280 285
 Cys Ile Phe Ala Asn Phe Ser Val Thr Gly Gly Lys Trp Ile Val Ser

290 295 300
 Gly Ser Glu Asp Asn Leu Val Tyr Ile Trp Asn Leu Gln Thr Lys Glu
 305 310 315 320
 Ile Val Gln Lys Leu Gln Gly His Thr Asp Val Val Ile Ser Thr Ala
 325 330 335
 Cys His Pro Thr Glu Asn Ile Ile Ala Ser Ala Ala Leu Glu Asn Asp
 340 345 350
 Lys Thr Ile Lys Leu Trp Lys Ser Asp Cys
 355 360

 <210> 150
 <211> 514
 <212> PRT
 <213> Homo sapiens

 <400> 150
 Met Ser Ile Ser Ser Asp Glu Val Asn Phe Leu Val Tyr Arg Tyr Leu
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 Gln Glu Ser Gly Phe Ser His Ser Ala Phe Thr Phe Gly Ile Glu Ser
 20 25 30
 His Ile Ser Gln Ser Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala
 35 40 45
 Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val
 50 55 60
 Ser Ile Asn Glu Asp Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser
 65 70 75 80
 Leu Ser Leu Ile Asp Ala Val Met Pro Asp Val Val Gln Thr Arg Gln
 85 90 95
 Gln Ala Tyr Arg Asp Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala Ala
 100 105 110
 Ala Ala Ala Ala Ala Ala Ser Gln Gln Gly Ser Ala Lys Asn Gly Glu
 115 120 125
 Asn Thr Ala Asn Gly Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn
 130 135 140
 His Thr Asp Met Met Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn
 145 150 155 160
 Lys Ala Val Val Leu Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala
 165 170 175
 Trp Asn Pro Val Ser Asp Leu Leu Ala Ser Gly Ser Gly Asp Ser Thr
 180 185 190
 Ala Arg Ile Trp Asn Leu Ser Glu Asn Ser Thr Ser Gly Ser Thr Gln
 195 200 205
 Leu Val Leu Arg His Cys Ile Arg Glu Gly Gly Gln Asp Val Pro Ser
 210 215 220

Asn Lys Asp Val Thr Ser Leu Asp Trp Asn Ser Glu Gly Thr Leu Leu
 225 230 235 240
 Ala Thr Gly Ser Tyr Asp Gly Phe Ala Arg Ile Trp Thr Lys Asp Gly
 245 250 255
 Asn Leu Ala Ser Thr Leu Gly Gln His Lys Gly Pro Ile Phe Ala Leu
 260 265 270
 Lys Trp Asn Lys Lys Gly Asn Phe Ile Leu Ser Ala Gly Val Asp Lys
 275 280 285
 Thr Thr Ile Ile Trp Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe
 290 295 300
 Pro Phe His Ser Ala Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn
 305 310 315 320
 Thr Phe Ala Ser Cys Ser Thr Asp Met Cys Ile His Val Cys Lys Leu
 325 330 335
 Gly Gln Asp Arg Pro Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val
 340 345 350
 Asn Ala Ile Lys Trp Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser
 355 360 365
 Asp Asp Met Thr Leu Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val
 370 375 380
 His Asp Leu Gln Ala His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser
 385 390 395 400
 Pro Thr Gly Pro Gly Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala
 405 410 415
 Ser Ala Ser Phe Asp Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly
 420 425 430
 Ile Cys Ile His Thr Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val
 435 440 445
 Ala Phe Ser Pro Asp Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys
 450 455 460
 Cys Val His Ile Trp Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr
 465 470 475 480
 Arg Gly Thr Gly Gly Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp
 485 490 495
 Lys Val Gly Ala Ser Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu
 500 505 510

Arg Lys

<210> 151
 <211> 619
 <212> PRT
 <213> Homo sapiens

<400> 151

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Met Ser Val Ala His Met Ser Leu Gln Ala Ala Ala Ala Leu Leu Lys
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Gly Arg Ser Val Leu Asp Ala Thr Gly Gln Arg Cys Arg Val Val Lys
20          25          30

Arg Ser Phe Ala Phe Pro Ser Phe Leu Glu Glu Asp Val Val Asp Gly
35          40          45

Ala Asp Thr Phe Asp Ser Ser Phe Phe Ser Lys Glu Glu Met Ser Ser
50          55          60

Met Pro Asp Asp Val Phe Glu Ser Pro Pro Leu Ser Ala Ser Tyr Phe
65          70          75          80

Arg Gly Ile Pro His Ser Ala Ser Pro Val Ser Pro Asp Gly Val Gln
85          90          95

Ile Pro Leu Lys Glu Tyr Gly Arg Ala Pro Val Pro Gly Pro Arg Arg
100         105         110

Gly Lys Arg Ile Ala Ser Lys Val Lys His Phe Ala Phe Asp Arg Lys
115         120         125

Lys Arg His Tyr Gly Leu Gly Val Val Gly Asn Trp Leu Asn Arg Ser
130         135         140

Tyr Arg Arg Ser Ile Ser Ser Thr Val Gln Arg Gln Leu Glu Ser Phe
145         150         155         160

Asp Ser His Arg Pro Tyr Phe Thr Tyr Trp Leu Thr Phe Val His Val
165         170         175

Ile Ile Thr Leu Leu Val Ile Cys Thr Tyr Gly Ile Ala Pro Val Gly
180         185         190

Phe Ala Gln His Val Thr Thr Gln Leu Val Leu Arg Asn Lys Gly Val
195         200         205

Tyr Glu Ser Val Lys Tyr Ile Gln Gln Glu Asn Phe Trp Val Gly Pro
210         215         220

Ser Ser Ile Asp Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys Ile
225         230         235         240

Arg Lys Asp Gly Gln Ile Glu Gln Leu Val Leu Arg Glu Arg Asp Leu
245         250         255

Glu Arg Asp Ser Gly Cys Cys Val Gln Asn Asp His Ser Gly Cys Ile
260         265         270

Gln Thr Gln Arg Lys Asp Cys Ser Glu Thr Leu Ala Thr Phe Val Lys
275         280         285

Trp Gln Asp Asp Thr Gly Pro Pro Met Asp Lys Ser Asp Leu Gly Gln
290         295         300

Lys Arg Thr Ser Gly Ala Val Cys His Gln Asp Pro Arg Thr Cys Glu
305         310         315         320

Glu Pro Ala Ser Ser Gly Ala His Ile Trp Pro Asp Asp Ile Thr Lys

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325	330	335
Trp Pro Ile Cys Thr Glu Gln Ala Arg Ser Asn His Thr Gly Phe Leu		
340	345	350
His Met Asp Cys Glu Ile Lys Gly Arg Pro Cys Cys Ile Gly Thr Lys		
355	360	365
Gly Ser Cys Glu Ile Thr Thr Arg Glu Tyr Cys Glu Phe Met His Gly		
370	375	380
Tyr Phe His Glu Glu Ala Thr Leu Cys Ser Gln Val His Cys Leu Asp		
385	390	400
Lys Val Cys Gly Leu Leu Pro Phe Leu Asn Pro Glu Val Pro Asp Gln		
405	410	415
Phe Tyr Arg Leu Trp Leu Ser Leu Phe Leu His Ala Gly Val Val His		
420	425	430
Cys Leu Val Ser Val Val Phe Gln Met Thr Ile Leu Arg Asp Leu Glu		
435	440	445
Lys Leu Ala Gly Trp His Arg Ile Ala Ile Ile Phe Ile Leu Ser Gly		
450	455	460
Ile Thr Gly Asn Leu Ala Ser Ala Ile Phe Leu Pro Tyr Arg Ala Glu		
465	470	475
Val Gly Pro Ala Gly Ser Gln Phe Gly Leu Leu Ala Cys Leu Phe Val		
485	490	495
Glu Leu Phe Gln Ser Trp Pro Leu Leu Glu Arg Pro Trp Lys Ala Phe		
500	505	510
Leu Asn Leu Ser Ala Ile Val Leu Phe Leu Phe Ile Cys Gly Leu Leu		
515	520	525
Pro Trp Ile Asp Asn Ile Ala His Ile Phe Gly Phe Leu Ser Gly Leu		
530	535	540
Leu Leu Ala Phe Ala Phe Leu Pro Tyr Ile Thr Phe Gly Thr Ser Asp		
545	550	555
Lys Tyr Arg Lys Arg Ala Leu Ile Leu Val Ser Leu Leu Ala Phe Ala		
565	570	575
Gly Leu Phe Ala Ala Leu Val Leu Trp Leu Tyr Ile Tyr Pro Ile Asn		
580	585	590
Trp Pro Trp Ile Glu His Leu Thr Cys Phe Pro Phe Thr Ser Arg Phe		
595	600	605
Cys Glu Lys Tyr Glu Leu Asp Gln Val Leu His		
610	615	

<210> 152
 <211> 607
 <212> PRT
 <213> Homo sapiens
 <400> 152

Met Glu Ala Pro Ala Ala Gly Leu Phe Leu Leu Leu Leu Leu Gly Thr
 1 5 10 15
 Trp Ala Pro Ala Pro Gly Ser Ala Ser Ser Glu Ala Pro Pro Leu Ile
 20 25 30
 Asn Glu Asp Val Lys Arg Thr Val Asp Leu Ser Ser His Leu Ala Lys
 35 40 45
 Val Thr Ala Glu Val Val Leu Ala His Leu Gly Gly Gly Ser Thr Ser
 50 55 60
 Arg Ala Thr Ser Phe Leu Leu Ala Leu Glu Pro Glu Leu Glu Ala Arg
 65 70 75 80
 Leu Ala His Leu Gly Val Gln Val Lys Gly Glu Asp Glu Glu Glu Asn
 85 90 95
 Asn Leu Glu Val Arg Glu Thr Lys Ile Lys Gly Lys Ser Gly Arg Phe
 100 105 110
 Phe Thr Val Lys Leu Pro Val Ala Leu Asp Pro Gly Ala Lys Ile Ser
 115 120 125
 Val Ile Val Glu Thr Val Tyr Thr His Val Leu His Pro Tyr Pro Thr
 130 135 140
 Gln Ile Thr Gln Ser Glu Lys Gln Phe Val Val Phe Glu Gly Asn His
 145 150 155 160
 Tyr Phe Tyr Ser Pro Tyr Pro Thr Lys Thr Gln Thr Met Arg Val Lys
 165 170 175
 Leu Ala Ser Arg Asn Val Glu Ser Tyr Thr Lys Leu Gly Asn Pro Thr
 180 185 190
 Arg Ser Glu Asp Leu Leu Asp Tyr Gly Pro Phe Arg Asp Val Pro Ala
 195 200 205
 Tyr Ser Gln Asp Thr Phe Lys Val His Tyr Glu Asn Asn Ser Pro Phe
 210 215 220
 Leu Thr Ile Thr Ser Met Thr Arg Val Ile Glu Val Ser His Trp Gly
 225 230 235 240
 Asn Ile Ala Val Glu Glu Asn Val Asp Leu Lys His Thr Gly Ala Val
 245 250 255
 Leu Lys Gly Pro Phe Ser Arg Tyr Asp Tyr Gln Arg Gln Pro Asp Ser
 260 265 270
 Gly Ile Ser Ser Ile Arg Ser Phe Lys Thr Ile Leu Pro Ala Ala Ala
 275 280 285
 Gln Asp Val Tyr Tyr Arg Asp Glu Ile Gly Asn Val Ser Thr Ser His
 290 295 300
 Leu Leu Ile Leu Asp Asp Ser Val Glu Met Glu Ile Arg Pro Arg Phe
 305 310 315 320
 Pro Leu Phe Gly Gly Trp Lys Thr His Tyr Ile Val Gly Tyr Asn Leu
 325 330 335

Pro Ser Tyr Glu Tyr Leu Tyr Asn Leu Gly Asp Gln Tyr Ala Leu Lys
 340 345 350
 Met Arg Phe Val Asp His Val Phe Asp Glu Gln Val Ile Asp Ser Leu
 355 360 365
 Thr Val Lys Ile Ile Leu Pro Glu Gly Ala Lys Asn Ile Glu Ile Asp
 370 375 380
 Ser Pro Tyr Glu Ile Ser Arg Ala Pro Asp Glu Leu His Tyr Thr Tyr
 385 390 395 400
 Leu Asp Thr Phe Gly Arg Pro Val Ile Val Ala Tyr Lys Lys Asn Leu
 405 410 415
 Val Glu Gln His Ile Gln Asp Ile Val Val His Tyr Thr Phe Asn Lys
 420 425 430
 Val Leu Met Leu Gln Glu Pro Leu Leu Val Val Ala Ala Phe Tyr Ile
 435 440 445
 Leu Phe Phe Thr Val Ile Ile Tyr Val Arg Leu Asp Phe Ser Ile Thr
 450 455 460
 Lys Asp Pro Ala Ala Glu Ala Arg Met Lys Val Ala Cys Ile Thr Glu
 465 470 475 480
 Gln Val Leu Thr Leu Val Asn Lys Arg Ile Gly Leu Tyr Arg His Phe
 485 490 495
 Asp Glu Thr Val Asn Arg Tyr Lys Gln Ser Arg Asp Ile Ser Thr Leu
 500 505 510
 Asn Ser Gly Lys Lys Ser Leu Glu Thr Glu His Lys Ala Leu Thr Ser
 515 520 525
 Glu Ile Ala Leu Leu Gln Ser Arg Leu Lys Thr Glu Gly Ser Asp Leu
 530 535 540
 Cys Asp Arg Val Ser Glu Met Gln Lys Leu Asp Ala Gln Val Lys Glu
 545 550 555 560
 Leu Val Leu Lys Ser Ala Val Glu Ala Glu Arg Leu Val Ala Gly Lys
 565 570 575
 Leu Lys Lys Asp Thr Tyr Ile Glu Asn Glu Lys Leu Ile Ser Gly Lys
 580 585 590
 Arg Gln Glu Leu Val Thr Lys Ile Asp His Ile Leu Asp Ala Leu
 595 600 605
 <210> 153
 <211> 601
 <212> PRT
 <213> Homo sapiens
 <400> 153
 Arg Trp Leu Arg Arg Ala Pro Ala Asp Met Ala Ala Ala Val Ala Ala
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 Ala Leu Ala Arg Leu Leu Ala Ala Phe Leu Leu Leu Ala Ala Gln Val

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Ala	Cys	Glu	Tyr	Gly	Met	Val	His	Val	Val	Ser	Gln	Ala	Gly	Gly	Pro
		35					40					45			
Glu	Gly	Lys	Asp	Tyr	Cys	Ile	Leu	Tyr	Asn	Pro	Gln	Trp	Ala	His	Leu
	50					55					60				
Pro	His	Asp	Leu	Ser	Lys	Ala	Ser	Phe	Leu	Gln	Leu	Arg	Asn	Trp	Thr
65					70					75					80
Ala	Ser	Leu	Leu	Cys	Ser	Ala	Ala	Asp	Leu	Pro	Ala	Arg	Gly	Phe	Ser
				85					90					95	
Asn	Gln	Ile	Pro	Leu	Val	Ala	Arg	Gly	Asn	Cys	Thr	Phe	Tyr	Glu	Lys
			100					105						110	
Val	Arg	Leu	Ala	Gln	Gly	Ser	Gly	Ala	Arg	Gly	Leu	Leu	Ile	Val	Ser
		115					120					125			
Arg	Glu	Arg	Leu	Val	Pro	Pro	Gly	Gly	Asn	Lys	Thr	Gln	Tyr	Asp	Glu
	130					135					140				
Ile	Gly	Ile	Pro	Val	Ala	Leu	Leu	Ser	Tyr	Lys	Asp	Met	Leu	Asp	Ile
145					150					155					160
Phe	Thr	Arg	Phe	Gly	Arg	Thr	Val	Arg	Ala	Ala	Leu	Tyr	Ala	Pro	Lys
				165					170					175	
Glu	Pro	Val	Leu	Asp	Tyr	Asn	Met	Val	Ile	Ile	Phe	Ile	Met	Ala	Val
			180					185					190		
Gly	Thr	Val	Ala	Ile	Gly	Gly	Tyr	Trp	Ala	Gly	Ser	Arg	Asp	Val	Lys
		195					200					205			
Lys	Arg	Tyr	Met	Lys	His	Lys	Arg	Asp	Asp	Gly	Pro	Glu	Lys	Gln	Glu
	210					215					220				
Asp	Glu	Ala	Val	Asp	Val	Thr	Pro	Val	Met	Thr	Cys	Val	Phe	Val	Val
225					230					235					240
Met	Cys	Cys	Ser	Met	Leu	Val	Leu	Leu	Tyr	Tyr	Phe	Tyr	Asp	Leu	Leu
				245					250					255	
Val	Tyr	Val	Val	Ile	Gly	Ile	Phe	Cys	Leu	Ala	Ser	Ala	Thr	Gly	Leu
			260					265					270		
Tyr	Ser	Cys	Leu	Ala	Pro	Cys	Val	Arg	Arg	Leu	Pro	Phe	Gly	Lys	Cys
		275				280						285			
Arg	Ile	Pro	Asn	Asn	Ser	Leu	Pro	Tyr	Phe	His	Lys	Arg	Pro	Gln	Ala
	290					295					300				
Arg	Met	Leu	Leu	Leu	Ala	Leu	Phe	Cys	Val	Ala	Val	Ser	Val	Val	Trp
305					310					315					320
Gly	Val	Phe	Arg	Asn	Glu	Asp	Gln	Trp	Ala	Trp	Val	Leu	Gln	Asp	Ala
				325					330					335	
Leu	Gly	Ile	Ala	Phe	Cys	Leu	Tyr	Met	Leu	Lys	Thr	Ile	Arg	Leu	Pro
			340					345					350		

Thr Phe Lys Ala Cys Thr Leu Leu Leu Val Leu Phe Leu Tyr Asp
 355 360 365
 Ile Phe Phe Val Phe Ile Thr Pro Phe Leu Thr Lys Ser Gly Ser Ser
 370 375 380
 Ile Met Val Glu Val Ala Thr Gly Pro Ser Asp Ser Ala Thr Arg Glu
 385 390 395 400
 Lys Leu Pro Met Val Leu Lys Val Pro Arg Leu Asn Ser Ser Pro Leu
 405 410 415
 Ala Leu Cys Asp Arg Pro Phe Ser Leu Leu Gly Phe Gly Asp Ile Leu
 420 425 430
 Val Pro Gly Leu Leu Val Ala Tyr Cys His Arg Phe Asp Ile Gln Val
 435 440 445
 Gln Ser Ser Arg Val Tyr Phe Val Ala Cys Thr Ile Ala Tyr Gly Val
 450 455 460
 Gly Leu Leu Val Thr Phe Val Ala Leu Ala Leu Met Gln Arg Gly Gln
 465 470 475 480
 Pro Ala Leu Leu Tyr Leu Val Pro Cys Thr Leu Val Thr Ser Cys Ala
 485 490 495
 Val Ala Leu Trp Arg Arg Glu Leu Gly Val Phe Trp Thr Gly Ser Gly
 500 505 510
 Phe Ala Lys Val Leu Pro Pro Ser Pro Trp Ala Pro Ala Pro Ala Asp
 515 520 525
 Gly Pro Gln Pro Pro Lys Asp Ser Ala Thr Pro Leu Ser Pro Gln Pro
 530 535 540
 Pro Ser Glu Glu Pro Ala Thr Ser Pro Trp Pro Ala Glu Gln Ser Pro
 545 550 555 560
 Lys Ser Arg Thr Ser Glu Glu Met Gly Ala Gly Ala Pro Met Arg Glu
 565 570 575
 Pro Gly Ser Pro Ala Glu Ser Glu Gly Arg Asp Gln Ala Gln Pro Ser
 580 585 590
 Pro Val Thr Gln Pro Gly Ala Ser Ala
 595 600
 <210> 154
 <211> 377
 <212> PRT
 <213> Homo sapiens
 <400> 154
 Met Asp Ser Ala Leu Ser Asp Pro His Asn Gly Ser Ala Glu Ala Gly
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 Gly Pro Thr Asn Ser Thr Thr Arg Pro Pro Ser Thr Pro Glu Gly Ile
 20 25 30
 Ala Leu Ala Tyr Gly Ser Leu Leu Leu Met Ala Leu Leu Pro Ile Phe
 35 40 45

Phe Gly Ala Leu Arg Ser Val Arg Cys Ala Arg Gly Lys Asn Ala Ser
 50 55 60
 Asp Met Pro Glu Thr Ile Thr Ser Arg Asp Ala Ala Arg Phe Pro Ile
 65 70 75 80
 Ile Ala Ser Cys Thr Leu Leu Gly Leu Tyr Leu Phe Phe Lys Ile Phe
 85 90 95
 Ser Gln Glu Tyr Ile Asn Leu Leu Leu Ser Met Tyr Phe Phe Val Leu
 100 105 110
 Gly Ile Leu Ala Leu Ser His Thr Ile Ser Pro Phe Met Asn Lys Phe
 115 120 125
 Phe Pro Ala Ser Phe Pro Asn Arg Gln Tyr Gln Leu Leu Phe Thr Gln
 130 135 140
 Gly Ser Gly Glu Asn Lys Glu Glu Ile Ile Asn Tyr Glu Phe Asp Thr
 145 150 155 160
 Lys Asp Leu Val Cys Leu Gly Leu Ser Ser Ile Val Gly Val Trp Tyr
 165 170 175
 Leu Leu Arg Lys His Trp Ile Ala Asn Asn Leu Phe Gly Leu Ala Phe
 180 185 190
 Ser Leu Asn Gly Val Glu Leu Leu His Leu Asn Asn Val Ser Thr Gly
 195 200 205
 Cys Ile Leu Leu Gly Gly Leu Phe Ile Tyr Asp Val Phe Trp Val Phe
 210 215 220
 Gly Thr Asn Val Met Val Thr Val Ala Lys Ser Phe Glu Ala Pro Ile
 225 230 235 240
 Lys Leu Val Phe Pro Gln Asp Leu Leu Glu Lys Gly Leu Glu Ala Asn
 245 250 255
 Asn Phe Ala Met Leu Gly Leu Gly Asp Val Val Ile Pro Gly Ile Phe
 260 265 270
 Ile Ala Leu Leu Leu Arg Phe Asp Ile Ser Leu Lys Lys Asn Thr His
 275 280 285
 Thr Tyr Phe Tyr Thr Ser Phe Ala Ala Tyr Ile Phe Gly Leu Gly Leu
 290 295 300
 Thr Ile Phe Ile Met His Ile Phe Lys His Ala Gln Pro Ala Leu Leu
 305 310 315 320
 Tyr Leu Val Pro Ala Cys Ile Gly Phe Pro Val Leu Val Ala Leu Ala
 325 330 335
 Lys Gly Glu Val Thr Glu Met Phe Ser Tyr Glu Glu Ser Asn Pro Lys
 340 345 350
 Asp Pro Ala Ala Val Thr Glu Ser Lys Glu Gly Thr Glu Ala Ser Ala
 355 360 365
 Ser Lys Gly Leu Glu Lys Lys Glu Lys

370 375

<210> 155
 <211> 743
 <212> PRT
 <213> Homo sapiens

<400> 155
 Met Ala Val Ala Val Arg Thr Leu Gln Glu Gln Leu Glu Lys Ala Lys
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 Glu Ser Leu Lys Asn Val Asp Glu Asn Ile Arg Lys Leu Thr Gly Arg
 20 25 30
 Asp Pro Asn Asp Val Arg Pro Ile Gln Ala Arg Leu Leu Ala Leu Ser
 35 40 45
 Gly Pro Gly Gly Gly Arg Gly Arg Gly Ser Leu Leu Leu Arg Arg Gly
 50 55 60
 Phe Ser Asp Ser Gly Gly Pro Pro Ala Lys Gln Arg Asp Leu Glu Gly
 65 70 75 80
 Ala Val Ser Arg Leu Gly Gly Glu Arg Arg Thr Arg Arg Glu Ser Arg
 85 90 95
 Gln Glu Ser Asp Pro Glu Asp Asp Asp Val Lys Lys Pro Ala Leu Gln
 100 105 110
 Ser Ser Val Val Ala Thr Ser Lys Glu Arg Thr Arg Arg Asp Leu Ile
 115 120 125
 Gln Asp Gln Asn Met Asp Glu Lys Gly Lys Gln Arg Asn Arg Arg Ile
 130 135 140
 Phe Gly Leu Leu Met Gly Thr Leu Gln Lys Phe Lys Gln Glu Ser Thr
 145 150 155 160
 Val Ala Thr Glu Arg Gln Asn Arg Arg Gln Glu Ile Glu Gln Lys Leu
 165 170 175
 Glu Val Gln Ala Glu Glu Glu Arg Lys Gln Val Glu Asn Glu Arg Arg
 180 185 190
 Glu Leu Phe Glu Glu Arg Arg Ala Lys Gln Thr Glu Leu Arg Leu Leu
 195 200 205
 Glu Gln Lys Val Glu Leu Ala Gln Leu Gln Glu Glu Trp Asn Glu His
 210 215 220
 Asn Ala Lys Ile Ile Lys Tyr Ile Arg Thr Lys Thr Lys Pro His Leu
 225 230 235 240
 Phe Tyr Ile Pro Gly Arg Met Cys Pro Ala Thr Gln Lys Leu Ile Glu
 245 250 255
 Glu Ser Gln Arg Lys Met Asn Ala Leu Phe Asp Gly Arg Arg Ile Glu
 260 265 270
 Phe Ala Glu Gln Ile Asn Lys Met Glu Ala Arg Pro Arg Arg Gln Ser
 275 280 285

Met Lys Glu Lys Glu His Gln Val Val Arg Asn Glu Glu His Lys Ala
 290 295 300
 Glu Gln Glu Glu Gly Lys Val Ala Gln Arg Glu Glu Glu Leu Val Glu
 305 310 315 320
 Thr Gly Asn Gln His Asn Asp Val Glu Ile Glu Glu Ala Gly Glu Glu
 325 330 335
 Glu Glu Lys Glu Ile Gly Ile Val His Ser Asp Ala Glu Lys Glu Gln
 340 345 350
 Glu Glu Glu Glu Gln Lys Gln Glu Met Glu Val Lys Met Glu Glu Glu
 355 360 365
 Thr Glu Val Arg Glu Ser Glu Lys Gln Gln Asp Ser Gln Pro Glu Glu
 370 375 380
 Val Met Asp Val Leu Glu Met Val Glu Asn Val Lys His Val Ile Ala
 385 390 395 400
 Asp Gln Glu Val Met Glu Thr Asn Arg Val Glu Ser Val Glu Pro Ser
 405 410 415
 Glu Asn Glu Ala Ser Lys Glu Leu Glu Pro Glu Met Glu Phe Glu Ile
 420 425 430
 Glu Pro Asp Lys Glu Cys Lys Ser Leu Ser Pro Gly Lys Glu Asn Val
 435 440 445
 Ser Ala Leu Asp Met Glu Lys Glu Ser Asp Glu Lys Glu Glu Lys Glu
 450 455 460
 Ser Glu Pro Gln Pro Glu Pro Val Ala Gln Pro Gln Ala Gln Ser Gln
 465 470 475 480
 Pro Gln Leu Gln Leu Gln Ser Gln Ser Glu Pro Gln Pro Gln Leu Gln
 485 490 495
 Pro Glu Pro Ala Gln Pro Gln Leu Gln Ser Gln Pro Gln Leu Gln Leu
 500 505 510
 Gln Ser Gln Cys His Ala Val Leu Gln Ser His Pro Pro Ser Gln Pro
 515 520 525
 Glu Asp Leu Ser Leu Ala Val Leu Gln Pro Thr Pro Gln Val Thr Gln
 530 535 540
 Glu His Gly His Phe Leu Pro Glu Arg Lys Asp Phe Pro Val Glu Ser
 545 550 555 560
 Val Lys Leu Thr Glu Val Pro Val Asp Pro Val Leu Thr Val His Pro
 565 570 575
 Glu Ser Glu Ser Glu Thr Asn Thr Arg Ser Arg Ser Arg Gly Arg Thr
 580 585 590
 Arg Asn Arg Thr Thr Lys Ser Arg Ser Arg Ser Ser Ser Ser Ser
 595 600 605
 Ser Ser Ser Ser Ser Thr Ser Ser Ser Ser Gly Ser Ser Ser Ser
 610 615 620

Gly Ser Ser Ser Ser Arg Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser
 625 630 635 640
 Gly Ser Ser Ser Arg Asp Ser Ser Ser Ser Thr Ser Ser Ser Ser Glu
 645 650 655
 Ser Arg Ser Arg Ser Arg Gly Arg Gly His Asn Arg Asp Arg Lys His
 660 665 670
 Arg Arg Ser Val Asp Arg Lys Arg Arg Asp Thr Ser Gly Leu Glu Arg
 675 680 685
 Ser His Lys Ser Ser Lys Gly Gly Ser Ser Arg Asp Thr Lys Gly Ser
 690 695 700
 Lys Asp Lys Asn Ser Arg Ser Asp Arg Lys Arg Ser Ile Ser Glu Ser
 705 710 715 720
 Ser Arg Ser Gly Lys Arg Ser Ser Arg Ser Glu Arg Asp Arg Lys Ser
 725 730 735
 Asp Arg Lys Asp Lys Arg Arg
 740

<210> 156
 <211> 442
 <212> PRT
 <213> Homo sapiens

<400> 156
 Met Ala Ser Val Val Leu Pro Ser Gly Ser Gln Cys Ala Ala Ala Ala
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 Ala Ala Ala Ala Pro Pro Gly Leu Arg Leu Arg Leu Leu Leu Leu Leu
 20 25 30
 Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe
 35 40 45
 Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys
 50 55 60
 Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn
 65 70 75 80
 Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg
 85 90 95
 Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr
 100 105 110
 Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr
 115 120 125
 Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro
 130 135 140
 Arg Asn Leu Met Ile Asp Ile Gln Arg Asp Thr Ala Val Glu Gly Glu
 145 150 155 160
 Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr

				165				170				175			
Ile	Arg	Trp	Phe 180	Lys	Gly	Asn	Thr	Glu 185	Leu	Lys	Gly	Lys	Ser 190	Glu	Val
Glu	Glu	Trp 195	Ser	Asp	Met	Tyr	Thr 200	Val	Thr	Ser	Gln	Leu 205	Met	Leu	Lys
Val	His 210	Lys	Glu	Asp	Asp	Gly 215	Val	Pro	Val	Ile	Cys 220	Gln	Val	Glu	His
Pro 225	Ala	Val	Thr	Gly	Asn 230	Leu	Gln	Thr	Gln	Arg 235	Tyr	Leu	Glu	Val	Gln 240
Tyr	Lys	Pro	Gln	Val 245	His	Ile	Gln	Met	Thr 250	Tyr	Pro	Leu	Gln	Gly 255	Leu
Thr	Arg	Glu	Gly 260	Asp	Ala	Leu	Glu 265	Leu	Thr	Cys	Glu	Ala	Ile 270	Gly	Lys
Pro	Gln	Pro 275	Val	Met	Val	Thr	Trp 280	Val	Arg	Val	Asp	Asp 285	Glu	Met	Pro
Gln	His 290	Ala	Val	Leu	Ser	Gly 295	Pro	Asn	Leu	Phe	Ile 300	Asn	Asn	Leu	Asn
Lys 305	Thr	Asp	Asn	Gly	Thr 310	Tyr	Arg	Cys	Glu	Ala 315	Ser	Asn	Ile	Val	Gly 320
Lys	Ala	His	Ser	Asp 325	Tyr	Met	Leu	Tyr	Val 330	Tyr	Asp	Pro	Pro	Thr 335	Thr
Ile	Pro	Pro	Pro 340	Thr	Thr	Thr	Thr 345	Thr	Thr	Thr	Thr	Thr	Thr 350	Thr	Thr
Thr	Ile 355	Leu	Thr	Ile	Ile	Thr	Asp 360	Ser	Arg	Ala	Gly	Glu 365	Glu	Gly	Ser
Ile 370	Arg	Ala	Val	Asp	His	Ala 375	Val	Ile	Gly	Gly	Val 380	Val	Ala	Val	Val
Val 385	Phe	Ala	Met	Leu	Cys 390	Leu	Leu	Ile	Ile	Leu 395	Gly	Arg	Tyr	Phe	Ala 400
Arg	His	Lys	Gly	Thr 405	Tyr	Phe	Thr	His	Glu 410	Ala	Lys	Gly	Ala	Asp 415	Asp
Ala	Ala	Asp	Ala 420	Asp	Thr	Ala	Ile	Ile 425	Asn	Ala	Glu	Gly	Gly 430	Gln	Asn
Asn	Ser	Glu 435	Glu	Lys	Lys	Glu	Tyr 440	Phe	Ile						
<210>	157														
<211>	1241														
<212>	PRT														
<213>	Homo sapiens														
<400>	157														
Met	Ala	Leu	Gly	Thr	Thr	Leu	Arg	Ala	Ser	Leu	Leu	Leu	Leu	Gly	Leu
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Leu Thr Glu Gly Leu Ala Gln Leu Ala Ile Pro Ala Ser Val Pro Arg
 20 25 30
 Gly Phe Trp Ala Leu Pro Glu Asn Leu Thr Val Val Glu Gly Ala Ser
 35 40 45
 Val Glu Leu Arg Cys Gly Val Ser Thr Pro Gly Ser Ala Val Gln Trp
 50 55 60
 Ala Lys Asp Gly Leu Leu Leu Gly Pro Asp Pro Arg Ile Pro Gly Phe
 65 70 75 80
 Pro Arg Tyr Arg Leu Glu Gly Asp Pro Ala Arg Gly Glu Phe His Leu
 85 90 95
 His Ile Glu Ala Cys Asp Leu Ser Asp Asp Ala Glu Tyr Glu Cys Gln
 100 105 110
 Val Gly Arg Ser Glu Met Gly Pro Glu Leu Val Ser Pro Arg Val Ile
 115 120 125
 Leu Ser Ile Leu Val Pro Pro Lys Leu Leu Leu Thr Pro Glu Ala
 130 135 140
 Gly Thr Met Val Thr Trp Val Ala Gly Gln Glu Tyr Val Val Asn Cys
 145 150 155 160
 Val Ser Gly Asp Ala Lys Pro Ala Pro Asp Ile Thr Ile Leu Leu Ser
 165 170 175
 Gly Gln Thr Ile Ser Asp Ile Ser Ala Asn Val Asn Glu Gly Ser Gln
 180 185 190
 Gln Lys Leu Phe Thr Val Glu Ala Thr Ala Arg Val Thr Pro Arg Ser
 195 200 205
 Ser Asp Asn Arg Gln Leu Leu Val Cys Glu Ala Ser Ser Pro Ala Leu
 210 215 220
 Glu Ala Pro Ile Lys Ala Ser Phe Thr Val Asn Val Leu Phe Pro Pro
 225 230 235 240
 Gly Pro Pro Val Ile Glu Trp Pro Gly Leu Asp Glu Gly His Val Arg
 245 250 255
 Ala Gly Gln Ser Leu Glu Leu Pro Cys Val Ala Arg Gly Gly Asn Pro
 260 265 270
 Leu Ala Thr Leu Gln Trp Leu Lys Asn Gly Gln Pro Val Ser Thr Ala
 275 280 285
 Trp Gly Thr Glu His Thr Gln Ala Val Ala Arg Ser Val Leu Val Met
 290 295 300
 Thr Val Arg Pro Glu Asp His Gly Ala Gln Leu Ser Cys Glu Ala His
 305 310 315 320
 Asn Ser Val Ser Ala Gly Thr Gln Glu His Gly Ile Thr Leu Gln Val
 325 330 335
 Thr Phe Pro Pro Ser Ala Ile Ile Ile Leu Gly Ser Ala Ser Gln Thr
 340 345 350

Glu Asn Lys Asn Val Thr Leu Ser Cys Val Ser Lys Ser Ser Arg Pro
 355 360 365
 Arg Val Leu Leu Arg Trp Trp Leu Gly Trp Arg Gln Leu Leu Pro Met
 370 375 380
 Glu Glu Thr Val Met Asp Gly Leu His Gly Gly His Ile Ser Met Ser
 385 390 395 400
 Asn Leu Thr Phe Leu Ala Arg Arg Glu Asp Asn Gly Leu Thr Leu Thr
 405 410 415
 Cys Glu Ala Phe Ser Glu Ala Phe Thr Lys Glu Thr Phe Lys Lys Ser
 420 425 430
 Leu Ile Leu Asn Val Lys Tyr Pro Ala Gln Lys Leu Trp Ile Glu Gly
 435 440 445
 Pro Pro Glu Gly Gln Lys Leu Arg Ala Gly Thr Arg Val Arg Leu Val
 450 455 460
 Cys Leu Ala Ile Gly Gly Asn Pro Glu Pro Ser Leu Met Trp Tyr Lys
 465 470 475 480
 Asp Ser Arg Thr Val Thr Glu Ser Arg Leu Pro Gln Glu Ser Arg Arg
 485 490 495
 Val His Leu Gly Ser Val Glu Lys Ser Gly Ser Thr Phe Ser Arg Glu
 500 505 510
 Leu Val Leu Val Thr Gly Pro Ser Asp Asn Gln Ala Lys Phe Thr Cys
 515 520 525
 Lys Ala Gly Gln Leu Ser Ala Ser Thr Gln Leu Ala Val Gln Phe Pro
 530 535 540
 Pro Thr Asn Val Thr Ile Leu Ala Asn Ala Ser Ala Leu Arg Pro Gly
 545 550 555 560
 Asp Ala Leu Asn Leu Thr Cys Val Ser Val Ser Ser Asn Pro Pro Val
 565 570 575
 Asn Leu Ser Trp Asp Lys Glu Gly Glu Arg Leu Glu Gly Val Ala Ala
 580 585 590
 Pro Pro Arg Arg Ala Pro Phe Lys Gly Ser Ala Ala Ala Arg Ser Val
 595 600 605
 Leu Leu Gln Val Ser Ser Arg Asp His Gly Gln Arg Val Thr Cys Arg
 610 615 620
 Ala His Ser Ala Glu Leu Arg Glu Thr Val Ser Ser Phe Tyr Arg Leu
 625 630 635 640
 Asn Val Leu Tyr Arg Pro Glu Phe Leu Gly Glu Gln Val Leu Val Val
 645 650 655
 Thr Ala Val Glu Gln Gly Glu Ala Leu Leu Pro Val Ser Val Ser Ala
 660 665 670
 Asn Pro Ala Pro Glu Ala Phe Asn Trp Thr Phe Arg Gly Tyr Arg Leu

675					680					685					
Ser	Pro	Ala	Gly	Gly	Pro	Arg	His	Arg	Ile	Leu	Ser	Ser	Gly	Ala	Leu
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His	Leu	Trp	Asn	Val	Thr	Arg	Ala	Asp	Asp	Gly	Leu	Tyr	Gln	Leu	His
705					710					715					720
Cys	Gln	Asn	Ser	Glu	Gly	Thr	Ala	Glu	Ala	Arg	Leu	Arg	Leu	Asp	Val
				725					730					735	
His	Tyr	Ala	Pro	Thr	Ile	Arg	Ala	Leu	Gln	Asp	Pro	Thr	Glu	Val	Asn
			740					745					750		
Val	Gly	Gly	Ser	Val	Asp	Ile	Val	Cys	Thr	Val	Asp	Ala	Asn	Pro	Ile
		755					760					765			
Leu	Pro	Gly	Met	Phe	Asn	Trp	Glu	Arg	Leu	Gly	Glu	Asp	Glu	Glu	Asp
	770					775					780				
Gln	Ser	Leu	Asp	Asp	Met	Glu	Lys	Ile	Ser	Arg	Gly	Pro	Thr	Gly	Arg
785					790					795					800
Leu	Arg	Ile	His	His	Ala	Lys	Leu	Ala	Gln	Ala	Gly	Ala	Tyr	Gln	Cys
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Ile	Val	Asp	Asn	Gly	Val	Ala	Pro	Pro	Ala	Arg	Arg	Leu	Leu	Arg	Leu
			820					825					830		
Val	Val	Arg	Phe	Ala	Pro	Gln	Val	Glu	His	Pro	Thr	Pro	Leu	Thr	Lys
		835					840					845			
Val	Ala	Ala	Ala	Gly	Asp	Ser	Thr	Ser	Ser	Ala	Thr	Leu	His	Cys	Arg
	850					855					860				
Ala	Arg	Gly	Val	Pro	Asn	Ile	Val	Phe	Thr	Trp	Thr	Lys	Asn	Gly	Val
865					870					875					880
Pro	Leu	Asp	Leu	Gln	Asp	Pro	Arg	Tyr	Thr	Glu	His	Thr	Tyr	His	Gln
				885					890					895	
Gly	Gly	Val	His	Ser	Ser	Leu	Leu	Thr	Ile	Ala	Asn	Val	Ser	Ala	Ala
		900						905					910		
Gln	Asp	Tyr	Ala	Leu	Phe	Thr	Cys	Thr	Ala	Thr	Asn	Ala	Leu	Gly	Ser
	915						920					925			
Asp	Gln	Thr	Asn	Ile	Gln	Leu	Val	Ser	Ile	Ser	Arg	Pro	Asp	Pro	Pro
	930					935					940				
Ser	Gly	Leu	Lys	Val	Val	Ser	Leu	Thr	Pro	His	Ser	Val	Gly	Leu	Glu
945					950					955					960
Trp	Lys	Pro	Gly	Phe	Asp	Gly	Gly	Leu	Pro	Gln	Arg	Phe	Cys	Ile	Arg
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Tyr	Glu	Ala	Leu	Gly	Thr	Pro	Gly	Phe	His	Tyr	Val	Asp	Val	Val	Pro
			980					985					990		
Pro	Gln	Ala	Thr	Thr	Phe	Thr	Leu	Thr	Gly	Leu	Gln	Pro	Ser	Thr	Arg
			995				1000						1005		

Tyr Arg Val Trp Leu Leu Ala Ser Asn Ala Leu Gly Asp Ser Gly
 1010 1015 1020
 Leu Ala Asp Lys Gly Thr Gln Leu Pro Ile Thr Thr Pro Gly Leu
 1025 1030 1035
 His Gln Pro Ser Gly Glu Pro Glu Asp Gln Leu Pro Thr Glu Pro
 1040 1045 1050
 Pro Ser Gly Pro Ser Gly Leu Pro Leu Leu Pro Val Leu Phe Ala
 1055 1060 1065
 Leu Gly Gly Leu Leu Leu Leu Ser Asn Ala Ser Cys Val Gly Gly
 1070 1075 1080
 Val Leu Trp Gln Arg Arg Leu Arg Arg Leu Ala Glu Gly Ile Ser
 1085 1090 1095
 Glu Lys Thr Glu Ala Gly Ser Glu Glu Asp Arg Val Arg Asn Glu
 1100 1105 1110
 Tyr Glu Glu Ser Gln Trp Thr Gly Glu Arg Asp Thr Gln Ser Ser
 1115 1120 1125
 Thr Val Ser Thr Thr Glu Ala Glu Pro Tyr Tyr Arg Ser Leu Arg
 1130 1135 1140
 Asp Phe Ser Pro Gln Leu Pro Pro Thr Gln Glu Glu Val Ser Tyr
 1145 1150 1155
 Ser Arg Gly Phe Thr Gly Glu Asp Glu Asp Met Ala Phe Pro Gly
 1160 1165 1170
 His Leu Tyr Asp Glu Val Glu Arg Thr Tyr Pro Pro Ser Gly Ala
 1175 1180 1185
 Trp Gly Pro Leu Tyr Asp Glu Val Gln Met Gly Pro Trp Asp Leu
 1190 1195 1200
 His Trp Pro Glu Asp Thr Tyr Gln Asp Pro Arg Gly Ile Tyr Asp
 1205 1210 1215
 Gln Val Ala Gly Asp Leu Asp Thr Leu Glu Pro Asp Ser Leu Pro
 1220 1225 1230
 Phe Glu Leu Arg Gly His Leu Val
 1235 1240

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<211> 372

<212> PRT

<213> Homo sapiens

<400> 158

Met Asp Val Leu Ser Pro Leu Ser Phe Ile Lys Val Ser His Val Arg
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Met Gln Gly Ile Leu Leu Leu Val Phe Ala Lys Tyr Gln His Leu Pro
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Tyr Ile Gln Ile Leu Ser Thr Lys Ser Thr Pro Thr Gly Leu Phe Gly
 35 40 45

Tyr Trp Gly Asn Lys Gly Gly Val Asn Ile Cys Leu Lys Leu Tyr Gly
 50 55 60
 Tyr Tyr Val Ser Ile Ile Asn Cys His Leu Pro Pro His Ile Ser Asn
 65 70 75 80
 Asn Tyr Gln Arg Leu Glu His Phe Asp Arg Ile Leu Glu Met Gln Asn
 85 90 95
 Cys Glu Gly Arg Asp Ile Pro Asn Ile Leu Asp His Asp Leu Ile Ile
 100 105 110
 Trp Phe Gly Asp Met Asn Phe Arg Ile Glu Asp Phe Gly Leu His Phe
 115 120 125
 Val Arg Glu Ser Ile Lys Asn Arg Cys Tyr Gly Gly Leu Trp Glu Lys
 130 135 140
 Asp Gln Leu Ser Ile Ala Lys Lys His Asp Pro Leu Leu Arg Glu Phe
 145 150 155 160
 Gln Glu Gly Arg Leu Leu Phe Pro Pro Thr Tyr Lys Phe Asp Arg Asn
 165 170 175
 Ser Asn Asp Tyr Asp Thr Ser Glu Lys Lys Arg Lys Pro Ala Trp Thr
 180 185 190
 Asp Arg Ile Leu Trp Arg Leu Lys Arg Gln Pro Cys Ala Gly Pro Asp
 195 200 205
 Thr Pro Ile Pro Pro Ala Ser His Phe Ser Leu Ser Leu Arg Gly Tyr
 210 215 220
 Ser Ser His Met Thr Tyr Gly Ile Ser Asp His Lys Pro Val Ser Gly
 225 230 235 240
 Thr Phe Asp Leu Glu Leu Lys Pro Leu Val Ser Ala Pro Leu Ile Val
 245 250 255
 Leu Met Pro Glu Asp Leu Trp Thr Val Glu Asn Asp Met Met Val Ser
 260 265 270
 Tyr Ser Ser Thr Ser Asp Phe Pro Ser Ser Pro Trp Asp Trp Ile Gly
 275 280 285
 Leu Tyr Lys Val Gly Leu Arg Asp Val Asn Asp Tyr Val Ser Tyr Ala
 290 295 300
 Trp Val Gly Asp Ser Lys Val Ser Cys Ser Asp Asn Leu Asn Gln Val
 305 310 315 320
 Tyr Ile Asp Ile Ser Asn Ile Pro Thr Thr Glu Asp Glu Phe Leu Leu
 325 330 335
 Cys Tyr Tyr Arg Asn Ser Leu Arg Ser Val Val Gly Ile Arg Arg Pro
 340 345 350
 Phe Gln Ile Pro Pro Gly Ser Leu Arg Glu Asp Pro Leu Gly Glu Ala
 355 360 365
 Gln Pro Gln Ile

370

<210> 159

<211> 1709

<212> PRT

<213> Homo sapiens

<400> 159

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          20          25          30

Gly Ser Ser Ser Gly Ser Ser Ser Asp Gly Ser Ser Ser Gln Ser Gly
          35          40          45

Ser Ser Asp Ser Asp Ser Gly Ser Glu Ser Gly Ser Gln Ser Glu Ser
          50          55          60

Glu Ser Asp Thr Ser Arg Glu Asn Lys Val Gln Ala Lys Pro Pro Lys
65          70          75          80

Val Asp Gly Ala Glu Phe Trp Lys Ser Ser Pro Ser Ile Leu Ala Val
          85          90          95

Gln Arg Ser Ala Ile Leu Lys Lys Gln Gln Gln Gln Gln Gln Gln
          100          105          110

Gln His Gln Ala Ser Ser Asn Ser Gly Ser Glu Glu Asp Ser Ser Ser
          115          120          125

Ser Glu Asp Ser Asp Asp Ser Ser Ser Glu Val Lys Arg Lys Lys His
          130          135          140

Lys Asp Glu Asp Trp Gln Met Ser Gly Ser Gly Ser Pro Ser Gln Ser
          145          150          155          160

Gly Ser Asp Ser Glu Ser Glu Glu Glu Arg Glu Lys Ser Ser Cys Asp
          165          170          175

Glu Thr Glu Ser Asp Tyr Glu Pro Lys Asn Lys Val Lys Ser Arg Lys
          180          185          190

Pro Gln Asn Arg Ser Lys Ser Lys Asn Gly Lys Lys Ile Leu Gly Gln
          195          200          205

Lys Lys Arg Gln Ile Asp Ser Ser Glu Glu Asp Asp Asp Glu Glu Asp
          210          215          220

Tyr Asp Asn Asp Lys Arg Ser Ser Arg Arg Gln Ala Thr Val Asn Val
          225          230          235          240

Ser Tyr Lys Glu Asp Glu Glu Met Lys Thr Asp Ser Asp Asp Leu Leu
          245          250          255

Glu Val Cys Gly Glu Asp Val Pro Gln Pro Glu Glu Glu Glu Phe Glu
          260          265          270

Thr Ile Glu Arg Phe Met Asp Cys Arg Ile Gly Arg Lys Gly Ala Thr
          275          280          285

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Gly Ala Thr Thr Thr Ile Tyr Ala Val Glu Ala Asp Gly Asp Pro Asn
 290 295 300
 Ala Gly Phe Glu Lys Asn Lys Glu Pro Gly Glu Ile Gln Tyr Leu Ile
 305 310 315 320
 Lys Trp Lys Gly Trp Ser His Ile His Asn Thr Trp Glu Thr Glu Glu
 325 330 335
 Thr Leu Lys Gln Gln Asn Val Arg Gly Met Lys Lys Leu Asp Asn Tyr
 340 345 350
 Lys Lys Lys Asp Gln Glu Thr Lys Arg Trp Leu Lys Asn Ala Ser Pro
 355 360 365
 Glu Asp Val Glu Tyr Tyr Asn Cys Gln Gln Glu Leu Thr Asp Asp Leu
 370 375 380
 His Lys Gln Tyr Gln Ile Val Gly Arg Ile Ile Ala His Ser Asn Gln
 385 390 395 400
 Lys Ser Ala Ala Gly Tyr Pro Asp Tyr Tyr Cys Lys Trp Gln Gly Leu
 405 410 415
 Pro Tyr Ser Glu Cys Ser Trp Glu Asp Gly Ala Leu Ile Ser Lys Lys
 420 425 430
 Phe Gln Ala Cys Ile Asp Glu Tyr Phe Ser Arg Asn Gln Ser Lys Thr
 435 440 445
 Thr Pro Phe Lys Asp Cys Lys Val Leu Lys Gln Arg Pro Arg Phe Val
 450 455 460
 Ala Leu Lys Lys Gln Pro Ser Tyr Ile Gly Gly His Glu Gly Leu Glu
 465 470 475 480
 Leu Arg Asp Tyr Gln Leu Asn Gly Leu Asn Trp Leu Ala His Ser Trp
 485 490 495
 Cys Lys Gly Asn Ser Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys
 500 505 510
 Thr Ile Gln Thr Ile Ser Phe Leu Asn Tyr Leu Phe His Glu His Gln
 515 520 525
 Leu Tyr Gly Pro Phe Leu Leu Val Val Pro Leu Ser Thr Leu Thr Ser
 530 535 540
 Trp Gln Arg Glu Ile Gln Thr Trp Ala Ser Gln Met Asn Ala Val Val
 545 550 555 560
 Tyr Leu Gly Asp Ile Asn Ser Arg Asn Met Ile Arg Thr His Glu Trp
 565 570 575
 Thr His His Gln Thr Lys Arg Leu Lys Phe Asn Ile Leu Leu Thr Thr
 580 585 590
 Tyr Glu Ile Leu Leu Lys Asp Lys Ala Phe Leu Gly Gly Leu Asn Trp
 595 600 605
 Ala Phe Ile Gly Val Asp Glu Ala His Arg Leu Lys Asn Asp Asp Ser
 610 615 620

Leu Leu Tyr Lys Thr Leu Ile Asp Phe Lys Ser Asn His Arg Leu Leu
 625 630 635 640
 Ile Thr Gly Thr Pro Leu Gln Asn Ser Leu Lys Glu Leu Trp Ser Leu
 645 650 655
 Leu His Phe Ile Met Pro Glu Lys Phe Ser Ser Trp Glu Asp Phe Glu
 660 665 670
 Glu Glu His Gly Lys Gly Arg Glu Tyr Gly Tyr Ala Ser Leu His Lys
 675 680 685
 Glu Leu Glu Pro Phe Leu Leu Arg Arg Val Lys Lys Asp Val Glu Lys
 690 695 700
 Ser Leu Pro Ala Lys Val Glu Gln Ile Leu Arg Met Glu Met Ser Ala
 705 710 715 720
 Leu Gln Lys Gln Tyr Tyr Lys Trp Ile Leu Thr Arg Asn Tyr Lys Ala
 725 730 735
 Leu Ser Lys Gly Ser Lys Gly Ser Thr Ser Gly Phe Leu Asn Ile Met
 740 745 750
 Met Glu Leu Lys Lys Cys Cys Asn His Cys Tyr Leu Ile Lys Pro Pro
 755 760 765
 Asp Asn Asn Glu Phe Tyr Asn Lys Gln Glu Ala Leu Gln His Leu Ile
 770 775 780
 Arg Ser Ser Gly Lys Leu Ile Leu Leu Asp Lys Leu Leu Ile Arg Leu
 785 790 795 800
 Arg Glu Arg Gly Asn Arg Val Leu Ile Phe Ser Gln Met Val Arg Met
 805 810 815
 Leu Asp Ile Leu Ala Glu Tyr Leu Lys Tyr Arg Gln Phe Pro Phe Gln
 820 825 830
 Arg Leu Asp Gly Ser Ile Lys Gly Glu Leu Arg Lys Gln Ala Leu Asp
 835 840 845
 His Phe Asn Ala Glu Gly Ser Glu Asp Phe Cys Phe Leu Leu Ser Thr
 850 855 860
 Arg Ala Gly Gly Leu Gly Ile Asn Leu Ala Ser Ala Asp Thr Val Val
 865 870 875 880
 Ile Phe Asp Ser Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala
 885 890 895
 Arg Ala His Arg Ile Gly Gln Lys Lys Gln Val Asn Ile Tyr Arg Leu
 900 905 910
 Val Thr Lys Gly Ser Val Glu Glu Asp Ile Leu Glu Arg Ala Lys Lys
 915 920 925
 Lys Met Val Leu Asp His Leu Val Ile Gln Arg Met Asp Thr Thr Gly
 930 935 940
 Lys Thr Val Leu His Thr Gly Ser Ala Pro Ser Ser Ser Thr Pro Phe

945		950		955		960
Asn Lys Glu Glu Leu Ser Ala Ile Leu Lys Phe Gly Ala Glu Glu Leu						
		965		970		975
Phe Lys Glu Pro Glu Gly Glu Glu Gln Glu Pro Gln Glu Met Asp Ile						
		980		985		990
Asp Glu Ile Leu Lys Arg Ala Glu Thr His Glu Asn Glu Pro Gly Pro						
		995		1000		1005
Leu Thr Val Gly Asp Glu Leu Leu Ser Gln Phe Lys Val Ala Asn						
		1010		1015		1020
Phe Ser Asn Met Asp Glu Asp Asp Ile Glu Leu Glu Pro Glu Arg						
		1025		1030		1035
Asn Ser Lys Asn Trp Glu Glu Ile Ile Pro Glu Asp Gln Arg Arg						
		1040		1045		1050
Arg Leu Glu Glu Glu Glu Arg Gln Lys Glu Leu Glu Glu Ile Tyr						
		1055		1060		1065
Met Leu Pro Arg Met Arg Asn Cys Ala Lys Gln Ile Ser Phe Asn						
		1070		1075		1080
Gly Ser Glu Gly Arg Arg Ser Arg Ser Arg Arg Tyr Ser Gly Ser						
		1085		1090		1095
Asp Ser Asp Ser Ile Ser Glu Gly Lys Arg Pro Lys Lys Arg Gly						
		1100		1105		1110
Arg Pro Arg Thr Ile Pro Arg Glu Asn Ile Lys Gly Phe Ser Asp						
		1115		1120		1125
Ala Glu Ile Arg Arg Phe Ile Lys Ser Tyr Lys Lys Phe Gly Gly						
		1130		1135		1140
Pro Leu Glu Arg Leu Asp Ala Ile Ala Arg Asp Ala Glu Leu Val						
		1145		1150		1155
Asp Lys Ser Glu Thr Asp Leu Arg Arg Leu Gly Glu Leu Val His						
		1160		1165		1170
Asn Gly Cys Ile Lys Ala Leu Lys Asp Ser Ser Ser Gly Thr Glu						
		1175		1180		1185
Arg Thr Gly Gly Arg Leu Gly Lys Val Lys Gly Pro Thr Phe Arg						
		1190		1195		1200
Ile Ser Gly Val Gln Val Asn Ala Lys Leu Val Ile Ser His Glu						
		1205		1210		1215
Glu Glu Leu Ile Pro Leu His Lys Ser Ile Pro Ser Asp Pro Glu						
		1220		1225		1230
Glu Arg Lys Gln Tyr Thr Ile Pro Cys His Thr Lys Ala Ala His						
		1235		1240		1245
Phe Asp Ile Asp Trp Gly Lys Glu Asp Asp Ser Asn Leu Leu Ile						
		1250		1255		1260

Gly Ile	Tyr Glu	Tyr Gly	Tyr Gly	Ser Trp	Glu Met	Ile Lys	Met
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Asp Pro	Asp Leu	Ser Leu	Thr	His Lys	Ile Leu	Pro	Asp Asp Pro
1280			1285			1290	
Asp Lys	Lys Pro	Gln Ala	Lys	Gln Leu	Gln Thr	Arg	Ala Asp Tyr
1295			1300			1305	
Leu Ile	Lys Leu	Leu Ser	Arg	Asp Leu	Ala Lys	Lys	Glu Ala Leu
1310			1315			1320	
Ser Gly	Ala Gly	Ser Ser	Lys	Arg Arg	Lys Ala	Arg	Ala Lys Lys
1325			1330			1335	
Asn Lys	Ala Met	Lys Ser	Ile	Lys Val	Lys Glu	Glu	Ile Lys Ser
1340			1345			1350	
Asp Ser	Ser Pro	Leu Pro	Ser	Glu Lys	Ser Asp	Glu	Asp Asp Asp
1355			1360			1365	
Lys Leu	Ser Glu	Ser Lys	Ser	Asp Gly	Arg Glu	Arg	Ser Lys Lys
1370			1375			1380	
Ser Ser	Val Ser	Asp Ala	Pro	Val His	Ile Thr	Ala	Ser Gly Glu
1385			1390			1395	
Pro Val	Pro Ile	Ser Glu	Glu	Ser Glu	Glu Leu	Asp	Gln Lys Thr
1400			1405			1410	
Phe Ser	Ile Cys	Lys Glu	Arg	Met Arg	Pro Val	Lys	Ala Ala Leu
1415			1420			1425	
Lys Gln	Leu Asp	Arg Pro	Glu	Lys Gly	Leu Ser	Glu	Arg Glu Gln
1430			1435			1440	
Leu Glu	His Thr	Arg Gln	Cys	Leu Ile	Lys Ile	Gly	Asp His Ile
1445			1450			1455	
Thr Glu	Cys Leu	Lys Glu	Tyr	Thr Asn	Pro Glu	Gln	Ile Lys Gln
1460			1465			1470	
Trp Arg	Lys Asn	Leu Trp	Ile	Phe Val	Ser Lys	Phe	Thr Glu Phe
1475			1480			1485	
Asp Ala	Arg Lys	Leu His	Lys	Leu Tyr	Lys His	Ala	Ile Lys Lys
1490			1495			1500	
Arg Gln	Glu Ser	Gln Gln	Asn	Ser Asp	Gln Asn	Ser	Asn Leu Asn
1505			1510			1515	
Pro His	Val Ile	Arg Asn	Pro	Asp Val	Glu Arg	Leu	Lys Glu Asn
1520			1525			1530	
Thr Asn	His Asp	Asp Ser	Ser	Arg Asp	Ser Tyr	Ser	Ser Asp Arg
1535			1540			1545	
His Leu	Thr Gln	Tyr His	Asp	His His	Lys Asp	Arg	His Gln Gly
1550			1555			1560	
Asp Ser	Tyr Lys	Lys Ser	Asp	Ser Arg	Lys Arg	Pro	Tyr Ser Ser
1565			1570			1575	

Phe Ser Asn Gly Lys Asp His Arg Asp Trp Asp His Tyr Lys Gln
 1580 1585 1590
 Asp Ser Arg Tyr Tyr Ser Asp Arg Glu Lys His Arg Lys Leu Asp
 1595 1600 1605
 Asp His Arg Ser Arg Asp His Arg Ser Asn Leu Glu Gly Ser Leu
 1610 1615 1620
 Lys Asp Arg Ser His Ser Asp His Arg Ser His Ser Asp His Arg
 1625 1630 1635
 Leu His Ser Asp His Arg Ser Ser Ser Glu Tyr Thr His His Lys
 1640 1645 1650
 Ser Ser Arg Asp Tyr Arg Tyr His Ser Asp Trp Gln Met Asp His
 1655 1660 1665
 Arg Ala Ser Ser Ser Gly Pro Arg Ser Pro Leu Asp Gln Arg Ser
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 Tyr Gly Ser Arg Ser Pro Phe Glu His Ser Val Glu His Lys Ser
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 Thr Pro Glu His Thr Trp Ser Ser Arg Lys Thr
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 <213> Homo sapiens
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 His Asn Leu Pro Tyr Gly Val Phe Ser Thr Arg Gly Asp Pro Arg Pro
 35 40 45
 Arg Ile Gly Val Ala Ile Gly Asp Gln Ile Leu Asp Leu Ser Ile Ile
 50 55 60
 Lys His Leu Phe Thr Gly Pro Val Leu Ser Lys His Gln Asp Val Phe
 65 70 75 80
 Asn Gln Pro Thr Leu Asn Ser Phe Met Gly Leu Gly Gln Ala Ala Trp
 85 90 95
 Lys Glu Ala Arg Val Phe Leu Gln Asn Leu Leu Ser Val Ser Gln Ala
 100 105 110
 Arg Leu Arg Asp Asp Thr Glu Leu Arg Lys Cys Ala Phe Ile Ser Gln
 115 120 125
 Ala Ser Ala Thr Met His Leu Pro Ala Thr Ile Gly Asp Tyr Thr Asp
 130 135 140
 Phe Tyr Ser Ser Arg Gln His Ala Thr Asn Val Gly Ile Met Phe Arg

145											150											155											160
Asp	Lys	Glu	Asn	Ala	Leu	Met	Pro	Asn	Trp	Leu	His	Leu	Pro	Val	Gly																		
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Tyr	His	Gly	Arg	Ala	Ser	Ser	Val	Val	Val	Ser	Gly	Thr	Pro	Ile	Arg																		
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Arg	Pro	Met	Gly	Gln	Met	Lys	Pro	Asp	Asp	Ser	Lys	Pro	Pro	Val	Tyr																		
				195											200											205							
Gly	Ala	Cys	Lys	Leu	Leu	Asp	Met	Glu	Leu	Glu	Met	Ala	Phe	Phe	Val																		
				210											215											220							
Gly	Pro	Gly	Asn	Arg	Leu	Gly	Glu	Pro	Ile	Pro	Ile	Ser	Lys	Ala	His																		
				225											230											235							
Glu	His	Ile	Phe	Gly	Met	Val	Leu	Met	Asn	Asp	Trp	Ser	Ala	Arg	Asp																		
				245											250											255							
Ile	Gln	Lys	Trp	Glu	Tyr	Val	Pro	Leu	Gly	Pro	Phe	Leu	Gly	Lys	Ser																		
				260											265											270							
Phe	Gly	Thr	Thr	Val	Ser	Pro	Trp	Val	Val	Pro	Met	Asp	Ala	Leu	Met																		
				275											280											285							
Pro	Phe	Ala	Val	Pro	Asn	Pro	Lys	Gln	Asp	Pro	Arg	Pro	Leu	Pro	Tyr																		
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Leu	Cys	His	Asp	Glu	Pro	Tyr	Thr	Phe	Asp	Ile	Asn	Leu	Ser	Val	Asn																		
				305											310											315							
Leu	Lys	Gly	Glu	Gly	Met	Ser	Gln	Ala	Ala	Thr	Ile	Cys	Lys	Ser	Asn																		
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Phe	Lys	Tyr	Met	Tyr	Trp	Thr	Met	Leu	Gln	Gln	Leu	Thr	His	His	Ser																		
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Val	Asn	Gly	Cys	Asn	Leu	Arg	Pro	Gly	Asp	Leu	Leu	Ala	Ser	Gly	Thr																		
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Ile	Ser	Gly	Pro	Glu	Pro	Glu	Asn	Phe	Gly	Ser	Met	Leu	Glu	Leu	Ser																		
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Trp	Lys	Gly	Thr	Lys	Pro	Ile	Asp	Leu	Gly	Asn	Gly	Gln	Thr	Arg	Lys																		
				385											390											395							
Phe	Leu	Leu	Asp	Gly	Asp	Glu	Val	Ile	Ile	Thr	Gly	Tyr	Cys	Gln	Gly																		
				405											410											415							
Asp	Gly	Tyr	Arg	Ile	Gly	Phe	Gly	Gln	Cys	Ala	Gly	Lys	Val	Leu	Pro																		
				420											425											430							
Ala	Leu	Leu	Pro	Ser																													
				435																													
<210>	161																																
<211>	580																																
<212>	PRT																																
<213>	Homo sapiens																																
<400>	161																																

Met Lys Asp Arg Leu Tyr Phe Ala Thr Leu Arg Asn Arg Pro Lys Ser
 1 5 10 15
 Thr Val Asn Thr His Tyr Phe Ser Ile Asp Glu Glu Leu Val Tyr Glu
 20 25 30
 Asn Phe Tyr Ala Asp Phe Gly Pro Leu Asn Leu Ala Met Val Tyr Arg
 35 40 45
 Tyr Cys Cys Lys Leu Asn Lys Lys Leu Lys Ser Tyr Ser Leu Ser Arg
 50 55 60
 Lys Lys Ile Val His Tyr Thr Cys Phe Asp Gln Arg Lys Arg Ala Asn
 65 70 75 80
 Ala Ala Phe Leu Ile Gly Ala Tyr Ala Val Ile Tyr Leu Lys Lys Thr
 85 90 95
 Pro Glu Glu Ala Tyr Arg Ala Leu Leu Ser Gly Ser Asn Pro Pro Tyr
 100 105 110
 Leu Pro Phe Arg Asp Ala Ser Phe Gly Asn Cys Thr Tyr Asn Leu Thr
 115 120 125
 Ile Leu Asp Cys Leu Gln Gly Ile Arg Lys Gly Leu Gln His Gly Phe
 130 135 140
 Phe Asp Phe Glu Thr Ile Asp Val Asp Glu Tyr Glu His Tyr Glu Arg
 145 150 155 160
 Val Glu Asn Gly Asp Phe Asn Cys Ile Val Pro Gly Lys Phe Leu Ala
 165 170 175
 Phe Ser Gly Pro His Pro Lys Ser Lys Ile Glu Asn Gly Tyr Pro Leu
 180 185 190
 His Ala Pro Glu Ala Tyr Phe Pro Tyr Phe Lys Lys His Asn Val Thr
 195 200 205
 Ala Val Val Arg Leu Asn Lys Lys Ile Tyr Glu Ala Lys Arg Phe Thr
 210 215 220
 Asp Ala Gly Phe Glu His Tyr Asp Leu Phe Phe Ile Asp Gly Ser Thr
 225 230 235 240
 Pro Ser Asp Asn Ile Val Arg Arg Phe Leu Asn Ile Cys Glu Asn Thr
 245 250 255
 Glu Gly Ala Ile Ala Val His Cys Lys Ala Gly Leu Gly Arg Thr Gly
 260 265 270
 Thr Leu Ile Ala Cys Tyr Val Met Lys His Tyr Arg Phe Thr His Ala
 275 280 285
 Glu Ile Ile Ala Trp Ile Arg Ile Cys Arg Pro Gly Ser Ile Ile Gly
 290 295 300
 Pro Gln Gln His Phe Leu Glu Glu Lys Gln Ala Ser Leu Trp Val Gln
 305 310 315 320
 Gly Asp Ile Phe Arg Ser Lys Leu Lys Asn Arg Pro Ser Ser Glu Gly
 325 330 335

Ser Ile Asn Lys Ile Leu Ser Gly Leu Asp Asp Met Ser Ile Gly Gly
 340 345 350
 Asn Leu Ser Lys Thr Gln Asn Met Glu Arg Phe Gly Glu Asp Asn Leu
 355 360 365
 Glu Asp Asp Asp Val Glu Met Lys Asn Gly Ile Thr Gln Gly Asp Lys
 370 375 380
 Leu Arg Ala Leu Lys Ser Gln Arg Gln Pro Arg Thr Ser Pro Ser Cys
 385 390 395 400
 Ala Phe Arg Ser Asp Asp Thr Lys Gly His Pro Arg Ala Val Ser Gln
 405 410 415
 Pro Phe Arg Leu Ser Ser Ser Leu Gln Gly Ser Ala Val Thr Leu Lys
 420 425 430
 Thr Ser Lys Met Ala Leu Ser Pro Ser Ala Thr Ala Lys Arg Ile Asn
 435 440 445
 Arg Thr Ser Leu Ser Ser Gly Ala Thr Val Arg Ser Phe Ser Ile Asn
 450 455 460
 Ser Arg Leu Ala Ser Ser Leu Gly Asn Leu Asn Ala Ala Thr Asp Asp
 465 470 475 480
 Pro Glu Asn Lys Lys Thr Ser Ser Ser Ser Lys Ala Gly Phe Thr Ala
 485 490 495
 Ser Pro Phe Thr Asn Leu Leu Asn Gly Ser Ser Gln Pro Thr Thr Arg
 500 505 510
 Asn Tyr Pro Glu Leu Asn Asn Asn Gln Tyr Asn Arg Ser Ser Asn Ser
 515 520 525
 Asn Gly Gly Asn Leu Asn Ser Pro Pro Gly Pro His Ser Ala Lys Thr
 530 535 540
 Glu Glu His Thr Thr Ile Leu Arg Pro Ser Tyr Thr Gly Leu Ser Ser
 545 550 555 560
 Ser Ser Ala Arg Phe Leu Ser Arg Ser Ile Pro Ser Leu Gln Ser Glu
 565 570 575
 Tyr Val His Tyr
 580

<210> 162

<211> 447

<212> PRT

<213> Homo sapiens

<400> 162

Met Arg Ser Ser Thr Leu Gln Asp Pro Arg Arg Arg Asp Pro Gln Asp
 1 5 10 15

Asp Val Tyr Val Asp Ile Thr Asp Arg Leu Arg Phe Ala Ile Leu Tyr
 20 25 30

Ser Arg Pro Lys Ser Ala Ser Asn Val His Tyr Phe Ser Ile Asp Asn

35					40					45					
Glu	Leu	Glu	Tyr	Glu	Asn	Phe	Ser	Glu	Asp	Phe	Gly	Pro	Leu	Asn	Leu
50					55					60					
Ala	Met	Val	Tyr	Arg	Tyr	Cys	Cys	Lys	Ile	Asn	Lys	Lys	Leu	Lys	Ser
65					70					75					80
Ile	Thr	Met	Leu	Arg	Lys	Lys	Ile	Val	His	Phe	Thr	Gly	Ser	Asp	Gln
				85					90					95	
Arg	Lys	Gln	Ala	Asn	Ala	Ala	Phe	Leu	Val	Gly	Cys	Tyr	Met	Val	Ile
			100					105					110		
Tyr	Leu	Gly	Arg	Thr	Pro	Glu	Ala	Ala	Tyr	Arg	Ile	Leu	Ile	Phe	Gly
		115					120					125			
Asp	Thr	Pro	Tyr	Ile	Pro	Phe	Arg	Asp	Ala	Ala	Tyr	Gly	Ser	Cys	Asn
		130					135					140			
Phe	Tyr	Ile	Thr	Leu	Leu	Asp	Cys	Phe	His	Ala	Val	Lys	Lys	Ala	Met
145				150						155					160
Gln	Tyr	Gly	Phe	Leu	Asn	Phe	Asn	Ser	Phe	Asn	Leu	Asp	Glu	Tyr	Glu
			165						170					175	
His	Tyr	Glu	Lys	Ala	Glu	Asn	Gly	Asp	Leu	Asn	Trp	Ile	Ile	Pro	Asp
			180					185					190		
Arg	Phe	Ile	Ala	Phe	Cys	Gly	Pro	His	Ser	Arg	Ala	Arg	Leu	Glu	Ser
		195					200					205			
Gly	Tyr	His	Gln	His	Ser	Pro	Glu	Thr	Tyr	Ile	Gln	Tyr	Phe	Lys	Asn
		210					215					220			
His	Asn	Val	Thr	Thr	Ile	Ile	Arg	Leu	Asn	Lys	Arg	Met	Tyr	Asp	Ala
225				230						235					240
Lys	Arg	Phe	Thr	Asp	Ala	Gly	Phe	Asp	His	His	Asp	Leu	Phe	Phe	Ala
			245						250					255	
Asp	Gly	Ser	Thr	Pro	Thr	Asp	Ala	Ile	Val	Lys	Arg	Phe	Leu	Asp	Ile
			260					265					270		
Cys	Glu	Asn	Ala	Glu	Gly	Ala	Ile	Ala	Val	His	Cys	Lys	Ala	Gly	Leu
		275					280					285			
Gly	Arg	Thr	Gly	Thr	Leu	Ile	Ala	Cys	Tyr	Ile	Met	Lys	His	Tyr	Arg
		290					295					300			
Met	Thr	Ala	Ala	Glu	Thr	Ile	Ala	Trp	Val	Arg	Ile	Cys	Arg	Pro	Gly
305				310						315					320
Leu	Val	Ile	Gly	Pro	Gln	Gln	Gln	Phe	Leu	Val	Met	Lys	Gln	Thr	Ser
				325					330					335	
Leu	Trp	Leu	Glu	Gly	Asp	Tyr	Phe	Arg	Gln	Arg	Leu	Lys	Gly	Gln	Glu
			340				345						350		
Asn	Gly	Gln	His	Arg	Ala	Ala	Phe	Ser	Lys	Leu	Leu	Ser	Gly	Val	Asp
		355					360					365			

Asp Ile Ser Ile Asn Gly Val Glu Asn Gln Asp Gln Gln Glu Pro Lys
370 375 380

Pro Tyr Ser Asp Asp Asp Glu Ile Asn Gly Val Thr Gln Gly Asp Arg
385 390 395 400

Ser Arg Ala Leu Lys Arg Arg Arg Gln Ser Lys Thr Asn Asp Ile Leu
405 410 415

Leu Pro Ser Pro Leu Ala Val Leu Thr Phe Thr Leu Cys Ser Val Val
420 425 430

Ile Trp Trp Ile Val Cys Asp Tyr Ile Leu Pro Ile Leu Leu Phe
435 440 445

<210> 163

<211> 159

<212> PRT

<213> Homo sapiens

<400> 163

Met Ala Val Leu Trp Arg Leu Ser Ala Val Cys Gly Ala Leu Gly Gly
1 5 10 15

Arg Ala Leu Leu Leu Arg Thr Pro Val Val Arg Pro Ala His Ile Ser
20 25 30

Ala Phe Leu Gln Asp Arg Pro Ile Pro Glu Trp Cys Gly Val Gln His
35 40 45

Ile His Leu Ser Pro Ser His His Ser Gly Ser Lys Ala Ala Ser Leu
50 55 60

His Trp Thr Ser Glu Arg Val Val Ser Val Leu Leu Leu Gly Leu Leu
65 70 75 80

Pro Ala Ala Tyr Leu Asn Pro Cys Ser Ala Met Asp Tyr Ser Leu Ala
85 90 95

Ala Ala Leu Thr Leu His Gly His Trp Gly Leu Gly Gln Val Val Thr
100 105 110

Asp Tyr Val His Gly Asp Ala Leu Gln Lys Ala Ala Lys Ala Gly Leu
115 120 125

Leu Ala Leu Ser Ala Leu Thr Phe Ala Gly Leu Cys Tyr Phe Asn Tyr
130 135 140

His Asp Val Gly Ile Cys Lys Ala Val Ala Met Leu Trp Lys Leu
145 150 155

<210> 164

<211> 1924

<212> PRT

<213> Homo sapiens

<400> 164

Met Lys Ser Pro Ala Leu Gln Pro Leu Ser Met Ala Gly Leu Gln Leu
1 5 10 15

Met Thr Pro Ala Ser Ser Pro Met Gly Pro Phe Phe Gly Leu Pro Trp
20 25 30

Gln Gln Glu Ala Ile His Asp Asn Ile Tyr Thr Pro Arg Lys Tyr Gln
 35 40 45
 Val Glu Leu Leu Glu Ala Ala Leu Asp His Asn Thr Ile Val Cys Leu
 50 55 60
 Asn Thr Gly Ser Gly Lys Thr Phe Ile Ala Ser Thr Thr Leu Leu Lys
 65 70 75 80
 Ser Cys Leu Tyr Leu Asp Leu Gly Glu Thr Ser Ala Arg Asn Gly Lys
 85 90 95
 Arg Thr Val Phe Leu Val Asn Ser Ala Asn Gln Val Ala Gln Gln Val
 100 105 110
 Ser Ala Val Arg Thr His Ser Asp Leu Lys Val Gly Glu Tyr Ser Asn
 115 120 125
 Leu Glu Val Asn Ala Ser Trp Thr Lys Glu Arg Trp Asn Gln Glu Phe
 130 135 140
 Thr Lys His Gln Val Leu Ile Met Thr Cys Tyr Val Ala Leu Asn Val
 145 150 155 160
 Leu Lys Asn Gly Tyr Leu Ser Leu Ser Asp Ile Asn Leu Leu Val Phe
 165 170 175
 Asp Glu Cys His Leu Ala Ile Leu Asp His Pro Tyr Arg Glu Phe Met
 180 185 190
 Lys Leu Cys Glu Ile Cys Pro Ser Cys Pro Arg Ile Leu Gly Leu Thr
 195 200 205
 Ala Ser Ile Leu Asn Gly Lys Trp Asp Pro Glu Asp Leu Glu Glu Lys
 210 215 220
 Phe Gln Lys Leu Glu Lys Ile Leu Lys Ser Asn Ala Glu Thr Ala Thr
 225 230 235 240
 Asp Leu Val Val Leu Asp Arg Tyr Thr Ser Gln Pro Cys Glu Ile Val
 245 250 255
 Val Asp Cys Gly Pro Phe Thr Asp Arg Ser Gly Leu Tyr Glu Arg Leu
 260 265 270
 Leu Met Glu Leu Glu Glu Ala Leu Asn Phe Ile Asn Asp Cys Asn Ile
 275 280 285
 Ser Val His Ser Lys Glu Arg Asp Ser Thr Leu Ile Ser Lys Gln Ile
 290 295 300
 Leu Ser Asp Cys Arg Ala Val Leu Val Val Leu Gly Pro Trp Cys Ala
 305 310 315 320
 Asp Lys Val Ala Gly Met Met Val Arg Glu Leu Gln Lys Tyr Ile Lys
 325 330 335
 His Glu Gln Glu Glu Leu His Arg Lys Phe Leu Leu Phe Thr Asp Thr
 340 345 350
 Phe Leu Arg Lys Ile His Ala Leu Cys Glu Glu His Phe Ser Pro Ala

355					360					365						
Ser	Leu	Asp	Leu	Lys	Phe	Val	Thr	Pro	Lys	Val	Ile	Lys	Leu	Leu	Glu	
370					375					380						
Ile	Leu	Arg	Lys	Tyr	Lys	Pro	Tyr	Glu	Arg	His	Ser	Phe	Glu	Ser	Val	
385					390					395					400	
Glu	Trp	Tyr	Asn	Asn	Arg	Asn	Gln	Asp	Asn	Tyr	Val	Ser	Trp	Ser	Asp	
					405					410					415	
Ser	Glu	Asp	Asp	Asp	Glu	Asp	Glu	Glu	Ile	Glu	Glu	Lys	Glu	Lys	Pro	
					420					425					430	
Glu	Thr	Asn	Phe	Pro	Ser	Pro	Phe	Thr	Asn	Ile	Leu	Cys	Gly	Ile	Ile	
					435					440					445	
Phe	Val	Glu	Arg	Arg	Tyr	Thr	Ala	Val	Val	Leu	Asn	Arg	Leu	Ile	Lys	
					450					455					460	
Glu	Ala	Gly	Lys	Gln	Asp	Pro	Glu	Leu	Ala	Tyr	Ile	Ser	Ser	Asn	Phe	
465					470					475					480	
Ile	Thr	Gly	His	Gly	Ile	Gly	Lys	Asn	Gln	Pro	Arg	Asn	Asn	Thr	Met	
					485					490					495	
Glu	Ala	Glu	Phe	Arg	Lys	Gln	Glu	Glu	Val	Leu	Arg	Lys	Phe	Arg	Ala	
					500					505					510	
His	Glu	Thr	Asn	Leu	Leu	Ile	Ala	Thr	Ser	Ile	Val	Glu	Glu	Gly	Val	
					515					520					525	
Asp	Ile	Pro	Lys	Cys	Asn	Leu	Val	Val	Arg	Phe	Asp	Leu	Pro	Thr	Glu	
530					535					540						
Tyr	Arg	Ser	Tyr	Val	Gln	Ser	Lys	Gly	Arg	Ala	Arg	Ala	Pro	Ile	Ser	
545					550					555					560	
Asn	Tyr	Ile	Met	Leu	Ala	Asp	Thr	Asp	Lys	Ile	Lys	Ser	Phe	Glu	Glu	
					565					570					575	
Asp	Leu	Lys	Thr	Tyr	Lys	Ala	Ile	Glu	Lys	Ile	Leu	Arg	Asn	Lys	Cys	
					580					585					590	
Ser	Lys	Ser	Val	Asp	Thr	Gly	Glu	Thr	Asp	Ile	Asp	Pro	Val	Met	Asp	
					595					600					605	
Asp	Asp	His	Val	Phe	Pro	Pro	Tyr	Val	Leu	Arg	Pro	Asp	Asp	Gly	Gly	
610					615					620						
Pro	Arg	Val	Thr	Ile	Asn	Thr	Ala	Ile	Gly	His	Ile	Asn	Arg	Tyr	Cys	
625					630					635					640	
Ala	Arg	Leu	Pro	Ser	Asp	Pro	Phe	Thr	His	Leu	Ala	Pro	Lys	Cys	Arg	
					645					650					655	
Thr	Arg	Glu	Leu	Pro	Asp	Gly	Thr	Phe	Tyr	Ser	Thr	Leu	Tyr	Leu	Pro	
					660					665					670	
Ile	Asn	Ser	Pro	Leu	Arg	Ala	Ser	Ile	Val	Gly	Pro	Pro	Met	Ser	Cys	
					675					680					685	

Val Arg Leu Ala Glu Arg Val Val Ala Leu Ile Cys Cys Glu Lys Leu
 690 695 700
 His Lys Ile Gly Glu Leu Asp Asp His Leu Met Pro Val Gly Lys Glu
 705 710 715 720
 Thr Val Lys Tyr Glu Glu Glu Leu Asp Leu His Asp Glu Glu Glu Thr
 725 730 735
 Ser Val Pro Gly Arg Pro Gly Ser Thr Lys Arg Arg Gln Cys Tyr Pro
 740 745 750
 Lys Ala Ile Pro Glu Cys Leu Arg Asp Ser Tyr Pro Arg Pro Asp Gln
 755 760 765
 Pro Cys Tyr Leu Tyr Val Ile Gly Met Val Leu Thr Thr Pro Leu Pro
 770 775 780
 Asp Glu Leu Asn Phe Arg Arg Arg Lys Leu Tyr Pro Pro Glu Asp Thr
 785 790 795 800
 Thr Arg Cys Phe Gly Ile Leu Thr Ala Lys Pro Ile Pro Gln Ile Pro
 805 810 815
 His Phe Pro Val Tyr Thr Arg Ser Gly Glu Val Thr Ile Ser Ile Glu
 820 825 830
 Leu Lys Lys Ser Gly Phe Met Leu Ser Leu Gln Met Leu Glu Leu Ile
 835 840 845
 Thr Arg Leu His Gln Tyr Ile Phe Ser His Ile Leu Arg Leu Glu Lys
 850 855 860
 Pro Ala Leu Glu Phe Lys Pro Thr Asp Ala Asp Ser Ala Tyr Cys Val
 865 870 875 880
 Leu Pro Leu Asn Val Val Asn Asp Ser Ser Thr Leu Asp Ile Asp Phe
 885 890 895
 Lys Phe Met Glu Asp Ile Glu Lys Ser Glu Ala Arg Ile Gly Ile Pro
 900 905 910
 Ser Thr Lys Tyr Thr Lys Glu Thr Pro Phe Val Phe Lys Leu Glu Asp
 915 920 925
 Tyr Gln Asp Ala Val Ile Ile Pro Arg Tyr Arg Asn Phe Asp Gln Pro
 930 935 940
 His Arg Phe Tyr Val Ala Asp Val Tyr Thr Asp Leu Thr Pro Leu Ser
 945 950 955 960
 Lys Phe Pro Ser Pro Glu Tyr Glu Thr Phe Ala Glu Tyr Tyr Lys Thr
 965 970 975
 Lys Tyr Asn Leu Asp Leu Thr Asn Leu Asn Gln Pro Leu Leu Asp Val
 980 985 990
 Asp His Thr Ser Ser Arg Leu Asn Leu Leu Thr Pro Arg His Leu Asn
 995 1000 1005
 Gln Lys Gly Lys Ala Leu Pro Leu Ser Ser Ala Glu Lys Arg Lys
 1010 1015 1020

Ala Lys Trp Glu Ser Leu Gln Asn Lys Gln Ile Leu Val Pro Glu	1025	1030	1035
Leu Cys Ala Ile His Pro Ile Pro Ala Ser Leu Trp Arg Lys Ala	1040	1045	1050
Val Cys Leu Pro Ser Ile Leu Tyr Arg Leu His Cys Leu Leu Thr	1055	1060	1065
Ala Glu Glu Leu Arg Ala Gln Thr Ala Ser Asp Ala Gly Val Gly	1070	1075	1080
Val Arg Ser Leu Pro Ala Asp Phe Arg Tyr Pro Asn Leu Asp Phe	1085	1090	1095
Gly Trp Lys Lys Ser Ile Asp Ser Lys Ser Phe Ile Ser Ile Ser	1100	1105	1110
Asn Ser Ser Ser Ala Glu Asn Asp Asn Tyr Cys Lys His Ser Thr	1115	1120	1125
Ile Val Pro Glu Asn Ala Ala His Gln Gly Ala Asn Arg Thr Ser	1130	1135	1140
Ser Leu Glu Asn His Asp Gln Met Ser Val Asn Cys Arg Thr Leu	1145	1150	1155
Leu Ser Glu Ser Pro Gly Lys Leu His Val Glu Val Ser Ala Asp	1160	1165	1170
Leu Thr Ala Ile Asn Gly Leu Ser Tyr Asn Gln Asn Leu Ala Asn	1175	1180	1185
Gly Ser Tyr Asp Leu Ala Asn Arg Asp Phe Cys Gln Gly Asn Gln	1190	1195	1200
Leu Asn Tyr Tyr Lys Gln Glu Ile Pro Val Gln Pro Thr Thr Ser	1205	1210	1215
Tyr Ser Ile Gln Asn Leu Tyr Ser Tyr Glu Asn Gln Pro Gln Pro	1220	1225	1230
Ser Asp Glu Cys Thr Leu Leu Ser Asn Lys Tyr Leu Asp Gly Asn	1235	1240	1245
Ala Asn Lys Ser Thr Ser Asp Gly Ser Pro Val Met Ala Val Met	1250	1255	1260
Pro Gly Thr Thr Asp Thr Ile Gln Val Leu Lys Gly Arg Met Asp	1265	1270	1275
Ser Glu Gln Ser Pro Ser Ile Gly Tyr Ser Ser Arg Thr Leu Gly	1280	1285	1290
Pro Asn Pro Gly Leu Ile Leu Gln Ala Leu Thr Leu Ser Asn Ala	1295	1300	1305
Ser Asp Gly Phe Asn Leu Glu Arg Leu Glu Met Leu Gly Asp Ser	1310	1315	1320
Phe Leu Lys His Ala Ile Thr Thr Tyr Leu Phe Cys Thr Tyr Pro			

1325	1330	1335
Asp Ala His Glu Gly Arg 1340	Leu Ser Tyr Met Arg 1345	Ser Lys Lys Val 1350
Ser Asn Cys Asn Leu Tyr 1355	Arg Leu Gly Lys Lys 1360	Lys Gly Leu Pro 1365
Ser Arg Met Val Val Ser 1370	Ile Phe Asp Pro Pro 1375	Val Asn Trp Leu 1380
Pro Pro Gly Tyr Val Val 1385	Asn Gln Asp Lys Ser 1390	Asn Thr Asp Lys 1395
Trp Glu Lys Asp Glu Met 1400	Thr Lys Asp Cys Met 1405	Leu Ala Asn Gly 1410
Lys Leu Asp Glu Asp Tyr 1415	Glu Glu Asp Glu Glu 1420	Glu Glu Ser 1425
Leu Met Trp Arg Ala Pro 1430	Lys Glu Glu Ala Asp 1435	Tyr Glu Asp Asp 1440
Phe Leu Glu Tyr Asp Gln 1445	Glu His Ile Arg Phe 1450	Ile Asp Asn Met 1455
Leu Met Gly Ser Gly Ala 1460	Phe Val Lys Lys Ile 1465	Ser Leu Ser Pro 1470
Phe Ser Thr Thr Asp Ser 1475	Ala Tyr Glu Trp Lys 1480	Met Pro Lys Lys 1485
Ser Ser Leu Gly Ser Met 1490	Pro Phe Ser Ser Asp 1495	Phe Glu Asp Phe 1500
Asp Tyr Ser Ser Trp Asp 1505	Ala Met Cys Tyr Leu 1510	Asp Pro Ser Lys 1515
Ala Val Glu Glu Asp Asp 1520	Phe Val Val Gly Phe 1525	Trp Asn Pro Ser 1530
Glu Glu Asn Cys Gly Val 1535	Asp Thr Gly Lys Gln 1540	Ser Ile Ser Tyr 1545
Asp Leu His Thr Glu Gln 1550	Cys Ile Ala Asp Lys 1555	Ser Ile Ala Asp 1560
Cys Val Glu Ala Leu Leu 1565	Gly Cys Tyr Leu Thr 1570	Ser Cys Gly Glu 1575
Arg Ala Ala Gln Leu Phe 1580	Leu Cys Ser Leu Gly 1585	Leu Lys Val Leu 1590
Pro Val Ile Lys Arg Thr 1595	Asp Arg Glu Lys Ala 1600	Leu Cys Pro Thr 1605
Arg Glu Asn Phe Asn Ser 1610	Gln Gln Lys Asn Leu 1615	Ser Val Ser Cys 1620
Ala Ala Ala Ser Val Ala 1625	Ser Ser Arg Ser Ser 1630	Val Leu Lys Asp 1635

Ser Glu Tyr Gly Cys Leu Lys Ile Pro Pro Arg Cys Met Phe Asp
 1640 1645 1650
 His Pro Asp Ala Asp Lys Thr Leu Asn His Leu Ile Ser Gly Phe
 1655 1660 1665
 Glu Asn Phe Glu Lys Lys Ile Asn Tyr Arg Phe Lys Asn Lys Ala
 1670 1675 1680
 Tyr Leu Leu Gln Ala Phe Thr His Ala Ser Tyr His Tyr Asn Thr
 1685 1690 1695
 Ile Thr Asp Cys Tyr Gln Arg Leu Glu Phe Leu Gly Asp Ala Ile
 1700 1705 1710
 Leu Asp Tyr Leu Ile Thr Lys His Leu Tyr Glu Asp Pro Arg Gln
 1715 1720 1725
 His Ser Pro Gly Val Leu Thr Asp Leu Arg Ser Ala Leu Val Asn
 1730 1735 1740
 Asn Thr Ile Phe Ala Ser Leu Ala Val Lys Tyr Asp Tyr His Lys
 1745 1750 1755
 Tyr Phe Lys Ala Val Ser Pro Glu Leu Phe His Val Ile Asp Asp
 1760 1765 1770
 Phe Val Gln Phe Gln Leu Glu Lys Asn Glu Met Gln Gly Met Asp
 1775 1780 1785
 Ser Glu Leu Arg Arg Ser Glu Glu Asp Glu Glu Lys Glu Glu Asp
 1790 1795 1800
 Ile Glu Val Pro Lys Ala Met Gly Asp Ile Phe Glu Ser Leu Ala
 1805 1810 1815
 Gly Ala Ile Tyr Met Asp Ser Gly Met Ser Leu Glu Thr Val Trp
 1820 1825 1830
 Gln Val Tyr Tyr Pro Met Met Arg Pro Leu Ile Glu Lys Phe Ser
 1835 1840 1845
 Ala Asn Val Pro Arg Ser Pro Val Arg Glu Leu Leu Glu Met Glu
 1850 1855 1860
 Pro Glu Thr Ala Lys Phe Ser Pro Ala Glu Arg Thr Tyr Asp Gly
 1865 1870 1875
 Lys Val Arg Val Thr Val Glu Val Val Gly Lys Gly Lys Phe Lys
 1880 1885 1890
 Gly Val Gly Arg Ser Tyr Arg Ile Ala Lys Ser Ala Ala Ala Arg
 1895 1900 1905
 Arg Ala Leu Arg Ser Leu Lys Ala Asn Gln Pro Gln Val Pro Asn
 1910 1915 1920
 Ser
 <210> 165
 <211> 482

<212> PRT

<213> Homo sapiens

<400> 165

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Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
1          5          10          15

Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
20          25          30

His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
35          40          45

Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
50          55          60

Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
65          70          75          80

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
85          90          95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
100         105         110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
115         120         125

Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys
130         135         140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
145         150         155         160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
165         170         175

Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
180         185         190

Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
195         200         205

Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
210         215         220

Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile
225         230         235         240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala
245         250         255

Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly
260         265         270

Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val
275         280         285

Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr
290         295         300

Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu

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305 310 315 320
 Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr
 325 330 335
 Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn
 340 345 350
 Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu
 355 360 365
 Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile
 370 375 380
 Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp
 385 390 395 400
 Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys
 405 410 415
 Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys
 420 425 430
 Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
 435 440 445
 Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys
 450 455 460
 Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
 465 470 475 480
 Leu Ala

<210> 166
 <211> 556
 <212> PRT
 <213> Homo sapiens

<400> 166
 Phe Arg Ala Phe Gly Thr Ser Ala Gly Trp Tyr Arg Ala Phe Pro Ala
 1 5 10 15
 Pro Pro Pro Leu Leu Pro Pro Ala Cys Pro Ser Pro Arg Asp Tyr Arg
 20 25 30
 Pro His Val Ser Leu Ser Pro Phe Leu Ser Arg Pro Ser Arg Gly Gly
 35 40 45
 Ser Ser Ser Ser Ser Ser Ser Arg Arg Arg Ser Pro Val Ala Ala Val
 50 55 60
 Ala Gly Glu Pro Met Ala Tyr Ser Gln Gly Gly Gly Lys Lys Lys Val
 65 70 75 80
 Cys Tyr Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly
 85 90 95
 His Pro Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu
 100 105 110

Asn Tyr Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala
 115 120 125
 Thr Ala Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe
 130 135 140
 Leu Arg Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met
 145 150 155 160
 His Thr Val Asn Val Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe
 165 170 175
 Glu Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys
 180 185 190
 Leu Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu
 195 200 205
 His His Ala Lys Lys Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp
 210 215 220
 Ile Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu
 225 230 235 240
 Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly Val Glu Glu Ala Phe
 245 250 255
 Tyr Thr Thr Asp Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu
 260 265 270
 Tyr Phe Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly
 275 280 285
 Lys Tyr Tyr Ala Val Asn Phe Pro Met Arg Asp Gly Ile Asp Asp Glu
 290 295 300
 Ser Tyr Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met
 305 310 315 320
 Tyr Gln Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser
 325 330 335
 Gly Asp Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys
 340 345 350
 Cys Val Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly
 355 360 365
 Gly Gly Gly Tyr Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu
 370 375 380
 Thr Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn
 385 390 395 400
 Asp Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro
 405 410 415
 Ser Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys
 420 425 430
 Gln Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val
 435 440 445

Gln Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp
 450 455 460
 Glu Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp
 465 470 475 480
 Lys Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly
 485 490 495
 Glu Gly Gly Arg Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys
 500 505 510
 Ala Arg Ile Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp
 515 520 525
 Val Lys Glu Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp
 530 535 540
 Thr Lys Gly Thr Lys Ser Glu Gln Leu Ser Asn Pro
 545 550 555
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 <211> 428
 <212> PRT
 <213> Homo sapiens
 <400> 167
 Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
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 His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
 20 25 30
 His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
 35 40 45
 Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
 50 55 60
 Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
 65 70 75 80
 Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
 85 90 95
 Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
 100 105 110
 Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
 115 120 125
 Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe
 130 135 140
 Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
 145 150 155 160
 His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
 165 170 175
 Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe

332

Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
 50 55 60
 Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
 65 70 75 80
 Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
 85 90 95
 Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
 100 105 110
 Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
 115 120 125
 Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
 130 135 140
 Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
 145 150 155 160
 Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
 165 170 175
 Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
 180 185 190
 Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
 195 200 205
 Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
 210 215 220
 Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
 225 230 235 240
 Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
 245 250 255
 Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
 260 265 270
 Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
 275 280 285
 Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
 290 295 300
 Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
 305 310 315 320
 Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
 325 330 335
 Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
 340 345 350
 Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
 355 360 365
 Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
 370 375 380

Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
 385 390 395 400
 Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
 405 410 415
 Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
 420 425 430
 Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
 435 440 445
 His Leu
 450
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 <211> 507
 <212> PRT
 <213> Homo sapiens
 <400> 169
 Met Ala Gly Arg Gly Ser Leu Val Ser Trp Arg Ala Phe His Gly Cys
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 Asp Ser Ala Glu Glu Leu Pro Arg Val Ser Pro Arg Phe Leu Arg Ala
 20 25 30
 Trp His Pro Pro Pro Val Ser Ala Arg Met Pro Thr Arg Arg Trp Ala
 35 40 45
 Pro Gly Thr Gln Cys Ile Thr Lys Cys Glu His Thr Arg Pro Lys Pro
 50 55 60
 Gly Glu Leu Ala Phe Arg Lys Gly Asp Val Val Thr Ile Leu Glu Ala
 65 70 75 80
 Cys Glu Asn Lys Ser Trp Tyr Arg Val Lys His His Thr Ser Gly Gln
 85 90 95
 Glu Gly Leu Leu Ala Ala Gly Ala Leu Arg Glu Arg Glu Ala Leu Ser
 100 105 110
 Ala Asp Pro Lys Leu Ser Leu Met Pro Trp Phe His Gly Lys Ile Ser
 115 120 125
 Gly Gln Glu Ala Val Gln Gln Leu Gln Pro Pro Glu Asp Gly Leu Phe
 130 135 140
 Leu Val Arg Glu Ser Ala Arg His Pro Gly Asp Tyr Val Leu Cys Val
 145 150 155 160
 Ser Phe Gly Arg Asp Val Ile His Tyr Arg Val Leu His Arg Asp Gly
 165 170 175
 His Leu Thr Ile Asp Glu Ala Val Phe Phe Cys Asn Leu Met Asp Met
 180 185 190
 Val Glu His Tyr Ser Lys Asp Lys Gly Ala Ile Cys Thr Lys Leu Val
 195 200 205
 Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala Glu Glu Glu Leu Ala

210	215	220
Arg Ala Gly Trp Leu Leu Asn Leu Gln His	Leu Thr Leu Gly Ala Gln	
225	230	235 240
Ile Gly Glu Gly Glu Phe Gly Ala Val	Leu Gln Gly Glu Tyr Leu Gly	
	245	250 255
Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp Val Thr Ala Gln Ala		
	260	265 270
Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met Gln His Glu Asn Leu		
	275	280 285
Val Arg Leu Leu Gly Val Ile Leu His Gln Gly Leu Tyr Ile Val Met		
	290	295 300
Glu His Val Ser Lys Gly Asn Leu Val Asn Phe Leu Arg Thr Arg Gly		
	305	310 315 320
Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln Phe Ser Leu His Val		
	325	330 335
Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys Leu Val His Arg Asp		
	340	345 350
Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp Leu Val Ala Lys Val		
	355	360 365
Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys Gly Leu Asp Ser Ser		
	370	375 380
Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Lys His Gly Lys		
	385	390 395 400
Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu		
	405	410 415
Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys Met Ser Leu Lys Glu		
	420	425 430
Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met Glu Pro Pro Glu Gly		
	435	440 445
Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu		
	450	455 460
Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg		
	465	470 475 480
Glu Leu Arg Ser Ala Gly Ala Pro Ala Ser Val Ser Gly Gln Asp Ala		
	485	490 495
Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro		
	500	505

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 <211> 1332
 <212> PRT
 <213> Homo sapiens
 <400> 170

Met Arg Asn Leu Lys Leu Phe Arg Thr Leu Glu Phe Arg Asp Ile Gln
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 Gly Pro Gly Asn Pro Gln Cys Phe Ser Leu Arg Thr Glu Gln Gly Thr
 20 25 30
 Val Leu Ile Gly Ser Glu His Gly Leu Ile Glu Val Asp Pro Val Ser
 35 40 45
 Arg Glu Val Lys Asn Glu Val Ser Leu Val Ala Glu Gly Phe Leu Pro
 50 55 60
 Glu Asp Gly Ser Gly Arg Ile Val Gly Val Gln Asp Leu Leu Asp Gln
 65 70 75 80
 Glu Ser Val Cys Val Ala Thr Ala Ser Gly Asp Val Ile Leu Cys Ser
 85 90 95
 Leu Ser Thr Gln Gln Leu Glu Cys Val Gly Ser Val Ala Ser Gly Ile
 100 105 110
 Ser Val Met Ser Trp Ser Pro Asp Gln Glu Leu Val Leu Leu Ala Thr
 115 120 125
 Gly Gln Gln Thr Leu Ile Met Met Thr Lys Asp Phe Glu Pro Ile Leu
 130 135 140
 Glu Gln Gln Ile His Gln Asp Asp Phe Gly Glu Ser Lys Phe Ile Thr
 145 150 155 160
 Val Gly Trp Gly Arg Lys Glu Thr Gln Phe His Gly Ser Glu Gly Arg
 165 170 175
 Gln Ala Ala Phe Gln Met Gln Met His Glu Ser Ala Leu Pro Trp Asp
 180 185 190
 Asp His Arg Pro Gln Val Thr Trp Arg Gly Asp Gly Gln Phe Phe Ala
 195 200 205
 Val Ser Val Val Cys Pro Glu Thr Gly Ala Arg Lys Val Arg Val Trp
 210 215 220
 Asn Arg Glu Phe Ala Leu Gln Ser Thr Ser Glu Pro Val Ala Gly Leu
 225 230 235 240
 Gly Pro Ala Leu Ala Trp Lys Pro Ser Gly Ser Leu Ile Ala Ser Thr
 245 250 255
 Gln Asp Lys Pro Asn Gln Gln Asp Ile Val Phe Phe Glu Lys Asn Gly
 260 265 270
 Leu Leu His Gly His Phe Thr Leu Pro Phe Leu Lys Asp Glu Val Lys
 275 280 285
 Val Asn Asp Leu Leu Trp Asn Ala Asp Ser Ser Val Leu Ala Val Trp
 290 295 300
 Leu Glu Asp Leu Gln Arg Glu Glu Ser Ser Ile Pro Lys Thr Cys Val
 305 310 315 320
 Gln Leu Trp Thr Val Gly Asn Tyr His Trp Tyr Leu Lys Gln Ser Leu
 325 330 335

Ser Phe Ser Thr Cys Gly Lys Ser Lys Ile Val Ser Leu Met Trp Asp
 340 345 350
 Pro Val Thr Pro Tyr Arg Leu His Val Leu Cys Gln Gly Trp His Tyr
 355 360 365
 Leu Ala Tyr Asp Trp His Trp Thr Thr Asp Arg Ser Val Gly Asp Asn
 370 375 380
 Ser Ser Asp Leu Ser Asn Val Ala Val Ile Asp Gly Asn Arg Val Leu
 385 390 395 400
 Val Thr Val Phe Arg Gln Thr Val Val Pro Pro Pro Met Cys Thr Tyr
 405 410 415
 Gln Leu Leu Phe Pro His Pro Val Asn Gln Val Thr Phe Leu Ala His
 420 425 430
 Pro Gln Lys Ser Asn Asp Leu Ala Val Leu Asp Ala Ser Asn Gln Ile
 435 440 445
 Ser Val Tyr Lys Cys Gly Asp Cys Pro Ser Ala Asp Pro Thr Val Lys
 450 455 460
 Leu Gly Ala Val Gly Gly Ser Gly Phe Lys Val Cys Leu Arg Thr Pro
 465 470 475 480
 His Leu Glu Lys Arg Tyr Lys Ile Gln Phe Glu Asn Asn Glu Asp Gln
 485 490 495
 Asp Val Asn Pro Leu Lys Leu Gly Leu Leu Thr Trp Ile Glu Glu Asp
 500 505 510
 Val Phe Leu Ala Val Ser His Ser Glu Phe Ser Pro Arg Ser Val Ile
 515 520 525
 His His Leu Thr Ala Ala Ser Ser Glu Met Asp Glu Glu His Gly Gln
 530 535 540
 Leu Asn Val Ser Ser Ser Ala Ala Val Asp Gly Val Ile Ile Ser Leu
 545 550 555 560
 Cys Cys Asn Ser Lys Thr Lys Ser Val Val Leu Gln Leu Ala Asp Gly
 565 570 575
 Gln Ile Phe Lys Tyr Leu Trp Glu Ser Pro Ser Leu Ala Ile Lys Pro
 580 585 590
 Trp Lys Asn Ser Gly Gly Phe Pro Val Arg Phe Pro Tyr Pro Cys Thr
 595 600 605
 Gln Thr Glu Leu Ala Met Ile Gly Glu Glu Glu Cys Val Leu Gly Leu
 610 615 620
 Thr Asp Arg Cys Arg Phe Phe Ile Asn Asp Ile Glu Val Ala Ser Asn
 625 630 635 640
 Ile Thr Ser Phe Ala Val Tyr Asp Glu Phe Leu Leu Leu Thr Thr His
 645 650 655
 Ser His Thr Cys Gln Cys Phe Cys Leu Arg Asp Ala Ser Phe Lys Thr

660					665					670					
Leu	Gln	Ala	Gly	Leu	Ser	Ser	Asn	His	Val	Ser	His	Gly	Glu	Val	Leu
	675						680					685			
Arg	Lys	Val	Glu	Arg	Gly	Ser	Arg	Ile	Val	Thr	Val	Val	Pro	Gln	Asp
	690					695					700				
Thr	Lys	Leu	Val	Leu	Gln	Met	Pro	Arg	Gly	Asn	Leu	Glu	Val	Val	His
	705					710					715				720
His	Arg	Ala	Leu	Val	Leu	Ala	Gln	Ile	Arg	Lys	Trp	Leu	Asp	Lys	Leu
			725						730					735	
Met	Phe	Lys	Glu	Ala	Phe	Glu	Cys	Met	Arg	Lys	Leu	Arg	Ile	Asn	Leu
			740					745					750		
Asn	Leu	Ile	Tyr	Asp	His	Asn	Pro	Lys	Val	Phe	Leu	Gly	Asn	Val	Glu
		755					760					765			
Thr	Phe	Ile	Lys	Gln	Ile	Asp	Ser	Val	Asn	His	Ile	Asn	Leu	Phe	Phe
	770					775						780			
Thr	Glu	Leu	Lys	Glu	Glu	Asp	Val	Thr	Lys	Thr	Met	Tyr	Pro	Ala	Pro
	785					790					795				800
Val	Thr	Ser	Ser	Val	Tyr	Leu	Ser	Arg	Asp	Pro	Asp	Gly	Asn	Lys	Ile
				805					810					815	
Asp	Leu	Val	Cys	Asp	Ala	Met	Arg	Ala	Val	Met	Glu	Ser	Ile	Asn	Pro
			820					825					830		
His	Lys	Tyr	Cys	Leu	Ser	Ile	Leu	Thr	Ser	His	Val	Lys	Lys	Thr	Thr
		835					840					845			
Pro	Glu	Leu	Glu	Ile	Val	Leu	Gln	Lys	Val	His	Glu	Leu	Gln	Gly	Asn
	850					855					860				
Ala	Pro	Ser	Asp	Pro	Asp	Ala	Val	Ser	Ala	Glu	Glu	Ala	Leu	Lys	Tyr
	865					870					875				880
Leu	Leu	His	Leu	Val	Asp	Val	Asn	Glu	Leu	Tyr	Asp	His	Ser	Leu	Gly
			885						890					895	
Thr	Tyr	Asp	Phe	Asp	Leu	Val	Leu	Met	Val	Ala	Glu	Lys	Ser	Gln	Lys
		900						905					910		
Asp	Pro	Lys	Glu	Tyr	Leu	Pro	Phe	Leu	Asn	Thr	Leu	Lys	Lys	Met	Glu
		915					920					925			
Thr	Asn	Tyr	Gln	Arg	Phe	Thr	Ile	Asp	Lys	Tyr	Leu	Lys	Arg	Tyr	Glu
	930					935					940				
Lys	Ala	Ile	Gly	His	Leu	Ser	Lys	Cys	Gly	Pro	Glu	Tyr	Phe	Pro	Glu
	945					950					955				960
Cys	Leu	Asn	Leu	Ile	Lys	Asp	Lys	Asn	Leu	Tyr	Asn	Glu	Ala	Leu	Lys
			965						970					975	
Leu	Tyr	Ser	Pro	Ser	Ser	Gln	Gln	Tyr	Gln	Asp	Ile	Ser	Ile	Ala	Tyr
			980					985					990		

Gly	Glu	His	Leu	Met	Gln	Glu	His	Met	Tyr	Glu	Pro	Ala	Gly	Leu	Met
		995					1000						1005		
Phe	Ala	Arg	Cys	Gly	Ala	His	Glu	Lys	Ala	Leu	Ser	Ala	Phe	Leu	
	1010					1015					1020				
Thr	Cys	Gly	Asn	Trp	Lys	Gln	Ala	Leu	Cys	Val	Ala	Ala	Gln	Leu	
	1025					1030					1035				
Asn	Phe	Thr	Lys	Asp	Gln	Leu	Val	Gly	Leu	Gly	Arg	Thr	Leu	Ala	
	1040					1045					1050				
Gly	Lys	Leu	Val	Glu	Gln	Arg	Lys	His	Ile	Asp	Ala	Ala	Met	Val	
	1055					1060					1065				
Leu	Glu	Glu	Ser	Ala	Gln	Asp	Tyr	Glu	Glu	Ala	Val	Leu	Leu	Leu	
	1070					1075					1080				
Leu	Glu	Gly	Ala	Ala	Trp	Glu	Glu	Ala	Leu	Arg	Leu	Val	Tyr	Lys	
	1085					1090					1095				
Tyr	Asn	Arg	Leu	Asp	Ile	Ile	Glu	Thr	Asn	Val	Lys	Pro	Ser	Ile	
	1100					1105					1110				
Leu	Glu	Ala	Gln	Lys	Asn	Tyr	Met	Ala	Phe	Leu	Asp	Ser	Gln	Thr	
	1115					1120					1125				
Ala	Thr	Phe	Ser	Arg	His	Lys	Lys	Arg	Leu	Leu	Val	Val	Arg	Glu	
	1130					1135					1140				
Leu	Lys	Glu	Gln	Ala	Gln	Gln	Ala	Gly	Leu	Asp	Asp	Glu	Val	Pro	
	1145					1150					1155				
His	Gly	Gln	Glu	Ser	Asp	Leu	Phe	Ser	Glu	Thr	Ser	Ser	Val	Val	
	1160					1165					1170				
Ser	Gly	Ser	Glu	Met	Ser	Gly	Lys	Tyr	Ser	His	Ser	Asn	Ser	Arg	
	1175					1180					1185				
Ile	Ser	Ala	Arg	Ser	Ser	Lys	Asn	Arg	Arg	Lys	Ala	Glu	Arg	Lys	
	1190					1195					1200				
Lys	His	Ser	Leu	Lys	Glu	Gly	Ser	Pro	Leu	Glu	Asp	Leu	Ala	Leu	
	1205					1210					1215				
Leu	Glu	Ala	Leu	Ser	Glu	Val	Val	Gln	Asn	Thr	Glu	Asn	Leu	Lys	
	1220					1225					1230				
Asp	Glu	Val	Tyr	His	Ile	Leu	Lys	Val	Leu	Phe	Leu	Phe	Glu	Phe	
	1235					1240					1245				
Asp	Glu	Gln	Gly	Arg	Glu	Leu	Gln	Lys	Ala	Phe	Glu	Asp	Thr	Leu	
	1250					1255					1260				
Gln	Leu	Met	Glu	Arg	Ser	Leu	Pro	Glu	Ile	Trp	Thr	Leu	Thr	Tyr	
	1265					1270					1275				
Gln	Gln	Asn	Ser	Ala	Thr	Pro	Val	Leu	Gly	Pro	Asn	Ser	Thr	Ala	
	1280					1285					1290				
Asn	Ser	Ile	Met	Ala	Ser	Tyr	Gln	Gln	Gln	Lys	Thr	Ser	Val	Pro	
	1295					1300					1305				

Val Leu Asp Ala Glu Leu Phe Ile Pro Pro Lys Ile Asn Arg Arg
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 Thr Gln Trp Lys Leu Ser Leu Leu Asp
 1325 1330
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 <211> 3371
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 <213> Homo sapiens
 <400> 171
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 Val Gln Ser Ala Ala Val Pro Ala Pro Thr Ser Gln Leu Leu Ser Ser
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 Leu Glu Lys Asp Glu Pro Arg Lys Ser Phe Gly Ile Lys Val Gln Asn
 35 40 45
 Leu Pro Val Arg Ser Thr Asp Thr Ser Leu Lys Asp Gly Leu Phe His
 50 55 60
 Glu Phe Lys Lys Phe Gly Lys Val Thr Ser Val Gln Ile His Gly Thr
 65 70 75 80
 Ser Glu Glu Arg Tyr Gly Leu Val Phe Phe Arg Gln Gln Glu Asp Gln
 85 90 95
 Glu Lys Ala Leu Thr Ala Ser Lys Gly Lys Leu Phe Phe Gly Met Gln
 100 105 110
 Ile Glu Val Thr Ala Trp Ile Gly Pro Glu Thr Glu Ser Glu Asn Glu
 115 120 125
 Phe Arg Pro Leu Asp Glu Arg Ile Asp Glu Phe His Pro Lys Ala Thr
 130 135 140
 Arg Thr Leu Phe Ile Gly Asn Leu Glu Lys Thr Thr Thr Tyr His Asp
 145 150 155 160
 Leu Arg Asn Ile Phe Gln Arg Phe Gly Glu Ile Val Asp Ile Asp Ile
 165 170 175
 Lys Lys Val Asn Gly Val Pro Gln Tyr Ala Phe Leu Gln Tyr Cys Asp
 180 185 190
 Ile Ala Ser Val Cys Lys Ala Ile Lys Lys Met Asp Gly Glu Tyr Leu
 195 200 205
 Gly Asn Asn Arg Leu Lys Leu Gly Phe Gly Lys Ser Met Pro Thr Asn
 210 215 220
 Cys Val Trp Leu Asp Gly Leu Ser Ser Asn Val Ser Asp Gln Tyr Leu
 225 230 235 240
 Thr Arg His Phe Cys Arg Tyr Gly Pro Val Val Lys Val Val Phe Asp
 245 250 255
 Arg Leu Lys Gly Met Ala Leu Val Leu Tyr Asn Glu Ile Glu Tyr Ala

260	265	270
Gln Ala Ala Val Lys Glu Thr Lys Gly Arg Lys Ile Gly Gly Asn Lys		
275	280	285
Ile Lys Val Asp Phe Ala Asn Arg Glu Ser Gln Leu Ala Phe Tyr His		
290	295	300
Cys Met Glu Lys Ser Gly Gln Asp Ile Arg Asp Phe Tyr Glu Met Leu		
305	310	315
Ala Glu Arg Arg Glu Glu Arg Arg Ala Ser Tyr Asp Tyr Asn Gln Asp		
325	330	335
Arg Thr Tyr Tyr Glu Ser Val Arg Thr Pro Gly Thr Tyr Pro Glu Asp		
340	345	350
Ser Arg Arg Asp Tyr Pro Ala Arg Gly Arg Glu Phe Tyr Ser Glu Trp		
355	360	365
Glu Thr Tyr Gln Gly Asp Tyr Tyr Glu Ser Arg Tyr Tyr Asp Asp Pro		
370	375	380
Arg Glu Tyr Arg Asp Tyr Arg Asn Asp Pro Tyr Glu Gln Asp Ile Arg		
385	390	395
Glu Tyr Ser Tyr Arg Gln Arg Glu Arg Glu Arg Glu Arg Glu Arg Phe		
405	410	415
Glu Ser Asp Arg Asp Arg Asp His Glu Arg Arg Pro Ile Glu Arg Ser		
420	425	430
Gln Ser Pro Val His Leu Arg Arg Pro Gln Ser Pro Gly Ala Ser Pro		
435	440	445
Ser Gln Ala Glu Arg Leu Pro Ser Asp Ser Glu Arg Arg Leu Tyr Ser		
450	455	460
Arg Ser Ser Asp Arg Ser Gly Ser Cys Ser Ser Leu Ser Pro Pro Arg		
465	470	475
Tyr Glu Lys Leu Asp Lys Ser Arg Leu Glu Arg Tyr Thr Lys Asn Glu		
485	490	495
Lys Thr Asp Lys Glu Arg Thr Phe Asp Pro Glu Arg Val Glu Arg Glu		
500	505	510
Arg Arg Leu Ile Arg Lys Glu Lys Val Glu Lys Asp Lys Thr Asp Lys		
515	520	525
Gln Lys Arg Lys Gly Lys Val His Ser Pro Ser Ser Gln Ser Ser Glu		
530	535	540
Thr Asp Gln Glu Asn Glu Arg Glu Gln Ser Pro Glu Lys Pro Arg Ser		
545	550	555
Cys Asn Lys Leu Ser Arg Glu Lys Ala Asp Lys Glu Gly Ile Ala Lys		
565	570	575
Asn Arg Leu Glu Leu Met Pro Cys Val Val Leu Thr Arg Val Lys Glu		
580	585	590

Lys Glu Gly Lys Val Ile Asp His Thr Pro Val Glu Lys Leu Lys Ala
 595 600 605
 Lys Leu Asp Asn Asp Thr Val Lys Ser Ser Ala Leu Asp Gln Lys Leu
 610 615 620
 Gln Val Ser Gln Thr Glu Pro Ala Lys Ser Asp Leu Ser Lys Leu Glu
 625 630 635 640
 Ser Val Arg Met Lys Val Pro Lys Glu Lys Gly Leu Ser Ser His Val
 645 650 655
 Glu Val Val Glu Lys Glu Gly Arg Leu Lys Ala Arg Lys His Leu Lys
 660 665 670
 Pro Glu Gln Pro Ala Asp Gly Val Ser Ala Val Asp Leu Glu Lys Leu
 675 680 685
 Glu Ala Arg Lys Arg Arg Phe Ala Asp Ser Asn Leu Lys Ala Glu Lys
 690 695 700
 Gln Lys Pro Glu Val Lys Lys Ser Ser Pro Glu Met Glu Asp Ala Arg
 705 710 715 720
 Val Leu Ser Lys Lys Gln Pro Asp Val Ser Ser Arg Glu Val Ile Leu
 725 730 735
 Leu Arg Glu Gly Glu Ala Glu Arg Lys Pro Val Arg Lys Glu Ile Leu
 740 745 750
 Lys Arg Glu Ser Lys Lys Ile Lys Leu Asp Arg Leu Asn Thr Val Ala
 755 760 765
 Ser Pro Lys Asp Cys Gln Glu Leu Ala Ser Ile Ser Val Gly Ser Gly
 770 775 780
 Ser Arg Pro Ser Ser Asp Leu Gln Ala Arg Leu Gly Glu Leu Ala Gly
 785 790 795 800
 Glu Ser Val Glu Asn Gln Glu Val Gln Ser Lys Lys Pro Ile Pro Ser
 805 810 815
 Lys Pro Gln Leu Lys Gln Leu Gln Val Leu Asp Asp Gln Gly Pro Glu
 820 825 830
 Arg Glu Asp Val Arg Lys Asn Tyr Cys Ser Leu Arg Asp Glu Thr Pro
 835 840 845
 Glu Arg Lys Ser Gly Gln Glu Lys Ser His Ser Val Asn Thr Glu Glu
 850 855 860
 Lys Ile Gly Ile Asp Ile Asp His Thr Gln Ser Tyr Arg Lys Gln Met
 865 870 875 880
 Glu Gln Ser Arg Arg Lys Gln Gln Met Glu Met Glu Ile Ala Lys Ser
 885 890 895
 Glu Lys Phe Gly Ser Pro Lys Lys Asp Val Asp Glu Tyr Glu Arg Arg
 900 905 910
 Ser Leu Val His Glu Val Gly Lys Pro Pro Gln Asp Val Thr Asp Asp
 915 920 925

Ser Pro Pro Ser Lys Lys Lys Arg Met Asp His Val Asp Phe Asp Ile
 930 935 940
 Cys Thr Lys Arg Glu Arg Asn Tyr Arg Ser Ser Arg Gln Ile Ser Glu
 945 950 955 960
 Asp Ser Glu Arg Thr Gly Gly Ser Pro Ser Val Arg His Gly Ser Phe
 965 970 975
 His Glu Asp Glu Asp Pro Ile Gly Ser Pro Arg Leu Leu Ser Val Lys
 980 985 990
 Gly Ser Pro Lys Val Asp Glu Lys Val Leu Pro Tyr Ser Asn Ile Thr
 995 1000 1005
 Val Arg Glu Glu Ser Leu Lys Phe Asn Pro Tyr Asp Ser Ser Arg
 1010 1015 1020
 Arg Glu Gln Met Ala Asp Met Ala Lys Ile Lys Leu Ser Val Leu
 1025 1030 1035
 Asn Ser Glu Asp Glu Leu Asn Arg Trp Asp Ser Gln Met Lys Gln
 1040 1045 1050
 Asp Ala Gly Arg Phe Asp Val Ser Phe Pro Asn Ser Ile Ile Lys
 1055 1060 1065
 Arg Asp Ser Leu Arg Lys Arg Ser Val Arg Asp Leu Glu Pro Gly
 1070 1075 1080
 Glu Val Pro Ser Asp Ser Asp Glu Asp Gly Glu His Lys Ser His
 1085 1090 1095
 Ser Pro Arg Ala Ser Ala Leu Tyr Glu Ser Ser Arg Leu Ser Phe
 1100 1105 1110
 Leu Leu Arg Asp Arg Glu Asp Lys Leu Arg Glu Arg Asp Glu Arg
 1115 1120 1125
 Leu Ser Ser Ser Leu Glu Arg Asn Lys Phe Tyr Ser Phe Ala Leu
 1130 1135 1140
 Asp Lys Thr Ile Thr Pro Asp Thr Lys Ala Leu Leu Glu Arg Ala
 1145 1150 1155
 Lys Ser Leu Ser Ser Ser Arg Glu Glu Asn Trp Ser Phe Leu Asp
 1160 1165 1170
 Trp Asp Ser Arg Phe Ala Asn Phe Arg Asn Asn Lys Asp Lys Glu
 1175 1180 1185
 Lys Val Asp Ser Ala Pro Arg Pro Ile Pro Ser Trp Tyr Met Lys
 1190 1195 1200
 Lys Lys Lys Ile Arg Thr Asp Ser Glu Gly Lys Met Asp Asp Lys
 1205 1210 1215
 Lys Glu Asp His Lys Glu Glu Glu Gln Glu Arg Gln Glu Leu Phe
 1220 1225 1230
 Ala Ser Arg Phe Leu His Ser Ser Ile Phe Glu Gln Asp Ser Lys

1235	1240	1245
Arg Leu Gln His Leu Glu Arg 1250	Lys Glu Glu Asp Ser 1255	Asp Phe Ile 1260
Ser Gly Arg Ile Tyr Gly Lys 1265	Gln Thr Ser Glu Gly 1270	Ala Asn Ser 1275
Thr Thr Asp Ser Ile Gln Glu 1280	Pro Val Val Leu Phe 1285	His Ser Arg 1290
Phe Met Glu Leu Thr Arg Met 1295	Gln Gln Lys Glu Lys 1300	Glu Lys Asp 1305
Gln Lys Pro Lys Glu Val Glu 1310	Lys Gln Glu Asp Thr 1315	Glu Asn His 1320
Pro Lys Thr Pro Glu Ser Ala 1325	Pro Glu Asn Lys Asp 1330	Ser Glu Leu 1335
Lys Thr Pro Pro Ser Val Gly 1340	Pro Pro Ser Val Thr 1345	Val Val Thr 1350
Leu Glu Ser Ala Pro Ser Ala 1355	Leu Glu Lys Thr Thr 1360	Gly Asp Lys 1365
Thr Val Glu Ala Pro Leu Val 1370	Thr Glu Glu Lys Thr 1375	Val Glu Pro 1380
Ala Thr Val Ser Glu Glu Ala 1385	Lys Pro Ala Ser Glu 1390	Pro Ala Pro 1395
Ala Pro Val Glu Gln Leu Glu 1400	Gln Val Asp Leu Pro 1405	Pro Gly Ala 1410
Asp Pro Asp Lys Glu Ala Ala 1415	Met Met Pro Ala Gly 1420	Val Glu Glu 1425
Gly Ser Ser Gly Asp Gln Pro 1430	Pro Tyr Leu Asp Ala 1435	Lys Pro Pro 1440
Thr Pro Gly Ala Ser Phe Ser 1445	Gln Ala Glu Ser Asn 1450	Val Asp Pro 1455
Glu Pro Asp Ser Thr Gln Pro 1460	Leu Ser Lys Pro Ala 1465	Gln Lys Ser 1470
Glu Glu Ala Asn Glu Pro Lys 1475	Ala Glu Lys Pro Asp 1480	Ala Thr Ala 1485
Asp Ala Glu Pro Asp Ala Asn 1490	Gln Lys Ala Glu Ala 1495	Ala Pro Glu 1500
Ser Gln Pro Pro Ala Ser Glu 1505	Asp Leu Glu Val Asp 1510	Pro Pro Val 1515
Ala Ala Lys Asp Lys Lys Pro 1520	Asn Lys Ser Lys Arg 1525	Ser Lys Thr 1530
Pro Val Gln Ala Ala Ala Val 1535	Ser Ile Val Glu Lys 1540	Pro Val Thr 1545

Arg Lys	Ser Glu	Arg Ile	Asp	Arg Glu	Lys Leu	Lys	Arg Ser	Asn
1550			1555			1560		
Ser Pro	Arg Gly	Glu Ala	Gln	Lys Leu	Leu Glu	Leu	Lys Met	Glu
1565			1570			1575		
Ala Glu	Lys Ile	Thr Arg	Thr	Ala Ser	Lys Asn	Ser	Ala Ala	Asp
1580			1585			1590		
Leu Glu	His Pro	Glu Pro	Ser	Leu Pro	Leu Ser	Arg	Thr Arg	Arg
1595			1600			1605		
Arg Asn	Val Arg	Ser Val	Tyr	Ala Thr	Met Gly	Asp	His Glu	Asn
1610			1615			1620		
Arg Ser	Pro Val	Lys Glu	Pro	Val Glu	Gln Pro	Arg	Val Thr	Arg
1625			1630			1635		
Lys Arg	Leu Glu	Arg Glu	Leu	Gln Glu	Ala Ala	Ala	Val Pro	Thr
1640			1645			1650		
Thr Pro	Arg Arg	Gly Arg	Pro	Pro Lys	Thr Arg	Arg	Arg Ala	Asp
1655			1660			1665		
Glu Glu	Glu Glu	Asn Glu	Ala	Lys Glu	Pro Ala	Glu	Thr Leu	Lys
1670			1675			1680		
Pro Pro	Glu Gly	Trp Arg	Ser	Pro Arg	Ser Gln	Lys	Thr Ala	Ala
1685			1690			1695		
Gly Gly	Gly Pro	Gln Gly	Lys	Lys Gly	Lys Asn	Glu	Pro Lys	Val
1700			1705			1710		
Asp Ala	Thr Arg	Pro Glu	Ala	Thr Thr	Glu Val	Gly	Pro Gln	Ile
1715			1720			1725		
Gly Val	Lys Glu	Ser Ser	Met	Glu Pro	Lys Ala	Ala	Glu Glu	Glu
1730			1735			1740		
Ala Gly	Ser Glu	Gln Lys	Arg	Asp Arg	Lys Asp	Ala	Gly Thr	Asp
1745			1750			1755		
Lys Asn	Pro Pro	Glu Thr	Ala	Pro Val	Glu Val	Val	Glu Lys	Lys
1760			1765			1770		
Pro Ala	Pro Glu	Lys Asn	Ser	Lys Ser	Lys Arg	Gly	Arg Ser	Arg
1775			1780			1785		
Asn Ser	Arg Leu	Ala Val	Asp	Lys Ser	Ala Ser	Leu	Lys Asn	Val
1790			1795			1800		
Asp Ala	Ala Val	Ser Pro	Arg	Gly Ala	Ala Ala	Gln	Ala Gly	Glu
1805			1810			1815		
Arg Glu	Ser Gly	Val Val	Ala	Val Ser	Pro Glu	Lys	Ser Glu	Ser
1820			1825			1830		
Pro Gln	Lys Glu	Asp Gly	Leu	Ser Ser	Gln Leu	Lys	Ser Asp	Pro
1835			1840			1845		
Val Asp	Pro Asp	Lys Glu	Pro	Glu Lys	Glu Asp	Val	Ser Ala	Ser
1850			1855			1860		

Gly Pro 1865	Ser Pro Glu Ala Thr 1870	Gln Leu Ala Lys Gln 1875	Met Glu Leu
Glu Gln 1880	Ala Val Glu His Ile 1885	Ala Lys Leu Ala Glu 1890	Ala Ser Ala
Ser Ala 1895	Ala Tyr Lys Ala Asp 1900	Ala Pro Glu Gly Leu 1905	Ala Pro Glu
Asp Arg 1910	Asp Lys Pro Ala His 1915	Gln Ala Ser Glu Thr 1920	Glu Leu Ala
Ala Ala 1925	Ile Gly Ser Ile Ile 1930	Asn Asp Ile Ser Gly 1935	Glu Pro Glu
Asn Phe 1940	Pro Ala Pro Pro Pro 1945	Tyr Pro Gly Glu Ser 1950	Gln Thr Asp
Leu Gln 1955	Pro Pro Ala Gly Ala 1960	Gln Ala Leu Gln Pro 1965	Ser Glu Glu
Gly Met 1970	Glu Thr Asp Glu Ala 1975	Val Ser Gly Ile Leu 1980	Glu Thr Glu
Ala Ala 1985	Thr Glu Ser Ser Arg 1990	Pro Pro Val Asn Ala 1995	Pro Asp Pro
Ser Ala 2000	Gly Pro Thr Asp Thr 2005	Lys Glu Ala Arg Gly 2010	Asn Ser Ser
Glu Thr 2015	Ser His Ser Val Pro 2020	Glu Ala Lys Gly Ser 2025	Lys Glu Val
Glu Val 2030	Thr Leu Val Arg Lys 2035	Asp Lys Gly Arg Gln 2040	Lys Thr Thr
Arg Ser 2045	Arg Arg Lys Arg Asn 2050	Thr Asn Lys Lys Val 2055	Val Ala Pro
Val Glu 2060	Ser His Val Pro Glu 2065	Ser Asn Gln Ala Gln 2070	Gly Glu Ser
Pro Ala 2075	Ala Asn Glu Gly Thr 2080	Thr Val Gln His Pro 2085	Glu Ala Pro
Gln Glu 2090	Glu Lys Gln Ser Glu 2095	Lys Pro His Ser Thr 2100	Pro Pro Gln
Ser Cys 2105	Thr Ser Asp Leu Ser 2110	Lys Ile Pro Ser Thr 2115	Glu Asn Ser
Ser Gln 2120	Glu Ile Ser Val Glu 2125	Glu Arg Thr Pro Thr 2130	Lys Ala Ser
Val Pro 2135	Pro Asp Leu Pro Pro 2140	Pro Pro Gln Pro Ala 2145	Pro Val Asp
Glu Glu 2150	Pro Gln Ala Arg Phe 2155	Arg Val His Ser Ile 2160	Ile Glu Ser
Asp Pro	Val Thr Pro Pro Ser	Asp Pro Ser Ile Pro	Ile Pro Thr

2165	2170	2175
Leu Pro Ser Val Thr Ala 2180	Ala Lys Leu Ser Pro 2185	Pro Val Ala Ser 2190
Gly Gly Ile Pro His Gln 2195	Ser Pro Pro Thr Lys 2200	Val Thr Glu Trp 2205
Ile Thr Arg Gln Glu Glu 2210	Pro Arg Ala Gln Ser 2215	Thr Pro Ser Pro 2220
Ala Leu Pro Pro Asp Thr 2225	Lys Ala Ser Asp Val 2230	Asp Thr Ser Ser 2235
Ser Thr Leu Arg Lys Ile 2240	Leu Met Asp Pro Lys 2245	Tyr Val Ser Ala 2250
Thr Ser Val Thr Ser Thr 2255	Ser Val Thr Thr Ala 2260	Ile Ala Glu Pro 2265
Val Ser Ala Ala Pro Cys 2270	Leu His Glu Ala Pro 2275	Pro Pro Pro Val 2280
Asp Ser Lys Lys Pro Leu 2285	Glu Glu Lys Thr Ala 2290	Pro Pro Val Thr 2295
Asn Asn Ser Glu Ile Gln 2300	Ala Ser Glu Val Leu 2305	Val Ala Ala Asp 2310
Lys Glu Lys Val Ala Pro 2315	Val Ile Ala Pro Lys 2320	Ile Thr Ser Val 2325
Ile Ser Arg Met Pro Val 2330	Ser Ile Asp Leu Glu 2335	Asn Ser Gln Lys 2340
Ile Thr Leu Ala Lys Pro 2345	Ala Pro Gln Thr Leu 2350	Thr Gly Leu Val 2355
Ser Ala Leu Thr Gly Leu 2360	Val Asn Val Ser Leu 2365	Val Pro Val Asn 2370
Ala Leu Lys Gly Pro Val 2375	Lys Gly Ser Val Thr 2380	Thr Leu Lys Ser 2385
Leu Val Ser Thr Pro Ala 2390	Gly Pro Val Asn Val 2395	Leu Lys Gly Pro 2400
Val Asn Val Leu Thr Gly 2405	Pro Val Asn Val Leu 2410	Thr Thr Pro Val 2415
Asn Ala Thr Val Gly Thr 2420	Val Asn Ala Ala Pro 2425	Gly Thr Val Asn 2430
Ala Ala Ala Ser Ala Val 2435	Asn Ala Thr Ala Ser 2440	Ala Val Thr Val 2445
Thr Ala Gly Ala Val Thr 2450	Ala Ala Ser Gly Gly 2455	Val Thr Ala Thr 2460
Thr Gly Thr Val Thr Met 2465	Ala Gly Ala Val Ile 2470	Ala Pro Ser Thr 2475

Lys Cys	Lys Gln Arg Ala Ser	Ala Asn Glu Asn Ser	Arg Phe His
2480	2485	2490	
Pro Gly	Ser Met Pro Val Ile	Asp Asp Arg Pro Ala	Asp Ala Gly
2495	2500	2505	
Ser Gly	Ala Gly Leu Arg Val	Asn Thr Ser Glu Gly	Val Val Leu
2510	2515	2520	
Leu Ser	Tyr Ser Gly Gln Lys	Thr Glu Gly Pro Gln	Arg Ile Ser
2525	2530	2535	
Ala Lys	Ile Ser Gln Ile Pro	Pro Ala Ser Ala Met	Asp Ile Glu
2540	2545	2550	
Phe Gln	Gln Ser Val Ser Lys	Ser Gln Val Lys Pro	Asp Ser Val
2555	2560	2565	
Thr Ala	Ser Gln Pro Pro Ser	Lys Gly Pro Gln Ala	Pro Ala Gly
2570	2575	2580	
Tyr Ala	Asn Val Ala Thr His	Ser Thr Leu Val Leu	Thr Ala Gln
2585	2590	2595	
Thr Tyr	Asn Ala Ser Pro Val	Ile Ser Ser Val Lys	Ala Asp Arg
2600	2605	2610	
Pro Ser	Leu Glu Lys Pro Glu	Pro Ile His Leu Ser	Val Ser Thr
2615	2620	2625	
Pro Val	Thr Gln Gly Gly Thr	Val Lys Val Leu Thr	Gln Gly Ile
2630	2635	2640	
Asn Thr	Pro Pro Val Leu Val	His Asn Gln Leu Val	Leu Thr Pro
2645	2650	2655	
Ser Ile	Val Thr Thr Asn Lys	Lys Leu Ala Asp Pro	Val Thr Leu
2660	2665	2670	
Lys Ile	Glu Thr Lys Val Leu	Gln Pro Ala Asn Leu	Gly Ser Thr
2675	2680	2685	
Leu Thr	Pro His His Pro Pro	Ala Leu Pro Ser Lys	Leu Pro Thr
2690	2695	2700	
Glu Val	Asn His Val Pro Ser	Gly Pro Ser Ile Pro	Ala Asp Arg
2705	2710	2715	
Thr Val	Ser His Leu Ala Ala	Ala Lys Leu Asp Ala	His Ser Pro
2720	2725	2730	
Arg Pro	Ser Gly Pro Gly Pro	Ser Ser Phe Pro Arg	Ala Ser His
2735	2740	2745	
Pro Ser	Ser Thr Ala Ser Thr	Ala Leu Ser Thr Asn	Ala Thr Val
2750	2755	2760	
Met Leu	Ala Ala Gly Ile Pro	Val Pro Gln Phe Ile	Ser Ser Ile
2765	2770	2775	
His Pro	Glu Gln Ser Val Ile	Met Pro Pro His Ser	Ile Thr Gln
2780	2785	2790	

Thr Val 2795	Ser Leu Ser His 2800	Leu Ser Gln Gly Glu Val 2805	Arg Met Asn
Thr Pro 2810	Thr Leu Pro Ser Ile 2815	Thr Tyr Ser Ile Arg 2820	Pro Glu Ala
Leu His 2825	Ser Pro Arg Ala Pro 2830	Leu Gln Pro Gln Gln 2835	Ile Glu Val
Arg Ala 2840	Pro Gln Arg Ala Ser 2845	Thr Pro Gln Pro Ala 2850	Pro Ala Gly
Val Pro 2855	Ala Leu Ala Ser Gln 2860	His Pro Pro Glu Glu 2865	Glu Val His
Tyr His 2870	Leu Pro Val Ala Arg 2875	Ala Thr Ala Pro Val 2880	Gln Ser Glu
Val Leu 2885	Val Met Gln Ser Glu 2890	Tyr Arg Leu His Pro 2895	Tyr Thr Val
Pro Arg 2900	Asp Val Arg Ile Met 2905	Val His Pro His Val 2910	Thr Ala Val
Ser Glu 2915	Gln Pro Arg Ala Ala 2920	Asp Gly Val Val Lys 2925	Val Pro Pro
Ala Ser 2930	Lys Ala Pro Gln Gln 2935	Pro Gly Lys Glu Ala 2940	Ala Lys Thr
Pro Asp 2945	Ala Lys Ala Ala Pro 2950	Thr Pro Thr Pro Ala 2955	Pro Val Pro
Val Pro 2960	Val Pro Leu Pro Ala 2965	Pro Ala Pro Ala Pro 2970	His Gly Glu
Ala Arg 2975	Ile Leu Thr Val Thr 2980	Pro Ser Asn Gln Leu 2985	Gln Gly Leu
Pro Leu 2990	Thr Pro Pro Val Val 2995	Val Thr His Gly Val 3000	Gln Ile Val
His Ser 3005	Ser Gly Glu Leu Phe 3010	Gln Glu Tyr Arg Tyr 3015	Gly Asp Ile
Arg Thr 3020	Tyr His Pro Pro Ala 3025	Gln Leu Thr His Thr 3030	Gln Phe Pro
Ala Ala 3035	Ser Ser Val Gly Leu 3040	Pro Ser Arg Thr Lys 3045	Thr Ala Ala
Gln Gly 3050	Pro Pro Pro Glu Gly 3055	Glu Pro Leu Gln Pro 3060	Pro Gln Pro
Val Gln 3065	Ser Thr Gln Pro Ala 3070	Gln Pro Ala Pro Pro 3075	Cys Pro Pro
Ser Gln 3080	Leu Gly Gln Pro Gly 3085	Gln Pro Pro Ser Ser 3090	Lys Met Pro
Gln Val	Ser Gln Glu Ala Lys	Gly Thr Gln Thr Gly	Val Glu Gln

3095	3100	3105
Pro Arg Leu Pro Ala Gly 3110	Pro Ala Asn Arg Pro 3115	Pro Pro Glu Pro His 3120
Thr Gln Val Gln Arg Ala 3125	Gln Ala Glu Thr Gly 3130	Pro Thr Ser Phe 3135
Pro Ser Pro Val Ser Val 3140	Ser Met Lys Pro Asp 3145	Leu Pro Val Ser 3150
Leu Pro Thr Gln Thr Ala 3155	Pro Lys Gln Pro Leu 3160	Phe Val Pro Thr 3165
Thr Ser Gly Pro Ser Thr 3170	Pro Pro Gly Leu Val 3175	Leu Pro His Thr 3180
Glu Phe Gln Pro Ala Pro 3185	Lys Gln Asp Ser Ser 3190	Pro His Leu Thr 3195
Ser Gln Arg Pro Val Asp 3200	Met Val Gln Leu Leu 3205	Lys Lys Tyr Pro 3210
Ile Val Trp Gln Gly Leu 3215	Leu Ala Leu Lys Asn 3220	Asp Thr Ala Ala 3225
Val Gln Leu His Phe Val 3230	Ser Gly Asn Asn Val 3235	Leu Ala His Arg 3240
Ser Leu Pro Leu Ser Glu 3245	Gly Gly Pro Pro Leu 3250	Arg Ile Ala Gln 3255
Arg Met Arg Leu Glu Ala 3260	Thr Gln Leu Glu Gly 3265	Val Ala Arg Arg 3270
Met Thr Val Glu Thr Asp 3275	Tyr Cys Leu Leu Leu 3280	Ala Leu Pro Cys 3285
Gly Arg Asp Gln Glu Asp 3290	Val Val Ser Gln Thr 3295	Glu Ser Leu Lys 3300
Ala Ala Phe Ile Thr Tyr 3305	Leu Gln Ala Lys Gln 3310	Ala Ala Gly Ile 3315
Ile Asn Val Pro Asn Pro 3320	Gly Ser Asn Gln Pro 3325	Ala Tyr Val Leu 3330
Gln Ile Phe Pro Pro Cys 3335	Glu Phe Ser Glu Ser 3340	His Leu Ser Arg 3345
Leu Ala Pro Asp Leu Leu 3350	Ala Ser Ile Ser Asn 3355	Ile Ser Pro His 3360
Leu Met Ile Val Ile Ala 3365	Ser Val 3370	

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 <400> 172

Met Glu Asn Leu Gln Thr Asn Phe Ser Leu Val Gln Gly Ser Thr Lys
 1 5 10 15
 Lys Leu Asn Gly Met Gly Asp Asp Gly Ser Pro Pro Ala Lys Lys Met
 20 25 30
 Ile Thr Asp Ile His Val Asn Gly Lys Thr Ile Asn Lys Val Pro Thr
 35 40 45
 Val Lys Lys Glu His Leu Asp Asp Tyr Gly Glu Ala Pro Val Glu Thr
 50 55 60
 Asp Gly Glu His Val Lys Arg Thr Cys Thr Ser Val Pro Glu Thr Leu
 65 70 75 80
 His Leu Asn Pro Ser Leu Lys His Thr Leu Ala Gln Phe His Leu Ser
 85 90 95
 Ser Gln Ser Ser Leu Gly Gly Pro Ala Ala Phe Ser Ala Arg His Ser
 100 105 110
 Gln Glu Ser Met Ser Pro Thr Val Phe Leu Pro Leu Pro Ser Pro Gln
 115 120 125
 Val Leu Pro Gly Pro Leu Leu Ile Pro Ser Asp Ser Ser Thr Glu Leu
 130 135 140
 Thr Gln Thr Val Leu Glu Gly Glu Ser Ile Ser Cys Phe Gln Val Gly
 145 150 155 160
 Gly Glu Lys Arg Leu Cys Leu Pro Gln Val Leu Asn Ser Val Leu Arg
 165 170 175
 Glu Phe Thr Leu Gln Gln Ile Asn Thr Val Cys Asp Glu Leu Tyr Ile
 180 185 190
 Tyr Cys Ser Arg Cys Thr Ser Asp Gln Leu His Ile Leu Lys Val Leu
 195 200 205
 Gly Ile Leu Pro Phe Asn Ala Pro Ser Cys Gly Leu Ile Thr Leu Thr
 210 215 220
 Asp Ala Gln Arg Leu Cys Asn Ala Leu Leu Arg Pro Arg Thr Phe Pro
 225 230 235 240
 Gln Asn Gly Ser Val Leu Pro Ala Lys Ser Ser Leu Ala Gln Leu Lys
 245 250 255
 Glu Thr Gly Ser Ala Phe Glu Val Glu His Glu Cys Leu Gly Lys Cys
 260 265 270
 Gln Gly Leu Phe Ala Pro Gln Phe Tyr Val Gln Pro Asp Ala Pro Cys
 275 280 285
 Ile Gln Cys Leu Glu Cys Cys Gly Met Phe Ala Pro Gln Thr Phe Val
 290 295 300
 Met His Ser His Arg Ser Pro Asp Lys Arg Thr Cys His Trp Gly Phe
 305 310 315 320
 Glu Ser Ala Lys Trp His Cys Tyr Leu His Val Asn Gln Lys Tyr Leu
 325 330 335

Gly Thr Pro Glu Glu Lys Lys Leu Lys Ile Ile Leu Glu Glu Met Lys
 340 345 350
 Glu Lys Phe Ser Met Arg Ser Gly Lys Arg Asn Gln Ser Lys Thr Asp
 355 360 365
 Ala Pro Ser Gly Met Glu Leu Gln Ser Trp Tyr Pro Val Ile Lys Gln
 370 375 380
 Glu Gly Asp His Val Ser Gln Thr His Ser Phe Leu His Pro Ser Tyr
 385 390 395 400
 Tyr Leu Tyr Met Cys Asp Lys Val Val Ala Pro Asn Val Ser¹ Leu Thr
 405 410 415
 Ser Ala Val Ser Gln Ser Lys Glu Leu Thr Lys Thr Glu Ala Ser Lys
 420 425 430
 Ser Ile Ser Arg Gln Ser Glu Lys Ala His Ser Ser Gly Lys Leu Gln
 435 440 445
 Lys Thr Val Ser Tyr Pro Asp Val Ser Leu Glu Glu Gln Glu Lys Met
 450 455 460
 Asp Leu Lys Thr Ser Arg Glu Leu Cys Ser Arg Leu Asp Ala Ser Ile
 465 470 475 480
 Ser Asn Asn Ser Thr Ser Lys Arg Lys Ser Glu Ser Ala Thr Cys Asn
 485 490 495
 Leu Val Arg Asp Ile Asn Lys Val Gly Ile Gly Leu Val Ala Ala Ala
 500 505 510
 Ser Ser Pro Leu Leu Val Lys Asp Val Ile Cys Glu Asp Asp Lys Gly
 515 520 525
 Lys Ile Met Glu Glu Val Met Arg Thr Tyr Leu Lys Gln Gln Glu Lys
 530 535 540
 Leu Asn Leu Ile Leu Gln Lys Lys Gln Gln Leu Gln Met Glu Val Lys
 545 550 555 560
 Met Leu Ser Ser Ser Lys Ser Met Lys Glu Leu Thr Glu Glu Gln Gln
 565 570 575
 Asn Leu Gln Lys Glu Leu Glu Ser Leu Gln Asn Glu His Ala Gln Arg
 580 585 590
 Met Glu Glu Phe Tyr Val Glu Gln Lys Asp Leu Glu Lys Lys Leu Glu
 595 600 605
 Gln Ile Met Lys Gln Lys Cys Thr Cys Asp Ser Asn Leu Glu Lys Asp
 610 615 620
 Lys Glu Ala Glu Tyr Ala Gly Gln Leu Ala Glu Leu Arg Gln Arg Leu
 625 630 635 640
 Asp His Ala Glu Ala Asp Arg Gln Glu Leu Gln Asp Glu Leu Arg Gln
 645 650 655
 Glu Arg Glu Ala Arg Gln Lys Leu Glu Met Met Ile Lys Glu Leu Lys

353

Phe Gly Val Gln Ser Glu Arg Gln Asp Ser Ala Ala Val Gly Phe Asp
 275 280 285
 Tyr Lys Glu Lys Leu Ala Lys His Glu Ser Gln Gln Asp Tyr Ser Lys
 290 295 300
 Gly Phe Gly Gly Lys Tyr Gly Val Gln Lys Asp Arg Met Asp Lys Asn
 305 310 315 320
 Ala Ser Thr Phe Glu Asp Val Thr Gln Val Ser Ser Ala Tyr Gln Lys
 325 330 335
 Thr Val Pro Val Glu Ala Val Thr Ser Lys Thr Ser Asn Ile Arg Ala
 340 345 350
 Asn Phe Glu Asn Leu Ala Lys Glu Lys Glu Gln Glu Asp Arg Arg Lys
 355 360 365
 Ala Glu Ala Glu Arg Ala Gln Arg Met Ala Lys Glu Arg Gln Glu Gln
 370 375 380
 Glu Glu Ala Arg Arg Lys Leu Glu Glu Gln Ala Arg Ala Lys Thr Gln
 385 390 395 400
 Thr Pro Pro Val Ser Pro Ala Pro Gln Pro Thr Glu Glu Arg Leu Pro
 405 410 415
 Ser Ser Pro Val Tyr Glu Asp Ala Ala Ser Phe Lys Ala Glu Leu Ser
 420 425 430
 Tyr Arg Gly Pro Val Ser Gly Thr Glu Pro Glu Pro Val Tyr Ser Met
 435 440 445
 Glu Ala Ala Asp Tyr Arg Glu Ala Ser Ser Gln Gln Gly Leu Ala Tyr
 450 455 460
 Ala Thr Glu Ala Val Tyr Glu Ser Ala Glu Ala Pro Gly His Tyr Pro
 465 470 475 480
 Ala Glu Asp Ser Thr Tyr Asp Glu Tyr Glu Asn Asp Leu Gly Tyr Thr
 485 490 495
 Ala Val Ala Leu Tyr Asp Tyr Gln Ala Ala Gly Asp Asp Glu Ile Ser
 500 505 510
 Phe Asp Pro Asp Asp Ile Ile Thr Asn Ile Glu Met Ile Asp Asp Gly
 515 520 525
 Trp Trp Arg Gly Val Cys Lys Gly Arg Tyr Gly Leu Phe Pro Ala Asn
 530 535 540
 Tyr Val Glu Leu Arg Gln
 545 550
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Gln Gly Asp Asp Trp Asp Thr Asp Pro Asp Phe Val Asn Asp Ile Ser
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 Glu Lys Glu Gln Arg Trp Gly Ala Lys Thr Ile Glu Gly Ser Gly Arg
 35 40 45
 Thr Glu His Ile Asn Ile His Gln Leu Arg Asn Lys Val Ser Glu Glu
 50 55 60
 His Asp Val Leu Arg Lys Lys Glu Met Glu Ser Gly Pro Lys Ala Ser
 65 70 75 80
 His Gly Tyr Gly Gly Arg Phe Gly Val Glu Arg Asp Arg Met Asp Lys
 85 90 95
 Ser Ala Val Gly His Glu Tyr Val Ala Glu Val Glu Lys His Ser Ser
 100 105 110
 Gln Thr Asp Ala Ala Lys Gly Phe Gly Gly Lys Tyr Gly Val Glu Arg
 115 120 125
 Asp Arg Ala Asp Lys Ser Ala Val Gly Phe Asp Tyr Lys Gly Glu Val
 130 135 140
 Glu Lys His Thr Ser Gln Lys Asp Tyr Ser Arg Gly Phe Gly Gly Arg
 145 150 155 160
 Tyr Gly Val Glu Lys Asp Lys Trp Asp Lys Ala Ala Leu Gly Tyr Asp
 165 170 175
 Tyr Lys Gly Glu Thr Glu Lys His Glu Ser Gln Arg Asp Tyr Ala Lys
 180 185 190
 Gly Phe Gly Gly Gln Tyr Gly Ile Gln Lys Asp Arg Val Asp Lys Ser
 195 200 205
 Ala Val Gly Phe Asn Glu Met Glu Ala Pro Thr Thr Ala Tyr Lys Lys
 210 215 220
 Thr Thr Pro Ile Glu Ala Ala Ser Ser Gly Ala Arg Gly Leu Lys Ala
 225 230 235 240
 Lys Phe Glu Ser Met Ala Glu Glu Lys Arg Lys Arg Glu Glu Glu Glu
 245 250 255
 Lys Ala Gln Gln Val Ala Arg Arg Gln Gln Glu Arg Lys Ala Val Thr
 260 265 270
 Lys Arg Ser Pro Glu Ala Pro Gln Pro Val Ile Ala Met Glu Glu Pro
 275 280 285
 Ala Val Pro Ala Pro Leu Pro Lys Lys Ile Ser Ser Glu Ala Trp Pro
 290 295 300
 Pro Val Gly Thr Pro Pro Ser Ser Glu Ser Glu Pro Val Arg Thr Ser
 305 310 315 320
 Arg Glu His Pro Val Pro Leu Leu Pro Ile Arg Gln Thr Leu Pro Glu
 325 330 335
 Asp Asn Glu Glu Pro Pro Ala Leu Pro Pro Arg Thr Leu Glu Gly Leu

340										345					350				
Gln	Val	Glu	Glu	Glu	Pro	Val	Tyr	Glu	Ala	Glu	Pro	Glu	Pro	Glu	Pro				
		355					360					365							
Glu	Pro	Glu	Pro	Glu	Pro	Glu	Asn	Asp	Tyr	Glu	Asp	Val	Glu	Glu	Met				
		370				375					380								
Asp	Arg	His	Glu	Gln	Glu	Asp	Glu	Pro	Glu	Gly	Asp	Tyr	Glu	Glu	Val				
385					390					395					400				
Leu	Glu	Pro	Glu	Asp	Ser	Ser	Phe	Ser	Ser	Ala	Leu	Ala	Gly	Ser	Ser				
				405					410					415					
Gly	Cys	Pro	Ala	Gly	Ala	Gly	Ala	Gly	Ala	Val	Ala	Leu	Gly	Ile	Ser				
			420					425					430						
Ala	Val	Ala	Leu	Tyr	Asp	Tyr	Gln	Gly	Glu	Gly	Ser	Asp	Glu	Leu	Ser				
		435					440					445							
Phe	Asp	Pro	Asp	Asp	Val	Ile	Thr	Asp	Ile	Glu	Met	Val	Asp	Glu	Gly				
450						455					460								
Trp	Trp	Arg	Gly	Arg	Cys	His	Gly	His	Phe	Gly	Leu	Phe	Pro	Ala	Asn				
465					470					475					480				
Tyr	Val	Lys	Leu	Leu	Glu														
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1				5					10				15						
Tyr	Pro	Pro	Ala	Gly	Gln	Glu	Ser	Ser	Phe	Pro	Pro	Ser	Gly	Gln	Tyr				
			20					25					30						
Pro	Tyr	Pro	Ser	Gly	Phe	Pro	Pro	Met	Gly	Gly	Gly	Ala	Tyr	Pro	Gln				
		35					40					45							
Val	Pro	Ser	Ser	Gly	Tyr	Pro	Gly	Ala	Gly	Gly	Tyr	Pro	Ala	Pro	Gly				
50						55					60								
Gly	Tyr	Pro	Ala	Pro	Gly	Gly	Tyr	Pro	Gly	Ala	Pro	Gln	Pro	Gly	Gly				
65					70					75				80					
Ala	Pro	Ser	Tyr	Pro	Gly	Val	Pro	Pro	Gly	Gln	Gly	Phe	Gly	Val	Pro				
				85					90					95					
Pro	Gly	Gly	Ala	Gly	Phe	Ser	Gly	Tyr	Pro	Gln	Pro	Pro	Ser	Gln	Ser				
			100					105					110						
Tyr	Gly	Gly	Gly	Pro	Ala	Gln	Val	Pro	Leu	Pro	Gly	Gly	Phe	Pro	Gly				
		115					120					125							
Gly	Gln	Met	Pro	Ser	Gln	Tyr	Pro	Gly	Gly	Gln	Pro	Thr	Tyr	Pro	Ser				
	130					135					140								

Gln Pro Ala Thr Val Thr Gln Val Thr Gln Gly Thr Ile Arg Pro Ala
 145 150 155 160
 Ala Asn Phe Asp Ala Ile Arg Asp Ala Glu Ile Leu Arg Lys Ala Met
 165 170 175
 Lys Gly Phe Gly Thr Asp Glu Gln Ala Ile Val Asp Val Val Ala Asn
 180 185 190
 Arg Ser Asn Asp Gln Arg Gln Lys Ile Lys Ala Ala Phe Lys Thr Ser
 195 200 205
 Tyr Gly Lys Asp Leu Ile Lys Asp Leu Lys Ser Glu Leu Ser Gly Asn
 210 215 220
 Met Glu Glu Leu Ile Leu Ala Leu Phe Met Pro Pro Thr Tyr Tyr Asp
 225 230 235 240
 Ala Trp Ser Leu Arg Lys Ala Met Gln Gly Ala Gly Thr Gln Glu Arg
 245 250 255
 Val Leu Ile Glu Ile Leu Cys Thr Arg Thr Asn Gln Glu Ile Arg Glu
 260 265 270
 Ile Val Arg Cys Tyr Gln Ser Glu Phe Gly Arg Asp Leu Glu Lys Asp
 275 280 285
 Ile Arg Ser Asp Thr Ser Gly His Phe Glu Arg Leu Leu Val Ser Met
 290 295 300
 Cys Gln Gly Asn Arg Asp Glu Asn Gln Ser Ile Asn His Gln Met Ala
 305 310 315 320
 Gln Glu Asp Ala Gln Arg Leu Tyr Gln Ala Gly Glu Gly Arg Leu Gly
 325 330 335
 Thr Asp Glu Ser Cys Phe Asn Met Ile Leu Ala Thr Arg Ser Phe Pro
 340 345 350
 Gln Leu Arg Ala Thr Met Glu Ala Tyr Ser Arg Met Ala Asn Arg Asp
 355 360 365
 Leu Leu Ser Ser Val Ser Arg Glu Phe Ser Gly Tyr Val Glu Ser Gly
 370 375 380
 Leu Lys Thr Ile Leu Gln Cys Ala Leu Asn Arg Pro Ala Phe Phe Ala
 385 390 395 400
 Glu Arg Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp Asp Ser Thr
 405 410 415
 Leu Val Arg Ile Val Val Thr Arg Ser Glu Ile Asp Leu Val Gln Ile
 420 425 430
 Lys Gln Met Phe Ala Gln Met Tyr Gln Lys Thr Leu Gly Thr Met Ile
 435 440 445
 Ala Gly Asp Thr Ser Gly Asp Tyr Arg Arg Leu Leu Leu Ala Ile Val
 450 455 460
 Gly Gln
 465

<210> 176
 <211> 505
 <212> PRT
 <213> Homo sapiens

<400> 176

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Met Ser Tyr Pro Gly Tyr Pro Pro Pro Gly Gly Tyr Pro Pro Ala
1          5          10          15

Ala Pro Gly Gly Gly Pro Trp Gly Gly Ala Ala Tyr Pro Pro Pro
20          25          30

Ser Met Pro Pro Ile Gly Leu Asp Asn Val Ala Thr Tyr Ala Gly Gln
35          40          45

Phe Asn Gln Asp Tyr Leu Ser Gly Met Ala Ala Asn Met Ser Gly Thr
50          55          60

Phe Gly Gly Ala Asn Met Pro Asn Leu Tyr Pro Gly Ala Pro Gly Ala
65          70          75          80

Gly Tyr Pro Pro Val Pro Pro Gly Gly Phe Gly Gln Pro Pro Ser Ala
85          90          95

Gln Gln Pro Val Pro Pro Tyr Gly Met Tyr Pro Pro Pro Gly Gly Asn
100         105         110

Pro Pro Ser Arg Met Pro Ser Tyr Pro Pro Tyr Pro Gly Ala Pro Val
115         120         125

Pro Gly Gln Pro Met Pro Pro Pro Gly Gln Gln Pro Pro Gly Ala Tyr
130         135         140

Pro Gly Gln Pro Pro Val Thr Tyr Pro Gly Gln Pro Pro Val Pro Leu
145         150         155         160

Pro Gly Gln Gln Gln Pro Val Pro Ser Tyr Pro Gly Tyr Pro Gly Ser
165         170         175

Gly Thr Val Thr Pro Ala Val Pro Pro Thr Gln Phe Gly Ser Arg Gly
180         185         190

Thr Ile Thr Asp Ala Pro Gly Phe Asp Pro Leu Arg Asp Ala Glu Val
195         200         205

Leu Arg Lys Ala Met Lys Gly Phe Gly Thr Asp Glu Gln Ala Ile Ile
210         215         220

Asp Cys Leu Gly Ser Arg Ser Asn Lys Gln Arg Gln Gln Ile Leu Leu
225         230         235         240

Ser Phe Lys Thr Ala Tyr Gly Lys Asp Leu Ile Lys Asp Leu Lys Ser
245         250         255

Glu Leu Ser Gly Asn Phe Glu Lys Thr Ile Leu Ala Leu Met Lys Thr
260         265         270

Pro Val Leu Phe Asp Ile Tyr Glu Ile Lys Glu Ala Ile Lys Gly Val
275         280         285

Gly Thr Asp Glu Ala Cys Leu Ile Glu Ile Leu Ala Ser Arg Ser Asn

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290	295	300
Glu His Ile Arg Glu	Leu Asn Arg Ala Tyr Lys	Ala Glu Phe Lys Lys
305	310	315 320
Thr Leu Glu Glu Ala	Ile Arg Ser Asp Thr Ser Gly His Phe Gln Arg	
	325	330 335
Leu Leu Ile Ser Leu Ser Gln Gly Asn Arg Asp Glu Ser Thr Asn Val		
	340	345 350
Asp Met Ser Leu Ala Gln Arg Asp Ala Gln Glu Leu Tyr Ala Ala Gly		
	355	360 365
Glu Asn Arg Leu Gly Thr Asp Glu Ser Lys Phe Asn Ala Val Leu Cys		
	370	375 380
Ser Arg Ser Arg Ala His Leu Val Ala Val Phe Asn Glu Tyr Gln Arg		
	385	390 395 400
Met Thr Gly Arg Asp Ile Glu Lys Ser Ile Cys Arg Glu Met Ser Gly		
	405	410 415
Asp Leu Glu Glu Gly Met Leu Ala Val Val Lys Cys Leu Lys Asn Thr		
	420	425 430
Pro Ala Phe Phe Ala Glu Arg Leu Asn Lys Ala Met Arg Gly Ala Gly		
	435	440 445
Thr Lys Asp Arg Thr Leu Ile Arg Ile Met Val Ser Arg Ser Glu Thr		
	450	455 460
Asp Leu Leu Asp Ile Arg Ser Glu Tyr Lys Arg Met Tyr Gly Lys Ser		
	465	470 475 480
Leu Tyr His Asp Ile Ser Gly Asp Thr Ser Gly Asp Tyr Arg Lys Ile		
	485	490 495
Leu Leu Lys Ile Cys Gly Gly Asn Asp		
	500	505
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<211> 515		
<212> PRT		
<213> Homo sapiens		
<400> 177		
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Pro Asn Thr Ser Gln Ser Gln Val Glu Glu Asp Val Ser Ser Pro Pro		
	20	25 30
Gln Arg Ser Ser Glu Thr Met Gln Leu Lys Lys Glu Ile Ser Leu Leu		
	35	40 45
Asn Gly Val Ser Leu Val Val Gly Asn Met Ile Gly Ser Gly Ile Phe		
	50	55 60
Val Ser Pro Lys Gly Val Leu Val His Thr Ala Ser Tyr Gly Met Ser		
	65	70 75 80

Leu Ile Val Trp Ala Ile Gly Gly Leu Phe Ser Val Val Gly Ala Leu
 85 90 95
 Cys Tyr Ala Glu Leu Gly Thr Thr Ile Thr Lys Ser Gly Ala Ser Tyr
 100 105 110
 Ala Tyr Ile Leu Glu Ala Phe Gly Gly Phe Ile Ala Phe Ile Arg Leu
 115 120 125
 Trp Val Ser Leu Leu Val Val Glu Pro Thr Gly Gln Ala Ile Ile Ala
 130 135 140
 Ile Thr Phe Ala Asn Tyr Ile Ile Gln Pro Ser Phe Pro Ser Cys Asp
 145 150 155 160
 Pro Pro Tyr Leu Ala Cys Arg Leu Leu Ala Ala Ala Cys Ile Cys Leu
 165 170 175
 Leu Thr Phe Val Asn Cys Ala Tyr Val Lys Trp Gly Thr Arg Val Gln
 180 185 190
 Asp Thr Phe Thr Tyr Ala Lys Val Val Ala Leu Ile Ala Ile Ile Val
 195 200 205
 Met Gly Leu Val Lys Leu Cys Gln Gly His Ser Glu His Phe Gln Asp
 210 215 220
 Ala Phe Glu Gly Ser Ser Trp Asp Met Gly Asn Leu Ser Leu Ala Leu
 225 230 235 240
 Tyr Ser Ala Leu Phe Ser Tyr Ser Gly Trp Asp Thr Leu Asn Phe Val
 245 250 255
 Thr Glu Glu Ile Lys Asn Pro Glu Arg Asn Leu Pro Leu Ala Ile Gly
 260 265 270
 Ile Ser Met Pro Ile Val Thr Leu Ile Tyr Ile Leu Thr Asn Val Ala
 275 280 285
 Tyr Tyr Thr Val Leu Asn Ile Ser Asp Val Leu Ser Ser Asp Ala Val
 290 295 300
 Ala Val Thr Phe Ala Asp Gln Thr Phe Gly Met Phe Ser Trp Thr Ile
 305 310 315 320
 Pro Ile Ala Val Ala Leu Ser Cys Phe Gly Gly Leu Asn Ala Ser Ile
 325 330 335
 Phe Ala Ser Ser Arg Leu Phe Phe Val Gly Ser Arg Glu Gly His Leu
 340 345 350
 Pro Asp Leu Leu Ser Met Ile His Ile Glu Arg Phe Thr Pro Ile Pro
 355 360 365
 Ala Leu Leu Phe Asn Cys Thr Met Ala Leu Ile Tyr Leu Ile Val Glu
 370 375 380
 Asp Val Phe Gln Leu Ile Asn Tyr Phe Ser Phe Ser Tyr Trp Phe Phe
 385 390 395 400
 Val Gly Leu Ser Val Val Gly Gln Leu Tyr Leu Arg Trp Lys Glu Pro
 405 410 415

Lys Arg Pro Arg Pro Leu Lys Leu Ser Val Phe Phe Pro Ile Val Phe
 420 425 430
 Cys Ile Cys Ser Val Phe Leu Val Ile Val Pro Leu Phe Thr Asp Thr
 435 440 445
 Ile Asn Ser Leu Ile Gly Ile Gly Ile Ala Leu Ser Gly Val Pro Phe
 450 455 460
 Tyr Phe Met Gly Val Tyr Leu Pro Glu Ser Arg Arg Pro Leu Phe Ile
 465 470 475 480
 Arg Asn Val Leu Ala Ala Ile Thr Arg Gly Thr Gln Gln Leu Cys Phe
 485 490 495
 Cys Val Leu Thr Glu Leu Asp Val Ala Glu Glu Lys Lys Asp Glu Arg
 500 505 510
 Lys Thr Asp
 515

<210> 178
 <211> 334
 <212> PRT
 <213> Homo sapiens

<400> 178
 Met Ser Lys Leu Leu Asn Pro Glu Glu Met Thr Ser Arg Asp Tyr Tyr
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 Phe Asp Ser Tyr Ala His Phe Gly Ile His Glu Glu Met Leu Lys Asp
 20 25 30
 Glu Val Arg Thr Leu Thr Tyr Arg Asn Ser Met Tyr His Asn Lys His
 35 40 45
 Val Phe Lys Asp Lys Val Val Leu Asp Val Gly Ser Gly Thr Gly Ile
 50 55 60
 Leu Ser Met Phe Ala Ala Lys Ala Gly Ala Lys Lys Val Phe Gly Ile
 65 70 75 80
 Glu Cys Ser Ser Ile Ser Asp Tyr Ser Glu Lys Ile Ile Lys Ala Asn
 85 90 95
 His Leu Asp Asn Ile Ile Thr Ile Phe Lys Gly Lys Val Glu Glu Val
 100 105 110
 Glu Leu Pro Val Glu Lys Val Asp Ile Ile Ile Ser Glu Trp Met Gly
 115 120 125
 Tyr Cys Leu Phe Tyr Glu Ser Met Leu Asn Thr Val Ile Phe Ala Arg
 130 135 140
 Asp Lys Trp Leu Lys Pro Gly Gly Leu Met Phe Pro Asp Arg Ala Ala
 145 150 155 160
 Leu Tyr Val Val Ala Ile Glu Asp Arg Gln Tyr Lys Asp Phe Lys Ile
 165 170 175
 His Trp Trp Glu Asn Val Tyr Gly Phe Asp Met Thr Cys Ile Arg Asp

180										185										190										
Val	Ala	Met	Lys	Glu	Pro	Leu	Val	Asp	Ile	Val	Asp	Pro	Lys	Gln	Val															
		195						200				205																		
Val	Thr	Asn	Ala	Cys	Leu	Ile	Lys	Glu	Val	Asp	Ile	Tyr	Thr	Val	Lys															
	210					215					220																			
Thr	Glu	Glu	Leu	Ser	Phe	Thr	Ser	Ala	Phe	Cys	Leu	Gln	Ile	Gln	Arg															
	225				230					235					240															
Asn	Asp	Tyr	Val	His	Ala	Leu	Val	Thr	Tyr	Phe	Asn	Ile	Glu	Phe	Thr															
			245						250					255																
Lys	Cys	His	Lys	Lys	Met	Gly	Phe	Ser	Thr	Ala	Pro	Asp	Ala	Pro	Tyr															
			260					265					270																	
Thr	His	Trp	Lys	Gln	Thr	Val	Phe	Tyr	Leu	Glu	Asp	Tyr	Leu	Thr	Val															
	275					280						285																		
Arg	Arg	Gly	Glu	Glu	Ile	Tyr	Gly	Thr	Ile	Ser	Met	Lys	Pro	Asn	Ala															
	290				295						300																			
Lys	Asn	Val	Arg	Asp	Leu	Asp	Phe	Thr	Val	Asp	Leu	Asp	Phe	Lys	Gly															
	305				310					315					320															
Gln	Leu	Cys	Glu	Thr	Ser	Val	Ser	Asn	Asp	Tyr	Lys	Met	Arg																	
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<210>	179																													
<211>	347																													
<212>	PRT																													
<213>	Homo sapiens																													
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Met	Val	Gly	Val	Ala	Glu	Val	Ser	Cys	Gly	Gln	Ala	Glu	Ser	Ser	Glu															
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Lys	Pro	Asn	Ala	Glu	Asp	Met	Thr	Ser	Lys	Asp	Tyr	Tyr	Phe	Asp	Ser															
			20					25					30																	
Tyr	Ala	His	Phe	Gly	Ile	His	Glu	Glu	Met	Leu	Lys	Asp	Glu	Val	Arg															
	35					40						45																		
Thr	Leu	Thr	Tyr	Arg	Asn	Ser	Met	Phe	His	Asn	Arg	His	Leu	Phe	Lys															
	50					55					60																			
Asp	Lys	Val	Val	Leu	Asp	Val	Gly	Ser	Gly	Thr	Gly	Ile	Leu	Cys	Met															
	65				70				75					80																
Phe	Ala	Ala	Lys	Ala	Gly	Ala	Arg	Lys	Val	Ile	Gly	Ile	Glu	Cys	Ser															
			85						90					95																
Ser	Ile	Ser	Asp	Tyr	Ala	Val	Lys	Ile	Val	Lys	Ala	Asn	Lys	Leu	Asp															
			100					105					110																	
His	Val	Val	Thr	Ile	Ile	Lys	Gly	Lys	Val	Glu	Glu	Val	Glu	Leu	Pro															
	115					120							125																	
Val	Glu	Lys	Val	Asp	Ile	Ile	Ile	Ser	Glu	Trp	Met	Gly	Tyr	Cys	Leu															
	130					135					140																			

Phe Tyr Glu Ser Met Leu Asn Thr Val Leu Tyr Ala Arg Asp Lys Trp
 145 150 155 160
 Leu Ala Pro Asp Gly Leu Ile Phe Pro Asp Arg Ala Thr Leu Tyr Val
 165 170 175
 Thr Ala Ile Glu Asp Arg Gln Tyr Lys Asp Tyr Lys Ile His Trp Trp
 180 185 190
 Glu Asn Val Tyr Gly Phe Asp Met Ser Cys Ile Lys Asp Val Ala Ile
 195 200 205
 Lys Glu Pro Leu Val Asp Val Val Asp Pro Lys Gln Leu Val Thr Asn
 210 215 220
 Ala Cys Leu Ile Lys Glu Val Asp Ile Tyr Thr Val Lys Val Glu Asp
 225 230 235 240
 Leu Thr Phe Thr Ser Pro Phe Cys Leu Gln Val Lys Arg Asn Asp Tyr
 245 250 255
 Val His Ala Leu Val Ala Tyr Phe Asn Ile Glu Phe Thr Arg Cys His
 260 265 270
 Lys Arg Thr Gly Phe Ser Thr Ser Pro Glu Ser Pro Tyr Thr His Trp
 275 280 285
 Lys Gln Thr Val Phe Tyr Met Glu Asp Tyr Leu Thr Val Lys Thr Gly
 290 295 300
 Glu Glu Ile Phe Gly Thr Ile Gly Met Arg Pro Asn Ala Lys Asn Asn
 305 310 315 320
 Arg Asp Leu Asp Phe Thr Ile Asp Leu Asp Phe Lys Gly Gln Leu Cys
 325 330 335
 Glu Leu Ser Cys Ser Thr Asp Tyr Arg Met Arg
 340 345

<210> 180
 <211> 502
 <212> PRT
 <213> Homo sapiens

<400> 180
 Met Leu Leu Arg Ser Ala Gly Lys Leu Asn Val Gly Thr Lys Lys Glu
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 Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Val Leu Arg Cys
 20 25 30
 Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser
 35 40 45
 Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Leu
 50 55 60
 Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp Phe Gln
 65 70 75 80
 Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys
 85 90 95

Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro
 100 105 110
 Leu Lys Asn Arg Asp Phe Val Asp Gly Pro Ile His His Arg Ala Leu
 115 120 125
 Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu
 130 135 140
 Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Thr Arg Pro Arg Tyr Ser
 145 150 155 160
 Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu
 165 170 175
 Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu
 180 185 190
 Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys
 195 200 205
 Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg
 210 215 220
 Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser
 225 230 235 240
 Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu
 245 250 255
 Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp
 260 265 270
 Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr
 275 280 285
 Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu
 290 295 300
 Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe
 305 310 315 320
 Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys
 325 330 335
 Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly
 340 345 350
 Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro
 355 360 365
 Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp
 370 375 380
 Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met
 385 390 395 400
 Tyr Ser Phe Gly Leu Ile Leu Trp Glu Val Ala Arg Arg Cys Val Ser
 405 410 415
 Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro

420										425										430									
Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met	Arg	Glu	Ile	Val	Cys	Ile	Lys	Lys														
		435					440					445																	
Leu	Arg	Pro	Ser	Phe	Pro	Asn	Arg	Trp	Ser	Ser	Asp	Glu	Cys	Leu	Arg														
		450				455					460																		
Gln	Met	Gly	Lys	Leu	Met	Thr	Glu	Cys	Trp	Ala	His	Asn	Pro	Ala	Ser														
465					470					475					480														
Arg	Leu	Thr	Ala	Leu	Arg	Val	Lys	Lys	Thr	Leu	Ala	Lys	Met	Ser	Glu														
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Ser	Gln	Asp	Ile	Lys	Leu																								
			500																										
<210>	181																												
<211>	532																												
<212>	PRT																												
<213>	Homo sapiens																												
<400>	181																												
Met	Thr	Gln	Leu	Tyr	Ile	Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Tyr	Leu	Phe														
1				5				10						15															
Ile	Ile	Ser	Arg	Val	Gln	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly														
			20					25					30																
Thr	Gly	Met	Lys	Ser	Asp	Ser	Asp	Gln	Lys	Lys	Ser	Glu	Asn	Gly	Val														
		35					40					45																	
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser														
	50					55					60																		
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly														
65					70					75					80														
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu														
				85					90					95															
Ala	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp														
			100					105					110																
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn														
		115					120					125																	
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly														
		130				135					140																		
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Leu	Leu	Ile	Ser	Met														
145					150					155					160														
Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr														
				165					170					175															
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	Asn	Arg	Asp														
			180					18																					

Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu
 210 215 220
 Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Arg Gln Val
 225 230 235 240
 Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu
 245 250 255
 Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe
 260 265 270
 Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile
 275 280 285
 Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln
 290 295 300
 Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Phe
 305 310 315 320
 Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys Leu Ala Tyr
 325 330 335
 Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile Tyr Gly Thr
 340 345 350
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile
 355 360 365
 Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu Gly Leu Ala
 370 375 380
 Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro Leu Asn Thr
 385 390 395 400
 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser
 405 410 415
 Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser
 420 425 430
 Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly
 435 440 445
 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp
 450 455 460
 Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg
 465 470 475 480
 Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val
 485 490 495
 Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu
 500 505 510
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln
 515 520 525
 Asp Val Lys Ile
 530

<210> 182
 <211> 395
 <212> PRT
 <213> Homo sapiens

<400> 182

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Pro Ser Gly Lys Glu Val Leu Leu Leu Met Gln Ala Leu Asn Thr Leu
1          5          10          15

Ser Thr Pro Glu Glu Lys Leu Ala Ala Leu Cys Lys Lys Tyr Ala Asp
          20          25          30

Leu Leu Glu Glu Ser Arg Ser Val Gln Lys Gln Met Lys Ile Leu Gln
          35          40          45

Lys Lys Gln Ala Gln Ile Val Lys Glu Lys Val His Leu Gln Ser Glu
          50          55          60

His Ser Lys Ala Ile Leu Ala Arg Ser Lys Leu Glu Ser Leu Cys Arg
65          70          75          80

Glu Leu Gln Arg His Asn Lys Thr Leu Lys Glu Glu Asn Met Gln Gln
          85          90          95

Ala Arg Glu Glu Glu Glu Arg Arg Lys Glu Ala Thr Ala His Phe Gln
          100          105          110

Ile Thr Leu Asn Glu Ile Gln Ala Gln Leu Glu Gln His Asp Ile His
          115          120          125

Asn Ala Lys Leu Arg Gln Glu Asn Ile Glu Leu Gly Glu Lys Leu Lys
          130          135          140

Lys Leu Ile Glu Gln Tyr Ala Leu Arg Glu Glu His Ile Asp Lys Val
145          150          155          160

Phe Lys His Lys Glu Leu Gln Gln Gln Leu Val Asp Ala Lys Leu Gln
          165          170          175

Gln Thr Thr Gln Leu Ile Lys Glu Ala Asp Glu Lys His Gln Arg Glu
          180          185          190

Arg Glu Phe Leu Leu Lys Glu Ala Thr Glu Ser Arg His Lys Tyr Glu
          195          200          205

Gln Met Lys Gln Gln Glu Val Gln Leu Lys Gln Gln Leu Ser Leu Tyr
          210          215          220

Met Asp Lys Phe Glu Glu Phe Gln Thr Thr Met Ala Lys Ser Asn Glu
225          230          235          240

Leu Phe Thr Thr Phe Arg Gln Glu Met Glu Lys Met Thr Lys Lys Ile
          245          250          255

Lys Lys Leu Glu Lys Glu Thr Ile Ile Trp Arg Thr Lys Trp Glu Asn
          260          265          270

Asn Asn Lys Ala Leu Leu Gln Met Ala Glu Glu Lys Thr Val Arg Asp
          275          280          285

Lys Glu Tyr Lys Ala Leu Gln Ile Lys Leu Glu Arg Leu Glu Lys Leu

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290	295	300
Cys Arg Ala Leu Gln Thr Glu Arg Asn Glu Leu Asn Glu Lys Val Glu 305 310 315 320		
Val Leu Lys Glu Gln Val Ser Ile Lys Ala Ala Ile Lys Ala Ala Asn 325 330 335		
Arg Asp Leu Ala Thr Pro Val Met Gln Pro Cys Thr Ala Leu Asp Ser 340 345 350		
His Lys Glu Leu Asn Thr Ser Ser Lys Arg Ala Leu Gly Ala His Leu 355 360 365		
Glu Ala Glu Pro Lys Ser Gln Arg Ser Ala Val Gln Lys Pro Pro Ser 370 375 380		
Thr Gly Ser Ala Pro Ala Ile Glu Ser Val Asp 385 390 395		
<210> 183		
<211> 356		
<212> PRT		
<213> Homo sapiens		
<400> 183		
Ala Leu Cys Lys Lys Tyr Ala Glu Leu Leu Glu Glu His Arg Asn Ser 1 5 10 15		
Gln Lys Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln 20 25 30		
Glu Lys Asp His Leu Arg Gly Glu His Ser Lys Ala Val Leu Ala Arg 35 40 45		
Ser Lys Leu Glu Ser Leu Cys Arg Glu Leu Gln Arg His Asn Arg Ser 50 55 60		
Leu Lys Glu Glu Gly Val Gln Arg Ala Arg Glu Glu Glu Glu Lys Arg 65 70 75 80		
Lys Glu Val Thr Ser His Phe Gln Val Thr Leu Asn Asp Ile Gln Leu 85 90 95		
Gln Met Glu Gln His Asn Glu Arg Asn Ser Lys Leu Arg Gln Glu Asn 100 105 110		
Met Glu Leu Ala Glu Arg Leu Lys Lys Leu Ile Glu Gln Tyr Glu Leu 115 120 125		
Arg Glu Glu His Ile Asp Lys Val Phe Lys His Lys Asp Leu Gln Gln 130 135 140		
Gln Leu Val Asp Ala Lys Leu Gln Gln Ala Gln Glu Met Leu Lys Glu 145 150 155 160		
Ala Glu Glu Arg His Gln Arg Glu Lys Asp Phe Leu Leu Lys Glu Ala 165 170 175		
Val Glu Ser Gln Arg Met Cys Glu Leu Met Lys Gln Gln Glu Thr His 180 185 190		

Leu Lys Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln
 195 200 205
 Asn Thr Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu
 210 215 220
 Met Glu Lys Met Thr Lys Lys Ile Lys Lys Leu Glu Lys Glu Thr Thr
 225 230 235 240
 Met Tyr Arg Ser Arg Trp Glu Ser Ser Asn Lys Ala Leu Leu Glu Met
 245 250 255
 Ala Glu Glu Lys Thr Val Arg Asp Lys Glu Leu Glu Gly Leu Gln Val
 260 265 270
 Lys Ile Gln Arg Leu Glu Lys Leu Cys Arg Ala Leu Gln Thr Glu Arg
 275 280 285
 Asn Asp Leu Asn Lys Arg Val Gln Asp Leu Ser Ala Gly Gly Gln Gly
 290 295 300
 Ser Leu Thr Asp Ser Gly Pro Glu Arg Arg Pro Glu Gly Pro Gly Ala
 305 310 315 320
 Gln Ala Pro Ser Ser Pro Arg Val Thr Glu Ala Pro Cys Tyr Pro Gly
 325 330 335
 Ala Pro Ser Thr Glu Ala Ser Gly Gln Thr Gly Pro Gln Glu Pro Thr
 340 345 350
 Ser Ala Arg Ala
 355

<210> 184
 <211> 497
 <212> PRT
 <213> Homo sapiens

<400> 184
 Met Asp Pro Leu Gly Ala Pro Ser Gln Phe Val Asp Val Asp Thr Leu
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 Pro Ser Trp Gly Asp Ser Cys Gln Asp Glu Leu Asn Ser Ser Asp Thr
 20 25 30
 Thr Ala Glu Ile Phe Gln Glu Asp Thr Val Arg Ser Pro Phe Leu Tyr
 35 40 45
 Asn Lys Asp Val Asn Gly Lys Val Val Leu Trp Lys Gly Asp Val Ala
 50 55 60
 Leu Leu Asn Cys Thr Ala Ile Val Asn Thr Ser Asn Glu Ser Leu Thr
 65 70 75 80
 Asp Lys Asn Pro Val Ser Glu Ser Ile Phe Met Leu Ala Gly Pro Asp
 85 90 95
 Leu Lys Glu Asp Leu Gln Lys Leu Lys Gly Cys Arg Thr Gly Glu Ala
 100 105 110
 Lys Leu Thr Lys Gly Phe Asn Leu Ala Ala Arg Phe Ile Ile His Thr
 115 120 125

Val Gly Pro Lys Tyr Lys Ser Arg Tyr Arg Thr Ala Ala Glu Ser Ser
 130 135 140
 Leu Tyr Ser Cys Tyr Arg Asn Val Leu Gln Leu Ala Lys Glu Gln Ser
 145 150 155 160
 Met Ser Ser Val Gly Phe Cys Val Ile Asn Ser Ala Lys Arg Gly Tyr
 165 170 175
 Pro Leu Glu Asp Ala Thr His Ile Ala Leu Arg Thr Val Arg Arg Phe
 180 185 190
 Leu Glu Ile His Gly Glu Thr Ile Glu Lys Val Val Phe Ala Val Ser
 195 200 205
 Asp Leu Glu Glu Gly Thr Tyr Gln Lys Leu Leu Pro Leu Tyr Phe Pro
 210 215 220
 Arg Ser Leu Lys Glu Glu Asn Arg Ser Leu Pro Tyr Leu Pro Ala Asp
 225 230 235 240
 Ile Gly Asn Ala Glu Gly Glu Pro Val Val Pro Glu Arg Gln Ile Arg
 245 250 255
 Ile Ser Glu Lys Pro Gly Ala Pro Glu Asp Asn Gln Glu Glu Glu Asp
 260 265 270
 Glu Gly Leu Gly Val Asp Leu Ser Phe Ile Gly Ser His Ala Phe Ala
 275 280 285
 Arg Met Glu Gly Asp Ile Asp Lys Gln Arg Lys Leu Ile Leu Gln Gly
 290 295 300
 Gln Leu Ser Glu Ala Ala Leu Gln Lys Gln His Gln Arg Asn Tyr Asn
 305 310 315 320
 Arg Trp Leu Cys Gln Ala Arg Ser Glu Asp Leu Ser Asp Ile Ala Ser
 325 330 335
 Leu Lys Ala Leu Tyr Gln Thr Gly Val Asp Asn Cys Gly Arg Thr Val
 340 345 350
 Met Val Val Val Gly Arg Asn Ile Pro Val Thr Leu Ile Asp Met Asp
 355 360 365
 Lys Ala Leu Leu Tyr Phe Ile His Val Met Asp His Ile Ala Val Lys
 370 375 380
 Glu Tyr Val Leu Val Tyr Phe His Thr Leu Thr Ser Glu Tyr Asn His
 385 390 395 400
 Leu Asp Ser Asp Phe Leu Lys Lys Leu Tyr Asp Val Val Asp Val Lys
 405 410 415
 Tyr Lys Arg Asn Leu Lys Ala Val Tyr Phe Val His Pro Thr Phe Arg
 420 425 430
 Ser Lys Val Ser Thr Trp Phe Phe Thr Thr Phe Ser Val Ser Gly Leu
 435 440 445
 Lys Asp Lys Ile His His Val Asp Ser Leu His Gln Leu Phe Ser Ala

450		455		460	
Ile Ser Pro Glu Gln Ile Asp Phe Pro Pro Phe Val Leu Glu Tyr Asp					
465		470		475	480
Ala Arg Glu Asn Gly Pro Tyr Tyr Thr Ser Tyr Pro Pro Ser Pro Asp					
		485		490	495

Leu

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 <212> PRT
 <213> Homo sapiens

<400> 185
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 1 5 10 15
 Ala Ala Gly Asp Lys Leu Val Val Val Asp Phe Ser Ala Thr Trp Cys
 20 25 30
 Gly Pro Cys Lys Met Ile Lys Pro Phe Phe His Ser Leu Ser Glu Lys
 35 40 45
 Tyr Ser Asn Val Ile Phe Leu Glu Val Asp Val Asp Asp Cys Gln Asp
 50 55 60
 Val Ala Ser Glu Cys Glu Val Lys Cys Met Pro Thr Phe Gln Phe Phe
 65 70 75 80
 Lys Lys Gly Gln Lys Val Gly Glu Phe Ser Gly Ala Asn Lys Glu Lys
 85 90 95
 Leu Glu Ala Thr Ile Asn Glu Leu Val
 100 105

<210> 186
 <211> 3038
 <212> PRT
 <213> Homo sapiens

<400> 186
 Met Lys Ala Met Asp Val Leu Pro Ile Leu Lys Glu Lys Val Ala Tyr
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 Leu Ser Gly Gly Arg Asp Lys Arg Gly Gly Pro Ile Leu Thr Phe Pro
 20 25 30
 Ala Arg Ser Asn His Asp Arg Ile Arg Gln Glu Asp Leu Arg Arg Leu
 35 40 45
 Ile Ser Tyr Leu Ala Cys Ile Pro Ser Glu Glu Val Cys Lys Arg Gly
 50 55 60
 Phe Thr Val Ile Val Asp Met Arg Gly Ser Lys Trp Asp Ser Ile Lys
 65 70 75 80
 Pro Leu Leu Lys Ile Leu Gln Glu Ser Phe Pro Cys Cys Ile His Val
 85 90 95

Ala Leu Ile Ile Lys Pro Asp Asn Phe Trp Gln Lys Gln Arg Thr Asn
 100 105 110
 Phe Gly Ser Ser Lys Phe Glu Phe Glu Thr Asn Met Val Ser Leu Glu
 115 120 125
 Gly Leu Thr Lys Val Val Asp Pro Ser Gln Leu Thr Pro Glu Phe Asp
 130 135 140
 Gly Cys Leu Glu Tyr Asn His Glu Glu Trp Ile Glu Ile Arg Val Ala
 145 150 155 160
 Phe Glu Asp Tyr Ile Ser Asn Ala Thr His Met Leu Ser Arg Leu Glu
 165 170 175
 Glu Leu Gln Asp Ile Leu Ala Lys Lys Glu Leu Pro Gln Asp Leu Glu
 180 185 190
 Gly Ala Arg Asn Met Ile Glu Glu His Ser Gln Leu Lys Lys Lys Val
 195 200 205
 Ile Lys Ala Pro Ile Glu Asp Leu Asp Leu Glu Gly Gln Lys Leu Leu
 210 215 220
 Gln Arg Ile Gln Ser Ser Glu Ser Phe Pro Lys Lys Asn Ser Gly Ser
 225 230 235 240
 Gly Asn Ala Asp Leu Gln Asn Leu Leu Pro Lys Val Ser Thr Met Leu
 245 250 255
 Asp Arg Leu His Ser Thr Arg Gln His Leu His Gln Met Trp His Val
 260 265 270
 Arg Lys Leu Lys Leu Asp Gln Cys Phe Gln Leu Arg Leu Phe Glu Gln
 275 280 285
 Asp Ala Glu Lys Met Phe Asp Trp Ile Thr His Asn Lys Gly Leu Phe
 290 295 300
 Leu Asn Ser Tyr Thr Glu Ile Gly Thr Ser His Pro His Ala Met Glu
 305 310 315 320
 Leu Gln Thr Gln His Asn His Phe Ala Met Asn Cys Met Asn Val Tyr
 325 330 335
 Val Asn Ile Asn Arg Ile Met Ser Val Ala Asn Arg Leu Val Glu Ser
 340 345 350
 Gly His Tyr Ala Ser Gln Gln Ile Arg Gln Ile Ala Ser Gln Leu Glu
 355 360 365
 Gln Glu Trp Lys Ala Phe Ala Ala Ala Leu Asp Glu Arg Ser Thr Leu
 370 375 380
 Leu Asp Met Ser Ser Ile Phe His Gln Lys Ala Glu Lys Tyr Met Ser
 385 390 395 400
 Asn Val Asp Ser Trp Cys Lys Ala Cys Gly Glu Val Asp Leu Pro Ser
 405 410 415
 Glu Leu Gln Asp Leu Glu Asp Ala Ile His His His Gln Gly Ile Tyr
 420 425 430

Glu His Ile Thr Leu Ala Tyr Ser Glu Val Ser Gln Asp Gly Lys Ser
 435 440 445
 Leu Leu Asp Lys Leu Gln Arg Pro Leu Thr Pro Gly Ser Ser Asp Ser
 450 455 460
 Leu Thr Ala Ser Ala Asn Tyr Ser Lys Ala Val His His Val Leu Asp
 465 470 475 480
 Val Ile His Glu Val Leu His His Gln Arg His Val Arg Thr Ile Trp
 485 490 495
 Gln His Arg Lys Val Arg Leu His Gln Arg Leu Gln Leu Cys Val Phe
 500 505 510
 Gln Gln Glu Val Gln Gln Val Leu Asp Trp Ile Glu Asn His Gly Glu
 515 520 525
 Ala Phe Leu Ser Lys His Thr Gly Val Gly Lys Ser Leu His Arg Ala
 530 535 540
 Arg Ala Leu Gln Lys Arg His Glu Asp Phe Glu Glu Val Ala Gln Asn
 545 550 555 560
 Thr Tyr Thr Asn Ala Asp Lys Leu Leu Glu Ala Ala Glu Gln Leu Ala
 565 570 575
 Gln Thr Gly Glu Cys Asp Pro Glu Glu Ile Tyr Gln Ala Ala His Gln
 580 585 590
 Leu Glu Asp Arg Ile Gln Asp Phe Val Arg Arg Val Glu Gln Arg Lys
 595 600 605
 Ile Leu Leu Asp Met Ser Val Ser Phe His Thr His Val Lys Glu Leu
 610 615 620
 Trp Thr Trp Leu Glu Glu Leu Gln Lys Glu Leu Leu Asp Asp Val Tyr
 625 630 635 640
 Ala Glu Ser Val Glu Ala Val Gln Asp Leu Ile Lys Arg Phe Gly Gln
 645 650 655
 Gln Gln Gln Thr Thr Leu Gln Val Thr Val Asn Val Ile Lys Glu Gly
 660 665 670
 Glu Asp Leu Ile Gln Gln Leu Arg Asp Ser Ala Ile Ser Ser Asn Lys
 675 680 685
 Thr Pro His Asn Ser Ser Ile Asn His Ile Glu Thr Val Leu Gln Gln
 690 695 700
 Leu Asp Glu Ala Gln Ser Gln Met Glu Glu Leu Phe Gln Glu Arg Lys
 705 710 715 720
 Ile Lys Leu Glu Leu Phe Leu His Val Arg Ile Phe Glu Arg Asp Ala
 725 730 735
 Ile Asp Ile Ile Ser Asp Leu Glu Ser Trp Asn Asp Glu Leu Ser Gln
 740 745 750
 Gln Met Asn Asp Phe Asp Thr Glu Asp Leu Thr Ile Ala Glu Gln Arg

755					760					765					
Leu	Gln	His	His	Ala	Asp	Lys	Ala	Leu	Thr	Met	Asn	Asn	Leu	Thr	Phe
770						775					780				
Asp	Val	Ile	His	Gln	Gly	Gln	Asp	Leu	Leu	Gln	Tyr	Val	Asn	Glu	Val
785					790					795					800
Gln	Ala	Ser	Gly	Val	Glu	Leu	Leu	Cys	Asp	Arg	Asp	Val	Asp	Met	Ala
				805					810					815	
Thr	Arg	Val	Gln	Asp	Leu	Leu	Glu	Phe	Leu	His	Glu	Lys	Gln	Gln	Glu
			820					825					830		
Leu	Asp	Leu	Ala	Ala	Glu	Gln	His	Arg	Lys	His	Leu	Glu	Gln	Cys	Val
	835						840					845			
Gln	Leu	Arg	His	Leu	Gln	Ala	Glu	Val	Lys	Gln	Val	Leu	Gly	Trp	Ile
	850					855					860				
Arg	Asn	Gly	Glu	Ser	Met	Leu	Asn	Ala	Gly	Leu	Ile	Thr	Ala	Ser	Ser
865					870					875					880
Leu	Gln	Glu	Ala	Glu	Gln	Leu	Gln	Arg	Glu	His	Glu	Gln	Phe	Gln	His
				885					890					895	
Ala	Ile	Glu	Lys	Thr	His	Gln	Ser	Ala	Leu	Gln	Val	Gln	Gln	Lys	Ala
			900					905						910	
Glu	Ala	Met	Leu	Gln	Ala	Asn	His	Tyr	Asp	Met	Asp	Met	Ile	Arg	Asp
	915						920					925			
Cys	Ala	Glu	Lys	Val	Ala	Ser	His	Trp	Gln	Gln	Leu	Met	Leu	Lys	Met
	930					935					940				
Glu	Asp	Arg	Leu	Lys	Leu	Val	Asn	Ala	Ser	Val	Ala	Phe	Tyr	Lys	Thr
945					950					955					960
Ser	Glu	Gln	Val	Cys	Ser	Val	Leu	Glu	Ser	Leu	Glu	Gln	Glu	Tyr	Lys
			965						970					975	
Arg	Glu	Glu	Asp	Trp	Cys	Gly	Gly	Ala	Asp	Lys	Leu	Gly	Pro	Asn	Ser
			980					985					990		
Glu	Thr	Asp	His	Val	Thr	Pro	Met	Ile	Ser	Lys	His	Leu	Glu	Gln	Lys
	995						1000						1005		
Glu	Ala	Phe	Leu	Lys	Ala	Cys	Thr	Leu	Ala	Arg	Arg	Asn	Ala	Asp	
	1010					1015					1020				
Val	Phe	Leu	Lys	Tyr	Leu	His	Arg	Asn	Ser	Val	Asn	Met	Pro	Gly	
	1025					1030					1035				
Met	Val	Thr	His	Ile	Lys	Ala	Pro	Glu	Gln	Gln	Val	Lys	Asn	Ile	
	1040					1045					1050				
Leu	Asn	Glu	Leu	Phe	Gln	Arg	Glu	Asn	Arg	Val	Leu	His	Tyr	Trp	
	1055					1060					1065				
Thr	Met	Arg	Lys	Arg	Arg	Leu	Asp	Gln	Cys	Gln	Gln	Tyr	Val	Val	
	1070					1075						1080			

Phe	Glu	Arg	Ser	Ala	Lys	Gln	Ala	Leu	Glu	Trp	Ile	His	Asp	Asn
1085						1090					1095			
Gly	Glu	Phe	Tyr	Leu	Ser	Thr	His	Thr	Ser	Thr	Gly	Ser	Ser	Ile
1100						1105					1110			
Gln	His	Thr	Gln	Glu	Leu	Leu	Lys	Glu	His	Glu	Glu	Phe	Gln	Ile
1115						1120					1125			
Thr	Ala	Lys	Gln	Thr	Lys	Glu	Arg	Val	Lys	Leu	Leu	Ile	Gln	Leu
1130						1135					1140			
Ala	Asp	Gly	Phe	Cys	Glu	Lys	Gly	His	Ala	His	Ala	Ala	Glu	Ile
1145						1150					1155			
Lys	Lys	Cys	Val	Thr	Ala	Val	Asp	Lys	Arg	Tyr	Arg	Asp	Phe	Ser
1160						1165					1170			
Leu	Arg	Met	Glu	Lys	Tyr	Arg	Thr	Ser	Leu	Glu	Lys	Ala	Leu	Gly
1175						1180					1185			
Ile	Ser	Ser	Asp	Ser	Asn	Lys	Ser	Ser	Lys	Ser	Leu	Gln	Leu	Asp
1190						1195					1200			
Ile	Ile	Pro	Ala	Ser	Ile	Pro	Gly	Ser	Glu	Val	Lys	Leu	Arg	Asp
1205						1210					1215			
Ala	Ala	His	Glu	Leu	Asn	Glu	Glu	Lys	Arg	Lys	Ser	Ala	Arg	Arg
1220						1225					1230			
Lys	Glu	Phe	Ile	Met	Ala	Glu	Leu	Ile	Gln	Thr	Glu	Lys	Ala	Tyr
1235						1240					1245			
Val	Arg	Asp	Leu	Arg	Glu	Cys	Met	Asp	Thr	Tyr	Leu	Trp	Glu	Met
1250						1255					1260			
Thr	Ser	Gly	Val	Glu	Glu	Ile	Pro	Pro	Gly	Ile	Val	Asn	Lys	Glu
1265						1270					1275			
Leu	Ile	Ile	Phe	Gly	Asn	Met	Gln	Glu	Ile	Tyr	Glu	Phe	His	Asn
1280						1285					1290			
Asn	Ile	Phe	Leu	Lys	Glu	Leu	Glu	Lys	Tyr	Glu	Gln	Leu	Pro	Glu
1295						1300					1305			
Asp	Val	Gly	His	Cys	Phe	Val	Thr	Trp	Ala	Asp	Lys	Phe	Gln	Met
1310						1315					1320			
Tyr	Val	Thr	Tyr	Cys	Lys	Asn	Lys	Pro	Asp	Ser	Thr	Gln	Leu	Ile
1325						1330					1335			
Leu	Glu	His	Ala	Gly	Ser	Tyr	Phe	Asp	Glu	Ile	Gln	Gln	Arg	His
1340						1345					1350			
Gly	Leu	Ala	Asn	Ser	Ile	Ser	Ser	Tyr	Leu	Ile	Lys	Pro	Val	Gln
1355						1360					1365			
Arg	Ile	Thr	Lys	Tyr	Gln	Leu	Leu	Leu	Lys	Glu	Leu	Leu	Thr	Cys
1370						1375					1380			
Cys	Glu	Glu	Gly	Lys	Gly	Glu	Ile	Lys	Asp	Gly	Leu	Glu	Val	Met
1385						1390					1395			

Leu Ser Val Pro Lys Arg Ala	Asn Asp Ala Met His	Leu Ser Met
1400	1405	1410
Leu Glu Gly Phe Asp Glu Asn	Ile Glu Ser Gln Gly	Glu Leu Ile
1415	1420	1425
Leu Gln Glu Ser Phe Gln Val	Trp Asp Pro Lys Thr	Leu Ile Arg
1430	1435	1440
Lys Gly Arg Glu Arg His Leu	Phe Leu Phe Glu Met	Ser Leu Val
1445	1450	1455
Phe Ser Lys Glu Val Lys Asp	Ser Ser Gly Arg Ser	Lys Tyr Leu
1460	1465	1470
Tyr Lys Ser Lys Leu Phe Thr	Ser Glu Leu Gly Val	Thr Glu His
1475	1480	1485
Val Glu Gly Asp Pro Cys Lys	Phe Ala Leu Trp Val	Gly Arg Thr
1490	1495	1500
Pro Thr Ser Asp Asn Lys Ile	Val Leu Lys Ala Ser	Ser Ile Glu
1505	1510	1515
Asn Lys Gln Asp Trp Ile Lys	His Ile Arg Glu Val	Ile Gln Glu
1520	1525	1530
Arg Thr Ile His Leu Lys Gly	Ala Leu Lys Glu Pro	Ile His Ile
1535	1540	1545
Pro Lys Thr Ala Pro Ala Thr	Arg Gln Lys Gly Arg	Arg Asp Gly
1550	1555	1560
Glu Asp Leu Asp Ser Gln Gly	Asp Gly Ser Ser Gln	Pro Asp Thr
1565	1570	1575
Ile Ser Ile Ala Ser Arg Thr	Ser Gln Asn Thr Leu	Asp Ser Asp
1580	1585	1590
Lys Leu Ser Gly Gly Cys Glu	Leu Thr Val Val Ile	His Asp Phe
1595	1600	1605
Thr Ala Cys Asn Ser Asn Glu	Leu Thr Ile Arg Arg	Gly Gln Thr
1610	1615	1620
Val Glu Val Leu Glu Arg Pro	His Asp Lys Pro Asp	Trp Cys Leu
1625	1630	1635
Val Arg Thr Thr Asp Arg Ser	Pro Ala Ala Glu Gly	Leu Val Pro
1640	1645	1650
Cys Gly Ser Leu Cys Ile Ala	His Ser Arg Ser Ser	Met Glu Met
1655	1660	1665
Glu Gly Ile Phe Asn His Lys	Asp Ser Leu Ser Val	Ser Ser Asn
1670	1675	1680
Asp Ala Ser Pro Pro Ala Ser	Val Ala Ser Leu Gln	Pro His Met
1685	1690	1695
Ile Gly Ala Gln Ser Ser Pro	Gly Pro Lys Arg Pro	Gly Asn Thr

1700	1705	1710
Leu Arg Lys Trp Leu Thr Ser 1715	Pro Val Arg Arg 1720	Leu Ser Ser Gly 1725
Lys Ala Asp Gly His Val Lys 1730	Lys Leu Ala His 1735	Lys His Lys Lys 1740
Ser Arg Glu Val Arg Lys 1745	Ala Asp Ala Gly 1750	Ser Gln Lys Asp 1755
Ser Asp Asp Ser Ala Ala Thr 1760	Pro Gln Asp Glu Thr 1765	Val Glu Glu 1770
Arg Gly Arg Asn Glu Gly Leu 1775	Ser Ser Gly Thr 1780	Leu Ser Lys Ser 1785
Ser Ser Ser Gly Met Gln Ser 1790	Cys Gly Glu Glu 1795	Glu Gly Glu Glu 1800
Gly Ala Asp Ala Val Pro Leu 1805	Pro Pro Pro Met 1810	Ala Ile Gln Gln 1815
His Ser Leu Leu Gln Pro Asp 1820	Ser Gln Asp Asp 1825	Lys Ala Ser Ser 1830
Arg Leu Leu Val Arg Pro Thr 1835	Ser Ser Glu Thr 1840	Pro Ser Ala Ala 1845
Glu Leu Val Ser Ala Ile Glu 1850	Glu Leu Val Lys 1855	Ser Lys Met Ala 1860
Leu Glu Asp Arg Pro Ser Ser 1865	Leu Leu Val Asp 1870	Gln Gly Asp Ser 1875
Ser Ser Pro Ser Phe Asn Pro 1880	Ser Asp Asn Ser 1885	Leu Leu Ser Ser 1890
Ser Ser Pro Ile Asp Glu Met 1895	Glu Glu Arg Lys 1900	Ser Ser Ser Leu 1905
Lys Arg Arg His Tyr Val Leu 1910	Gln Glu Leu Val 1915	Glu Thr Glu Arg 1920
Asp Tyr Val Arg Asp Leu Gly 1925	Tyr Val Val Glu 1930	Gly Tyr Met Ala 1935
Leu Met Lys Glu Asp Gly Val 1940	Pro Asp Asp Met 1945	Lys Gly Lys Asp 1950
Lys Ile Val Phe Gly Asn Ile 1955	His Gln Ile Tyr 1960	Asp Trp His Arg 1965
Asp Phe Phe Leu Gly Glu Leu 1970	Glu Lys Cys Leu 1975	Glu Asp Pro Glu 1980
Lys Leu Gly Ser Leu Phe Val 1985	Lys His Glu Arg 1990	Arg Leu His Met 1995
Tyr Ile Ala Tyr Cys Gln Asn 2000	Lys Pro Lys Ser 2005	Glu His Ile Val 2010

Ser	Glu	Tyr	Ile	Asp	Thr	Phe	Phe	Glu	Asp	Leu	Lys	Gln	Arg	Leu
2015						2020					2025			
Gly	His	Arg	Leu	Gln	Leu	Thr	Asp	Leu	Leu	Ile	Lys	Pro	Val	Gln
2030						2035					2040			
Arg	Ile	Met	Lys	Tyr	Gln	Leu	Leu	Leu	Lys	Asp	Phe	Leu	Lys	Tyr
2045						2050					2055			
Ser	Lys	Lys	Ala	Ser	Leu	Asp	Thr	Ser	Glu	Leu	Glu	Arg	Ala	Val
2060						2065					2070			
Glu	Val	Met	Cys	Ile	Val	Pro	Arg	Arg	Cys	Asn	Asp	Met	Met	Asn
2075						2080					2085			
Val	Gly	Arg	Leu	Gln	Gly	Phe	Asp	Gly	Lys	Ile	Val	Ala	Gln	Gly
2090						2095					2100			
Lys	Leu	Leu	Leu	Gln	Asp	Thr	Phe	Leu	Val	Thr	Asp	Gln	Asp	Ala
2105						2110					2115			
Gly	Leu	Leu	Pro	Arg	Cys	Arg	Glu	Arg	Arg	Ile	Phe	Leu	Phe	Glu
2120						2125					2130			
Gln	Ile	Val	Ile	Phe	Ser	Glu	Pro	Leu	Asp	Lys	Lys	Lys	Gly	Phe
2135						2140					2145			
Ser	Met	Pro	Gly	Phe	Leu	Phe	Lys	Asn	Ser	Ile	Lys	Val	Ser	Cys
2150						2155					2160			
Leu	Cys	Leu	Glu	Glu	Asn	Val	Glu	Asn	Asp	Pro	Cys	Lys	Phe	Ala
2165						2170					2175			
Leu	Thr	Ser	Arg	Thr	Gly	Asp	Val	Val	Glu	Thr	Phe	Ile	Leu	His
2180						2185					2190			
Ser	Ser	Ser	Pro	Ser	Val	Arg	Gln	Thr	Trp	Ile	His	Glu	Ile	Asn
2195						2200					2205			
Gln	Ile	Leu	Glu	Asn	Gln	Arg	Asn	Phe	Leu	Asn	Ala	Leu	Thr	Ser
2210						2215					2220			
Pro	Ile	Glu	Tyr	Gln	Arg	Asn	His	Ser	Gly	Gly	Gly	Gly	Gly	Gly
2225						2230					2235			
Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
2240						2245					2250			
Ala	Pro	Ser	Gly	Gly	Ser	Gly	His	Ser	Gly	Gly	Pro	Ser	Ser	Cys
2255						2260					2265			
Gly	Gly	Ala	Pro	Ser	Thr	Ser	Arg	Ser	Arg	Pro	Ser	Arg	Ile	Pro
2270						2275					2280			
Gln	Pro	Val	Arg	His	His	Pro	Pro	Val	Leu	Val	Ser	Ser	Ala	Ala
2285						2290					2295			
Ser	Ser	Gln	Ala	Glu	Ala	Asp	Lys	Met	Ser	Gly	Thr	Ser	Thr	Pro
2300						2305					2310			
Gly	Pro	Ser	Leu	Pro	Pro	Pro	Gly	Ala	Ala	Pro	Glu	Ala	Gly	Pro
2315						2320					2325			

Ser 2330	Ala	Pro	Ser	Arg	Arg	Pro 2335	Pro	Gly	Ala	Asp	Ala 2340	Glu	Gly	Ser
Glu 2345	Arg	Glu	Ala	Glu	Pro	Ile 2350	Pro	Lys	Met	Lys	Val 2355	Leu	Glu	Ser
Pro 2360	Arg	Lys	Gly	Ala	Ala	Asn 2365	Ala	Ser	Gly	Ser	Ser 2370	Pro	Asp	Ala
Pro 2375	Ala	Lys	Asp	Ala	Arg	Ala 2380	Ser	Leu	Gly	Thr	Leu 2385	Pro	Leu	Gly
Lys 2390	Pro	Arg	Ala	Gly	Ala	Ala 2395	Ser	Pro	Leu	Asn	Ser 2400	Pro	Leu	Ser
Ser 2405	Ala	Val	Pro	Ser	Leu	Gly 2410	Lys	Glu	Pro	Phe	Pro 2415	Pro	Ser	Ser
Pro 2420	Leu	Gln	Lys	Gly	Gly	Ser 2425	Phe	Trp	Ser	Ser	Ile 2430	Pro	Ala	Ser
Pro 2435	Ala	Ser	Arg	Pro	Gly	Ser 2440	Phe	Thr	Phe	Pro	Gly 2445	Asp	Ser	Asp
Ser 2450	Leu	Gln	Arg	Gln	Thr	Pro 2455	Arg	His	Ala	Ala	Pro 2460	Gly	Lys	Asp
Thr 2465	Asp	Arg	Met	Ser	Thr	Cys 2470	Ser	Ser	Ala	Ser	Glu 2475	Gln	Ser	Val
Gln 2480	Ser	Thr	Gln	Ser	Asn	Gly 2485	Ser	Glu	Ser	Ser	Ser 2490	Ser	Ser	Asn
Ile 2495	Ser	Thr	Met	Leu	Val	Thr 2500	His	Asp	Tyr	Thr	Ala 2505	Val	Lys	Glu
Asp 2510	Glu	Ile	Asn	Val	Tyr	Gln 2515	Gly	Glu	Val	Val	Gln 2520	Ile	Leu	Ala
Ser 2525	Asn	Gln	Gln	Asn	Met	Phe 2530	Leu	Val	Phe	Arg	Ala 2535	Ala	Thr	Asp
Gln 2540	Cys	Pro	Ala	Ala	Glu	Gly 2545	Trp	Ile	Pro	Gly	Phe 2550	Val	Leu	Gly
His 2555	Thr	Ser	Ala	Val	Ile	Val 2560	Glu	Asn	Pro	Asp	Gly 2565	Thr	Leu	Lys
Lys 2570	Ser	Thr	Ser	Trp	His	Thr 2575	Ala	Leu	Arg	Leu	Arg 2580	Lys	Lys	Ser
Glu 2585	Lys	Lys	Asp	Lys	Asp	Gly 2590	Lys	Arg	Glu	Gly	Lys 2595	Leu	Glu	Asn
Gly 2600	Tyr	Arg	Lys	Ser	Arg	Glu 2605	Gly	Leu	Ser	Asn	Lys 2610	Val	Ser	Val
Lys 2615	Leu	Leu	Asn	Pro	Asn	Tyr 2620	Ile	Tyr	Asp	Val	Pro 2625	Pro	Glu	Phe
Val	Ile	Pro	Leu	Ser	Glu	Val	Thr	Cys	Glu	Thr	Gly	Glu	Thr	Val

2630	2635	2640
Val Leu Arg Cys Arg Val Cys Gly Arg Pro Lys Ala Ser Ile Thr 2645 2650 2655		
Trp Lys Gly Pro Glu His Asn Thr Leu Asn Asn Asp Gly His Tyr 2660 2665 2670		
Ser Ile Ser Tyr Ser Asp Leu Gly Glu Ala Thr Leu Lys Ile Val 2675 2680 2685		
Gly Val Thr Thr Glu Asp Asp Gly Ile Tyr Thr Cys Ile Ala Val 2690 2695 2700		
Asn Asp Met Gly Ser Ala Ser Ser Ser Ala Ser Leu Arg Val Leu 2705 2710 2715		
Gly Pro Gly Met Asp Gly Ile Met Val Thr Trp Lys Asp Asn Phe 2720 2725 2730		
Asp Ser Phe Tyr Ser Glu Val Ala Glu Leu Gly Arg Gly Arg Phe 2735 2740 2745		
Ser Val Val Lys Lys Cys Asp Gln Lys Gly Thr Lys Arg Ala Val 2750 2755 2760		
Ala Thr Lys Phe Val Asn Lys Lys Leu Met Lys Arg Asp Gln Val 2765 2770 2775		
Thr His Glu Leu Gly Ile Leu Gln Ser Leu Gln His Pro Leu Leu 2780 2785 2790		
Val Gly Leu Leu Asp Thr Phe Glu Thr Pro Thr Ser Tyr Ile Leu 2795 2800 2805		
Val Leu Glu Met Ala Asp Gln Gly Arg Leu Leu Asp Cys Val Val 2810 2815 2820		
Arg Trp Gly Ser Leu Thr Glu Gly Lys Ile Arg Ala His Leu Gly 2825 2830 2835		
Glu Val Leu Glu Ala Val Arg Tyr Leu His Asn Cys Arg Ile Ala 2840 2845 2850		
His Leu Asp Leu Lys Pro Glu Asn Ile Leu Val Asp Glu Ser Leu 2855 2860 2865		
Ala Lys Pro Thr Ile Lys Leu Ala Asp Phe Gly Asp Ala Val Gln 2870 2875 2880		
Leu Asn Thr Thr Tyr Tyr Ile His Gln Leu Leu Gly Asn Pro Glu 2885 2890 2895		
Phe Ala Ala Pro Glu Ile Ile Leu Gly Asn Pro Val Ser Leu Thr 2900 2905 2910		
Ser Asp Thr Trp Ser Val Gly Val Leu Thr Tyr Val Leu Leu Ser 2915 2920 2925		
Gly Val Ser Pro Phe Leu Asp Asp Ser Val Glu Glu Thr Cys Leu 2930 2935 2940		

Asn Ile Cys Arg Leu Asp Phe Ser Phe Pro Asp Asp Tyr Phe Lys
 2945 2950 2955
 Gly Val Ser Gln Lys Ala Lys Glu Phe Val Cys Phe Leu Leu Gln
 2960 2965 2970
 Glu Asp Pro Ala Lys Arg Pro Ser Ala Ala Leu Ala Leu Gln Glu
 2975 2980 2985
 Gln Trp Leu Gln Ala Gly Asn Gly Arg Ser Thr Gly Val Leu Asp
 2990 2995 3000
 Thr Ser Arg Leu Thr Ser Phe Ile Glu Arg Arg Lys His Gln Asn
 3005 3010 3015
 Asp Val Arg Pro Ile Arg Ser Ile Lys Asn Phe Leu Gln Ser Arg
 3020 3025 3030
 Leu Leu Pro Arg Val
 3035

<210> 187
 <211> 1663
 <212> PRT
 <213> Homo sapiens

<400> 187
 Met Thr Asp Arg Phe Trp Asp Gln Trp Tyr Leu Trp Tyr Leu Arg Leu
 1 5 10 15
 Leu Arg Leu Leu Asp Arg Gly Ser Phe Arg Asn Asp Gly Leu Lys Ala
 20 25 30
 Ser Asp Val Leu Pro Ile Leu Lys Glu Lys Val Ala Phe Val Ser Gly
 35 40 45
 Gly Arg Asp Lys Arg Gly Gly Pro Ile Leu Thr Phe Pro Ala Arg Ser
 50 55 60
 Asn His Asp Arg Ile Arg Gln Glu Asp Leu Arg Lys Leu Val Thr Tyr
 65 70 75 80
 Leu Ala Ser Val Pro Ser Glu Asp Val Cys Lys Arg Gly Phe Thr Val
 85 90 95
 Ile Ile Asp Met Arg Gly Ser Lys Trp Asp Leu Ile Lys Pro Leu Leu
 100 105 110
 Lys Thr Leu Gln Glu Ala Phe Pro Ala Glu Ile His Val Ala Leu Ile
 115 120 125
 Ile Lys Pro Asp Asn Phe Trp Gln Lys Gln Lys Thr Asn Phe Gly Ser
 130 135 140
 Ser Lys Phe Ile Phe Glu Thr Ser Met Val Ser Val Glu Gly Leu Thr
 145 150 155 160
 Lys Leu Val Asp Pro Ser Gln Leu Thr Glu Glu Phe Asp Gly Ser Leu
 165 170 175
 Asp Tyr Asn His Glu Glu Trp Ile Glu Leu Arg Leu Ser Leu Glu Glu
 180 185 190

Phe Phe Asn Ser Ala Val His Leu Leu Ser Arg Leu Glu Asp Leu Gln
 195 200 205
 Glu Met Leu Ala Arg Lys Glu Phe Pro Val Asp Val Glu Gly Ser Arg
 210 215 220
 Arg Leu Ile Asp Glu His Thr Gln Leu Lys Lys Lys Val Leu Lys Ala
 225 230 235 240
 Pro Val Glu Glu Leu Asp Arg Glu Gly Gln Arg Leu Leu Gln Cys Ile
 245 250 255
 Arg Cys Ser Asp Gly Phe Ser Gly Arg Asn Cys Ile Pro Gly Ser Ala
 260 265 270
 Asp Phe Gln Ser Leu Val Pro Lys Ile Thr Ser Leu Leu Asp Lys Leu
 275 280 285
 His Ser Thr Arg Gln His Leu His Gln Met Trp His Val Arg Lys Leu
 290 295 300
 Lys Leu Asp Gln Cys Phe Gln Leu Arg Leu Phe Glu Gln Asp Ala Glu
 305 310 315 320
 Lys Met Phe Asp Trp Ile Ser His Asn Lys Glu Leu Phe Leu Gln Ser
 325 330 335
 His Thr Glu Ile Gly Val Ser Tyr Gln Tyr Ala Leu Asp Leu Gln Thr
 340 345 350
 Gln His Asn His Phe Ala Met Asn Ser Met Asn Ala Tyr Val Asn Ile
 355 360 365
 Asn Arg Ile Met Ser Val Ala Ser Arg Leu Ser Glu Ala Gly His Tyr
 370 375 380
 Ala Ser Gln Gln Ile Lys Gln Ile Ser Thr Gln Leu Asp Gln Glu Trp
 385 390 395 400
 Lys Ser Phe Ala Ala Ala Leu Asp Glu Arg Ser Thr Ile Leu Ala Met
 405 410 415
 Ser Ala Val Phe His Gln Lys Ala Glu Gln Phe Leu Ser Gly Val Asp
 420 425 430
 Ala Trp Cys Lys Met Cys Ser Glu Gly Gly Leu Pro Ser Glu Met Gln
 435 440 445
 Asp Leu Glu Leu Ala Ile His His His Gln Thr Leu Tyr Glu Gln Val
 450 455 460
 Thr Gln Ala Tyr Thr Glu Val Ser Gln Asp Gly Lys Ala Leu Leu Asp
 465 470 475 480
 Val Leu Gln Arg Pro Leu Ser Pro Gly Asn Ser Glu Ser Leu Thr Ala
 485 490 495
 Thr Ala Asn Tyr Ser Lys Ala Val His Gln Val Leu Asp Val Val His
 500 505 510
 Glu Val Leu His His Gln Arg Arg Leu Glu Ser Ile Trp Gln His Arg

515					520					525					
Lys	Val	Arg	Leu	His	Gln	Arg	Leu	Gln	Leu	Cys	Val	Phe	Gln	Gln	Asp
530						535					540				
Val	Gln	Gln	Val	Leu	Asp	Trp	Ile	Glu	Asn	His	Gly	Glu	Ala	Phe	Leu
545					550					555					560
Ser	Lys	His	Thr	Gly	Val	Gly	Lys	Ser	Leu	His	Arg	Ala	Arg	Ala	Leu
				565					570					575	
Gln	Lys	Arg	His	Asp	Asp	Phe	Glu	Glu	Val	Ala	Gln	Asn	Thr	Tyr	Thr
			580					585					590		
Asn	Ala	Asp	Lys	Leu	Leu	Glu	Ala	Ala	Glu	Gln	Leu	Ala	Gln	Thr	Gly
		595					600					605			
Glu	Cys	Asp	Pro	Glu	Glu	Ile	Tyr	Lys	Ala	Ala	Arg	His	Leu	Glu	Val
	610					615					620				
Arg	Ile	Gln	Asp	Phe	Val	Arg	Arg	Val	Glu	Gln	Arg	Lys	Leu	Leu	Leu
625					630					635					640
Asp	Met	Ser	Val	Ser	Phe	His	Thr	His	Thr	Lys	Glu	Leu	Trp	Thr	Trp
				645					650					655	
Met	Glu	Asp	Leu	Gln	Lys	Glu	Met	Leu	Glu	Asp	Val	Cys	Ala	Asp	Ser
			660					665					670		
Val	Asp	Ala	Val	Gln	Glu	Leu	Ile	Lys	Gln	Phe	Gln	Gln	Gln	Gln	Thr
		675					680					685			
Ala	Thr	Leu	Asp	Ala	Thr	Leu	Asn	Val	Ile	Lys	Glu	Gly	Glu	Asp	Leu
	690					695					700				
Ile	Gln	Gln	Leu	Arg	Ser	Ala	Pro	Pro	Ser	Leu	Gly	Glu	Pro	Ser	Glu
705					710					715					720
Ala	Arg	Asp	Ser	Ala	Val	Ser	Asn	Asn	Lys	Thr	Pro	His	Ser	Ser	Ser
			725						730					735	
Ile	Ser	His	Ile	Glu	Ser	Val	Leu	Gln	Gln	Leu	Asp	Asp	Ala	Gln	Val
			740					745					750		
Gln	Met	Glu	Glu	Leu	Phe	His	Glu	Arg	Lys	Ile	Lys	Leu	Asp	Ile	Phe
		755					760					765			
Leu	Gln	Leu	Arg	Ile	Phe	Glu	Gln	Tyr	Thr	Ile	Glu	Val	Thr	Ala	Glu
		770				775					780				
Leu	Asp	Ala	Trp	Asn	Glu	Asp	Leu	Leu	Arg	Gln	Met	Asn	Asp	Phe	Asn
785					790					795					800
Thr	Glu	Asp	Leu	Thr	Leu	Ala	Glu	Gln	Arg	Leu	Gln	Arg	His	Thr	Glu
			805						810					815	
Arg	Lys	Leu	Ala	Met	Asn	Asn	Met	Thr	Phe	Glu	Val	Ile	Gln	Gln	Gly
			820					825					830		
Gln	Asp	Leu	His	Gln	Tyr	Ile	Thr	Glu	Val	Gln	Ala	Ser	Gly	Ile	Glu
		835					840					845			

Leu Ile Cys Glu Lys Asp Ile Asp Leu Ala Ala Gln Val Gln Glu Leu
 850 855 860
 Leu Glu Phe Leu His Glu Lys Gln His Glu Leu Glu Leu Asn Ala Glu
 865 870 875 880
 Gln Thr His Lys Arg Leu Glu Gln Cys Leu Gln Leu Arg His Leu Gln
 885 890 895
 Ala Glu Val Lys Gln Val Leu Gly Trp Ile Arg Asn Gly Glu Ser Met
 900 905 910
 Leu Asn Ala Ser Leu Val Asn Ala Ser Ser Leu Ser Glu Ala Glu Gln
 915 920 925
 Leu Gln Arg Glu His Glu Gln Phe Gln Leu Ala Ile Glu Ser Leu Phe
 930 935 940
 His Ala Thr Ser Leu Gln Lys Thr His Gln Ser Ala Leu Gln Val Gln
 945 950 955 960
 Gln Lys Ala Glu Val Leu Leu Gln Ala Gly His Tyr Asp Ala Asp Ala
 965 970 975
 Ile Arg Glu Cys Ala Glu Lys Val Ala Leu His Trp Gln Gln Leu Met
 980 985 990
 Leu Lys Met Glu Asp Arg Leu Lys Leu Val Asn Ala Ser Val Ala Phe
 995 1000 1005
 Tyr Lys Thr Ser Glu Gln Val Cys Ser Val Leu Glu Ser Leu Glu
 1010 1015 1020
 Gln Glu Tyr Arg Arg Asp Glu Asp Trp Cys Gly Gly Arg Asp Lys
 1025 1030 1035
 Leu Gly Pro Ala Ala Glu Ile Asp His Val Ile Pro Leu Ile Ser
 1040 1045 1050
 Lys His Leu Glu Gln Lys Glu Ala Phe Leu Lys Ala Cys Thr Leu
 1055 1060 1065
 Ala Arg Arg Asn Ala Glu Val Phe Leu Lys Tyr Ile His Arg Asn
 1070 1075 1080
 Asn Val Ser Met Pro Ser Val Ala Ser His Thr Arg Gly Pro Glu
 1085 1090 1095
 Gln Gln Val Lys Ala Ile Leu Ser Glu Leu Leu Gln Arg Glu Asn
 1100 1105 1110
 Arg Val Leu His Phe Trp Thr Leu Lys Lys Arg Arg Leu Asp Gln
 1115 1120 1125
 Cys Gln Gln Tyr Val Val Phe Glu Arg Ser Ala Lys Gln Ala Leu
 1130 1135 1140
 Asp Trp Ile Gln Glu Thr Gly Glu Phe Tyr Leu Ser Thr His Thr
 1145 1150 1155
 Ser Thr Gly Glu Thr Thr Glu Glu Thr Gln Glu Leu Leu Lys Glu
 1160 1165 1170

Tyr	Gly	Glu	Phe	Arg	Val	Pro	Ala	Lys	Gln	Thr	Lys	Glu	Lys	Val
1175						1180					1185			
Lys	Leu	Leu	Ile	Gln	Leu	Ala	Asp	Ser	Phe	Val	Glu	Lys	Gly	His
1190						1195					1200			
Ile	His	Ala	Thr	Glu	Ile	Arg	Lys	Trp	Val	Thr	Thr	Val	Asp	Lys
1205						1210					1215			
His	Tyr	Arg	Asp	Phe	Ser	Leu	Arg	Met	Gly	Lys	Tyr	Arg	Tyr	Ser
1220						1225					1230			
Leu	Glu	Lys	Ala	Leu	Gly	Val	Asn	Thr	Glu	Asp	Asn	Lys	Asp	Leu
1235						1240					1245			
Glu	Leu	Asp	Ile	Ile	Pro	Ala	Ser	Leu	Ser	Asp	Arg	Glu	Val	Lys
1250						1255					1260			
Leu	Arg	Asp	Ala	Asn	His	Glu	Val	Asn	Glu	Glu	Lys	Arg	Lys	Ser
1265						1270					1275			
Ala	Arg	Lys	Lys	Glu	Phe	Ile	Met	Ala	Glu	Leu	Leu	Gln	Thr	Glu
1280						1285					1290			
Lys	Ala	Tyr	Val	Arg	Asp	Leu	His	Glu	Cys	Leu	Glu	Thr	Tyr	Leu
1295						1300					1305			
Trp	Glu	Met	Thr	Ser	Gly	Val	Glu	Glu	Ile	Pro	Pro	Gly	Ile	Leu
1310						1315					1320			
Asn	Lys	Glu	His	Ile	Ile	Phe	Gly	Asn	Ile	Gln	Glu	Ile	Tyr	Asp
1325						1330					1335			
Phe	His	Asn	Asn	Ile	Phe	Leu	Lys	Glu	Leu	Glu	Lys	Tyr	Glu	Gln
1340						1345					1350			
Leu	Pro	Glu	Asp	Val	Gly	His	Cys	Phe	Val	Thr	Trp	Ala	Asp	Lys
1355						1360					1365			
Phe	Gln	Met	Tyr	Val	Thr	Tyr	Cys	Lys	Asn	Lys	Pro	Asp	Ser	Asn
1370						1375					1380			
Gln	Leu	Ile	Leu	Glu	His	Ala	Gly	Thr	Phe	Phe	Asp	Glu	Ile	Gln
1385						1390					1395			
Gln	Arg	His	Gly	Leu	Ala	Asn	Ser	Ile	Ser	Ser	Tyr	Leu	Ile	Lys
1400						1405					1410			
Pro	Val	Gln	Arg	Ile	Thr	Lys	Tyr	Gln	Leu	Leu	Leu	Lys	Glu	Leu
1415						1420					1425			
Leu	Thr	Cys	Cys	Glu	Glu	Gly	Lys	Gly	Glu	Leu	Lys	Asp	Gly	Leu
1430						1435					1440			
Glu	Val	Met	Leu	Ser	Val	Pro	Lys	Lys	Ala	Asn	Asp	Ala	Met	His
1445						1450					1455			
Val	Ser	Met	Leu	Glu	Gly	Phe	Asp	Glu	Asn	Leu	Asp	Val	Gln	Gly
1460						1465					1470			
Glu	Leu	Ile	Leu	Gln	Asp	Ala	Phe	Gln	Val	Trp	Asp	Pro	Lys	Ser

1475	1480	1485
Leu Ile Arg Lys Gly Arg Glu	Arg His Leu Phe Leu	Phe Glu Ile
1490	1495	1500
Ser Leu Val Phe Ser Lys Glu	Ile Lys Asp Ser Ser	Gly His Thr
1505	1510	1515
Lys Tyr Val Tyr Lys Asn Lys	Leu Leu Thr Ser Glu	Leu Gly Val
1520	1525	1530
Thr Glu His Val Glu Gly Asp	Pro Cys Lys Phe Ala	Leu Trp Ser
1535	1540	1545
Gly Arg Thr Pro Ser Ser Asp	Asn Lys Thr Val Leu	Lys Ala Ser
1550	1555	1560
Asn Ile Glu Thr Lys Gln Glu	Trp Ile Lys Asn Ile	Arg Glu Val
1565	1570	1575
Ile Gln Glu Arg Ile Ile His	Leu Lys Gly Ala Leu	Lys Glu Pro
1580	1585	1590
Leu Gln Leu Pro Lys Thr Pro	Ala Lys Gln Arg Asn	Asn Ser Lys
1595	1600	1605
Arg Asp Gly Val Glu Asp Ile	Asp Ser Gln Gly Asp	Gly Ser Ser
1610	1615	1620
Gln Pro Asp Thr Ile Ser Ile	Ala Ser Arg Thr Ser	Gln Asn Thr
1625	1630	1635
Val Asp Ser Asp Lys Asp Gly	Asn Leu Val Pro Arg	Trp His Leu
1640	1645	1650
Gly Pro Gly Asp Pro Phe Ser	Thr Tyr Val	
1655	1660	

<210> 188
 <211> 616
 <212> PRT
 <213> Homo sapiens

<400> 188
 Met Ser Ser Leu Ala Val Arg Asp Pro Ala Met Asp Arg Ser Leu Arg
 1 5 10 15
 Ser Val Phe Val Gly Asn Ile Pro Tyr Glu Ala Thr Glu Glu Gln Leu
 20 25 30
 Lys Asp Ile Phe Ser Glu Val Gly Ser Val Val Ser Phe Arg Leu Val
 35 40 45
 Tyr Asp Arg Glu Thr Gly Lys Pro Lys Gly Tyr Gly Phe Cys Glu Tyr
 50 55 60
 Gln Asp Gln Glu Thr Ala Leu Ser Ala Met Arg Asn Leu Asn Gly Arg
 65 70 75 80
 Glu Phe Ser Gly Arg Ala Leu Arg Val Asp Asn Ala Ala Ser Glu Lys
 85 90 95

Asn Lys Glu Glu Leu Lys Ser Leu Gly Pro Ala Ala Pro Ile Ile Asp
 100 105 110
 Ser Pro Tyr Gly Asp Pro Ile Asp Pro Glu Asp Ala Pro Glu Ser Ile
 115 120 125
 Thr Arg Ala Val Ala Ser Leu Pro Pro Glu Gln Met Phe Glu Leu Met
 130 135 140
 Lys Gln Met Lys Leu Cys Val Gln Asn Ser His Gln Glu Ala Arg Asn
 145 150 155 160
 Met Leu Leu Gln Asn Pro Gln Leu Ala Tyr Ala Leu Leu Gln Ala Gln
 165 170 175
 Val Val Met Arg Ile Met Asp Pro Glu Ile Ala Leu Lys Ile Leu His
 180 185 190
 Arg Lys Ile His Val Thr Pro Leu Ile Pro Gly Lys Ser Gln Ser Val
 195 200 205
 Ser Val Ser Gly Pro Gly Pro Gly Pro Gly Pro Gly Leu Cys Pro Gly
 210 215 220
 Pro Asn Val Leu Leu Asn Gln Gln Asn Pro Pro Ala Pro Gln Pro Gln
 225 230 235 240
 His Leu Ala Arg Arg Pro Val Lys Asp Ile Pro Pro Leu Met Gln Thr
 245 250 255
 Pro Ile Gln Gly Gly Ile Pro Ala Pro Gly Pro Ile Pro Ala Ala Val
 260 265 270
 Pro Gly Ala Gly Pro Gly Ser Leu Thr Pro Gly Gly Ala Met Gln Pro
 275 280 285
 Gln Leu Gly Met Pro Gly Val Gly Pro Val Pro Leu Glu Arg Gly Gln
 290 295 300
 Val Gln Met Ser Asp Pro Arg Ala Pro Ile Pro Arg Gly Pro Val Thr
 305 310 315 320
 Pro Gly Gly Leu Pro Pro Arg Gly Leu Leu Gly Asp Ala Pro Asn Asp
 325 330 335
 Pro Arg Gly Gly Thr Leu Leu Ser Val Thr Gly Glu Val Glu Pro Arg
 340 345 350
 Gly Tyr Leu Gly Pro Pro His Gln Gly Pro Pro Met His His Ala Ser
 355 360 365
 Gly His Asp Thr Arg Gly Pro Ser Ser His Glu Met Arg Gly Gly Pro
 370 375 380
 Leu Gly Asp Pro Arg Leu Leu Ile Gly Glu Pro Arg Gly Pro Met Ile
 385 390 395 400
 Asp Gln Arg Gly Leu Pro Met Asp Gly Arg Gly Gly Arg Asp Ser Arg
 405 410 415
 Ala Met Glu Thr Arg Ala Met Glu Thr Glu Val Leu Glu Thr Arg Val
 420 425 430

Met Glu Arg Arg Gly Met Glu Thr Cys Ala Met Glu Thr Arg Gly Met
 435 440 445

Glu Ala Arg Gly Met Asp Ala Arg Gly Leu Glu Met Arg Gly Pro Val
 450 455 460

Pro Ser Ser Arg Gly Pro Met Thr Gly Gly Ile Gln Gly Pro Gly Pro
 465 470 475 480

Ile Asn Ile Gly Ala Gly Gly Pro Pro Gln Gly Pro Arg Gln Val Pro
 485 490 495

Gly Ile Ser Gly Val Gly Asn Pro Gly Ala Gly Met Gln Gly Thr Gly
 500 505 510

Ile Gln Gly Thr Gly Met Gln Gly Ala Gly Ile Gln Gly Gly Gly Met
 515 520 525

Gln Gly Ala Gly Ile Gln Gly Val Ser Ile Gln Gly Gly Gly Ile Gln
 530 535 540

Gly Gly Gly Ile Gln Gly Ala Ser Lys Gln Gly Gly Ser Gln Pro Ser
 545 550 555 560

Ser Phe Ser Pro Gly Gln Ser Gln Val Thr Pro Gln Asp Gln Glu Lys
 565 570 575

Ala Ala Leu Ile Met Gln Val Leu Gln Leu Thr Ala Asp Gln Ile Ala
 580 585 590

Met Leu Pro Pro Glu Gln Arg Gln Ser Ile Leu Ile Leu Lys Glu Gln
 595 600 605

Ile Gln Lys Ser Thr Gly Ala Ser
 610 615

<210> 189
 <211> 577
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Ala Gly Leu Thr Val Arg Asp Pro Ala Val Asp Arg Ser Leu Arg
 1 5 10 15

Ser Val Phe Val Gly Asn Ile Pro Tyr Glu Ala Thr Glu Glu Gln Leu
 20 25 30

Lys Asp Ile Phe Ser Glu Val Gly Pro Val Val Ser Phe Arg Leu Val
 35 40 45

Tyr Asp Arg Glu Thr Gly Lys Pro Lys Gly Tyr Gly Phe Cys Glu Tyr
 50 55 60

Gln Asp Gln Glu Thr Ala Leu Ser Ala Met Arg Asn Leu Asn Gly Arg
 65 70 75 80

Glu Phe Ser Gly Arg Ala Leu Arg Val Asp Asn Ala Ala Ser Glu Lys
 85 90 95

Asn Lys Glu Glu Leu Lys Ser Leu Gly Thr Gly Ala Pro Val Ile Glu

100							105					110				
Ser	Pro	Tyr	Gly	Glu	Thr	Ile	Ser	Pro	Glu	Asp	Ala	Pro	Glu	Ser	Ile	
		115					120					125				
Ser	Lys	Ala	Val	Ala	Ser	Leu	Pro	Pro	Glu	Gln	Met	Phe	Glu	Leu	Met	
	130					135					140					
Lys	Gln	Met	Lys	Leu	Cys	Val	Gln	Asn	Ser	Pro	Gln	Glu	Ala	Arg	Asn	
145					150					155				160		
Met	Leu	Leu	Gln	Asn	Pro	Gln	Leu	Ala	Tyr	Ala	Leu	Leu	Gln	Ala	Gln	
				165					170					175		
Val	Val	Met	Arg	Ile	Val	Asp	Pro	Glu	Ile	Ala	Leu	Lys	Ile	Leu	His	
			180					185					190			
Arg	Gln	Thr	Asn	Ile	Pro	Thr	Leu	Ile	Ala	Gly	Asn	Pro	Gln	Pro	Val	
		195					200					205				
His	Gly	Ala	Gly	Pro	Gly	Ser	Gly	Ser	Asn	Val	Ser	Met	Asn	Gln	Gln	
	210					215					220					
Asn	Pro	Gln	Ala	Pro	Gln	Ala	Gln	Ser	Leu	Gly	Gly	Met	His	Val	Asn	
225					230					235					240	
Gly	Ala	Pro	Pro	Leu	Met	Gln	Ala	Ser	Met	Gln	Gly	Gly	Val	Pro	Ala	
				245					250					255		
Pro	Gly	Gln	Met	Pro	Ala	Ala	Val	Thr	Gly	Pro	Gly	Pro	Gly	Ser	Leu	
			260					265					270			
Ala	Pro	Gly	Gly	Gly	Met	Gln	Ala	Gln	Val	Gly	Met	Pro	Gly	Ser	Gly	
		275				280						285				
Pro	Val	Ser	Met	Glu	Arg	Gly	Gln	Val	Pro	Met	Gln	Asp	Pro	Arg	Ala	
	290					295					300					
Ala	Met	Gln	Arg	Gly	Ser	Leu	Pro	Ala	Asn	Val	Pro	Thr	Pro	Arg	Gly	
305					310					315					320	
Leu	Leu	Gly	Asp	Ala	Pro	Asn	Asp	Pro	Arg	Gly	Gly	Thr	Leu	Leu	Ser	
				325					330					335		
Val	Thr	Gly	Glu	Val	Glu	Pro	Arg	Gly	Tyr	Leu	Gly	Pro	Pro	His	Gln	
			340					345					350			
Gly	Pro	Pro	Met	His	His	Val	Pro	Gly	His	Glu	Ser	Arg	Gly	Pro	Pro	
		355				360						365				
Pro	His	Glu	Leu	Arg	Gly	Gly	Pro	Leu	Pro	Glu	Pro	Arg	Pro	Leu	Met	
	370					375					380					
Ala	Glu	Pro	Arg	Gly	Pro	Met	Leu	Asp	Gln	Arg	Gly	Pro	Pro	Leu	Asp	
385					390					395					400	
Gly	Arg	Gly	Gly	Arg	Asp	Pro	Arg	Gly	Ile	Asp	Ala	Arg	Gly	Met	Glu	
				405					410					415		
Ala	Arg	Ala	Met	Glu	Ala	Arg	Gly	Leu	Asp	Ala	Arg	Gly	Leu	Glu	Ala	
			420					425					430			

Arg Ala Met Glu Ala Arg Ala Met Glu Ala Arg Ala Met Glu Ala Arg
 435 440 445
 Ala Met Glu Ala Arg Ala Met Glu Val Arg Gly Met Glu Ala Arg Gly
 450 455 460
 Met Asp Thr Arg Gly Pro Val Pro Gly Pro Arg Gly Pro Ile Pro Ser
 465 470 475 480
 Gly Met Gln Gly Pro Ser Pro Ile Asn Met Gly Ala Val Val Pro Gln
 485 490 495
 Gly Ser Arg Gln Val Pro Val Met Gln Gly Thr Gly Met Gln Gly Ala
 500 505 510
 Ser Ile Gln Gly Gly Ser Gln Pro Gly Gly Phe Ser Pro Gly Gln Asn
 515 520 525
 Gln Val Thr Pro Gln Asp His Glu Lys Ala Ala Leu Ile Met Gln Val
 530 535 540
 Leu Gln Leu Thr Ala Asp Gln Ile Ala Met Leu Pro Pro Glu Gln Arg
 545 550 555 560
 Gln Ser Ile Leu Ile Leu Lys Glu Gln Ile Gln Lys Ser Thr Gly Ala
 565 570 575

Pro

<210> 190
 <211> 717
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Ser Gly Asp Gly Ala Thr Glu Gln Ala Ala Glu Tyr Val Pro Glu
 1 5 10 15
 Lys Val Lys Lys Ala Glu Lys Lys Leu Glu Glu Asn Pro Tyr Asp Leu
 20 25 30
 Asp Ala Trp Ser Ile Leu Ile Arg Glu Ala Gln Asn Gln Pro Ile Asp
 35 40 45
 Lys Ala Arg Lys Thr Tyr Glu Arg Leu Val Ala Gln Phe Pro Ser Ser
 50 55 60
 Gly Arg Phe Trp Lys Leu Tyr Ile Glu Ala Glu Ile Lys Ala Lys Asn
 65 70 75 80
 Tyr Asp Lys Val Glu Lys Leu Phe Gln Arg Cys Leu Met Lys Val Leu
 85 90 95
 His Ile Asp Leu Trp Lys Cys Tyr Leu Ser Tyr Val Arg Glu Thr Lys
 100 105 110
 Gly Lys Leu Pro Ser Tyr Lys Glu Lys Met Ala Gln Ala Tyr Asp Phe
 115 120 125
 Ala Leu Asp Lys Ile Gly Met Glu Ile Met Ser Tyr Gln Ile Trp Val
 130 135 140

Asp Tyr Ile Asn Phe Leu Lys Gly Val Glu Ala Val Gly Ser Tyr Ala
 145 150 155 160
 Glu Asn Gln Arg Ile Thr Ala Val Arg Arg Val Tyr Gln Arg Gly Cys
 165 170 175
 Val Asn Pro Met Ile Asn Ile Glu Gln Leu Trp Arg Asp Tyr Asn Lys
 180 185 190
 Tyr Glu Glu Gly Ile Asn Ile His Leu Ala Lys Lys Met Ile Glu Asp
 195 200 205
 Arg Ser Arg Asp Tyr Met Asn Ala Arg Arg Val Ala Lys Glu Tyr Glu
 210 215 220
 Thr Val Met Lys Gly Leu Asp Arg Asn Ala Pro Ser Val Pro Pro Gln
 225 230 235 240
 Asn Thr Pro Gln Glu Ala Gln Gln Val Asp Met Trp Lys Lys Tyr Ile
 245 250 255
 Gln Trp Glu Lys Ser Asn Pro Leu Arg Thr Glu Asp Gln Thr Leu Ile
 260 265 270
 Thr Lys Arg Val Met Phe Ala Tyr Glu Gln Cys Leu Leu Val Leu Gly
 275 280 285
 His His Pro Asp Ile Trp Tyr Glu Ala Ala Gln Tyr Leu Glu Gln Ser
 290 295 300
 Ser Lys Leu Leu Ala Glu Lys Gly Asp Met Asn Asn Ala Lys Leu Phe
 305 310 315 320
 Ser Asp Glu Ala Ala Asn Ile Tyr Glu Arg Ala Ile Ser Thr Leu Leu
 325 330 335
 Lys Lys Asn Met Leu Leu Tyr Phe Ala Tyr Ala Asp Tyr Glu Glu Ser
 340 345 350
 Arg Met Lys Tyr Glu Lys Val His Ser Ile Tyr Asn Arg Leu Leu Ala
 355 360 365
 Ile Glu Asp Ile Asp Pro Thr Leu Val Tyr Ile Gln Tyr Met Lys Phe
 370 375 380
 Ala Arg Arg Ala Glu Gly Ile Lys Ser Gly Arg Met Ile Phe Lys Lys
 385 390 395 400
 Ala Arg Glu Asp Thr Arg Thr Arg His His Val Tyr Val Thr Ala Ala
 405 410 415
 Leu Met Glu Tyr Tyr Cys Ser Lys Asp Lys Ser Val Ala Phe Lys Ile
 420 425 430
 Phe Glu Leu Gly Leu Lys Lys Tyr Gly Asp Ile Pro Glu Tyr Val Leu
 435 440 445
 Ala Tyr Ile Asp Tyr Leu Ser His Leu Asn Glu Asp Asn Asn Thr Arg
 450 455 460
 Val Leu Phe Glu Arg Val Leu Thr Ser Gly Ser Leu Pro Pro Glu Lys

465				470				475				480					
Ser	Gly	Glu	Ile	Trp	Ala	Arg	Phe	Leu	Ala	Phe	Glu	Ser	Asn	Ile	Gly		
				485					490				495				
Asp	Leu	Ala	Ser	Ile	Leu	Lys	Val	Glu	Lys	Arg	Arg	Phe	Thr	Ala	Phe		
				500					505				510				
Lys	Glu	Glu	Tyr	Glu	Gly	Lys	Glu	Thr	Ala	Leu	Leu	Val	Asp	Arg	Tyr		
				515					520				525				
Lys	Phe	Met	Asp	Leu	Tyr	Pro	Cys	Ser	Ala	Ser	Glu	Leu	Lys	Ala	Leu		
				530					535				540				
Gly	Tyr	Lys	Asp	Val	Ser	Arg	Ala	Lys	Leu	Ala	Ala	Ile	Ile	Pro	Asp		
				545					550				555				
Pro	Val	Val	Ala	Pro	Ser	Ile	Val	Pro	Val	Leu	Lys	Asp	Glu	Val	Asp		
				565					570				575				
Arg	Lys	Pro	Glu	Tyr	Pro	Lys	Pro	Asp	Thr	Gln	Gln	Met	Ile	Pro	Phe		
				580					585				590				
Gln	Pro	Arg	His	Leu	Ala	Pro	Pro	Gly	Leu	His	Pro	Val	Pro	Gly	Gly		
				595					600				605				
Val	Phe	Pro	Val	Pro	Pro	Ala	Ala	Val	Val	Leu	Met	Lys	Leu	Leu	Pro		
				610					615				620				
Pro	Pro	Ile	Cys	Phe	Gln	Gly	Pro	Phe	Val	Gln	Val	Asp	Glu	Leu	Met		
				625					630				635				
Glu	Ile	Phe	Arg	Arg	Cys	Lys	Ile	Pro	Asn	Thr	Val	Glu	Glu	Ala	Val		
				645					650				655				
Arg	Ile	Ile	Thr	Gly	Gly	Ala	Pro	Glu	Leu	Ala	Val	Glu	Gly	Asn	Gly		
				660					665				670				
Pro	Val	Glu	Ser	Asn	Ala	Val	Leu	Thr	Lys	Ala	Val	Lys	Arg	Pro	Asn		
				675					680				685				
Glu	Asp	Ser	Asp	Glu	Asp	Glu	Glu	Lys	Gly	Ala	Val	Val	Pro	Pro	Val		
				690					695				700				
His	Asp	Ile	Tyr	Arg	Ala	Arg	Gln	Gln	Lys	Arg	Ile	Arg					
				705					710				715				
<210> 191																	
<211> 442																	
<212> PRT																	
<213> Homo sapiens																	
<400> 191																	
Met	Ala	Ser	Val	Val	Leu	Pro	Ser	Gly	Ser	Gln	Cys	Ala	Ala	Ala	Ala		
1					5					10				15			
Ala	Ala	Ala	Ala	Pro	Pro	Gly	Leu	Arg	Leu	Arg	Leu	Leu	Leu	Leu	Leu		
				20					25				30				
Phe	Ser	Ala	Ala	Ala	Leu	Ile	Pro	Thr	Gly	Asp	Gly	Gln	Asn	Leu	Phe		
				35					40				45				

Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys
 50 55 60
 Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn
 65 70 75 80
 Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg
 85 90 95
 Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr
 100 105 110
 Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr
 115 120 125
 Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro
 130 135 140
 Arg Asn Leu Met Ile Asp Ile Gln Arg Asp Thr Ala Val Glu Gly Glu
 145 150 155 160
 Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr
 165 170 175
 Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val
 180 185 190
 Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys
 195 200 205
 Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His
 210 215 220
 Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln
 225 230 235 240
 Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu
 245 250 255
 Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys
 260 265 270
 Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro
 275 280 285
 Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn
 290 295 300
 Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly
 305 310 315 320
 Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Pro Pro Thr Thr
 325 330 335
 Ile Pro Pro Pro Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr Thr
 340 345 350
 Thr Ile Leu Thr Ile Ile Thr Asp Ser Arg Ala Gly Glu Glu Gly Ser
 355 360 365
 Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val Val Ala Val Val
 370 375 380

Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly Arg Tyr Phe Ala
 385 390 395 400
 Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys Gly Ala Asp Asp
 405 410 415
 Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu Gly Gly Gln Asn
 420 425 430
 Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile
 435 440
 <210> 192
 <211> 288
 <212> PRT
 <213> Homo sapiens
 <400> 192
 Met Ala Ala Val Leu Gln Arg Val Glu Arg Leu Ser Asn Arg Val Val
 1 5 10 15
 Arg Val Leu Gly Cys Asn Pro Gly Pro Met Thr Leu Gln Gly Thr Asn
 20 25 30
 Thr Tyr Leu Val Gly Thr Gly Pro Arg Arg Ile Leu Ile Asp Thr Gly
 35 40 45
 Glu Pro Ala Ile Pro Glu Tyr Ile Ser Cys Leu Lys Gln Ala Leu Thr
 50 55 60
 Glu Phe Asn Thr Ala Ile Gln Glu Ile Val Val Thr His Trp His Arg
 65 70 75 80
 Asp His Ser Gly Gly Ile Gly Asp Ile Cys Lys Ser Ile Asn Asn Asp
 85 90 95
 Thr Thr Tyr Cys Ile Lys Lys Leu Pro Arg Asn Pro Gln Arg Glu Glu
 100 105 110
 Ile Ile Gly Asn Gly Glu Gln Gln Tyr Val Tyr Leu Lys Asp Gly Asp
 115 120 125
 Val Ile Lys Thr Glu Gly Ala Thr Leu Arg Val Leu Tyr Thr Pro Gly
 130 135 140
 His Thr Asp Asp His Met Ala Leu Leu Leu Glu Glu Glu Asn Ala Ile
 145 150 155 160
 Phe Ser Gly Asp Cys Ile Leu Gly Glu Gly Thr Thr Val Phe Glu Asp
 165 170 175
 Leu Tyr Asp Tyr Met Asn Ser Leu Lys Glu Leu Leu Lys Ile Lys Ala
 180 185 190
 Asp Ile Ile Tyr Pro Gly His Gly Pro Val Ile His Asn Ala Glu Ala
 195 200 205
 Lys Ile Gln Gln Tyr Ile Ser His Arg Asn Ile Arg Glu Gln Gln Ile
 210 215 220
 Leu Thr Leu Phe Arg Glu Asn Phe Glu Lys Ser Phe Thr Val Met Glu

225		230		235		240
Leu Val Lys Ile Ile Tyr Lys Asn Thr Pro Glu Asn Leu His Glu Met						
		245		250		255
Ala Lys His Asn Leu Leu Leu His Leu Lys Lys Leu Glu Lys Glu Gly		260		265		270
Lys Ile Phe Ser Asn Thr Asp Pro Asp Lys Lys Trp Lys Ala His Leu		275		280		285
<210> 193						
<211> 872						
<212> PRT						
<213> Homo sapiens						
<400> 193						
Met Ala Pro Gly Ala Ala Gln Glu Leu Gln Ala Lys Leu Ala Glu Ile						
1		5		10		15
Gly Ala Pro Ile Gln Gly Asn Arg Glu Glu Leu Val Glu Arg Leu Gln		20		25		30
Ser Tyr Thr Arg Gln Thr Gly Ile Val Leu Asn Arg Pro Val Leu Arg		35		40		45
Gly Glu Asp Gly Asp Lys Ala Ala Pro Pro Pro Met Ser Ala Gln Leu		50		55		60
Pro Gly Ile Pro Met Pro Pro Pro Pro Leu Gly Leu Pro Pro Leu Gln		65		70		75
Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Gly Leu Gly Leu Gly Phe		85		90		95
Pro Met Ala His Pro Pro Asn Leu Gly Pro Pro Pro Pro Leu Arg Val		100		105		110
Gly Glu Pro Val Ala Leu Ser Glu Glu Glu Arg Leu Lys Leu Ala Gln		115		120		125
Gln Gln Ala Ala Leu Leu Met Gln Gln Glu Glu Arg Ala Lys Gln Gln		130		135		140
Gly Asp His Ser Leu Lys Glu His Glu Leu Leu Glu Gln Gln Lys Arg		145		150		155
Ala Ala Val Leu Leu Glu Gln Glu Arg Gln Gln Glu Ile Ala Lys Met		165		170		175
Gly Thr Pro Val Pro Arg Pro Pro Gln Asp Met Gly Gln Ile Gly Val		180		185		190
Arg Thr Pro Leu Gly Pro Arg Val Ala Ala Pro Val Gly Pro Val Gly		195		200		205
Pro Thr Pro Thr Val Leu Pro Met Gly Ala Pro Val Pro Arg Pro Arg		210		215		220
Gly Pro Pro Pro Pro Pro Gly Asp Glu Asn Arg Glu Met Asp Asp Pro		225		230		235
						240

Ser Val Gly Pro Lys Ile Pro Gln Ala Leu Glu Lys Ile Leu Gln Leu
 245 250 255
 Lys Glu Ser Arg Gln Glu Glu Met Asn Ser Gln Gln Glu Glu Glu Glu
 260 265 270
 Met Glu Thr Asp Ala Arg Ser Ser Leu Gly Gln Ser Ala Ser Glu Thr
 275 280 285
 Glu Glu Asp Thr Val Ser Val Ser Lys Lys Glu Lys Asn Arg Lys Arg
 290 295 300
 Arg Asn Arg Lys Lys Lys Lys Lys Pro Gln Arg Val Arg Gly Val Ser
 305 310 315 320
 Ser Glu Ser Ser Gly Asp Arg Glu Lys Asp Ser Thr Arg Ser Arg Gly
 325 330 335
 Ser Asp Ser Pro Ala Ala Asp Val Glu Ile Glu Tyr Val Thr Glu Glu
 340 345 350
 Pro Glu Ile Tyr Glu Pro Asn Phe Ile Phe Phe Lys Arg Ile Phe Glu
 355 360 365
 Ala Phe Lys Leu Thr Asp Asp Val Lys Lys Glu Lys Glu Lys Glu Pro
 370 375 380
 Glu Lys Leu Asp Lys Leu Glu Asn Ser Ala Ala Pro Lys Lys Lys Gly
 385 390 395 400
 Phe Glu Glu Glu His Lys Asp Ser Asp Asp Asp Ser Ser Asp Asp Glu
 405 410 415
 Gln Glu Lys Lys Pro Glu Ala Pro Lys Leu Ser Lys Lys Lys Leu Arg
 420 425 430
 Arg Met Asn Arg Phe Thr Val Ala Glu Leu Lys Gln Leu Val Ala Arg
 435 440 445
 Pro Asp Val Val Glu Met His Asp Val Thr Ala Gln Asp Pro Lys Leu
 450 455 460
 Leu Val His Leu Lys Ala Thr Arg Asn Ser Val Pro Val Pro Arg His
 465 470 475 480
 Trp Cys Phe Lys Arg Lys Tyr Leu Gln Gly Lys Arg Gly Ile Glu Lys
 485 490 495
 Pro Pro Phe Glu Leu Pro Asp Phe Ile Lys Arg Thr Gly Ile Gln Glu
 500 505 510
 Met Arg Glu Ala Leu Gln Glu Lys Glu Glu Gln Lys Thr Met Lys Ser
 515 520 525
 Lys Met Arg Glu Lys Val Arg Pro Lys Met Gly Lys Ile Asp Ile Asp
 530 535 540
 Tyr Gln Lys Leu His Asp Ala Phe Phe Lys Trp Gln Thr Lys Pro Lys
 545 550 555 560
 Leu Thr Ile His Gly Asp Leu Tyr Tyr Glu Gly Lys Glu Phe Glu Thr
 565 570 575

Arg Leu Lys Glu Lys Lys Pro Gly Asp Leu Ser Asp Glu Leu Arg Ile
 580 585 590
 Ser Leu Gly Met Pro Val Gly Pro Asn Ala His Lys Val Pro Pro Pro
 595 600 605
 Trp Leu Ile Ala Met Gln Arg Tyr Gly Pro Pro Pro Ser Tyr Pro Asn
 610 615 620
 Leu Lys Ile Pro Gly Leu Asn Ser Pro Ile Pro Glu Ser Cys Ser Phe
 625 630 635 640
 Gly Tyr His Ala Gly Gly Trp Gly Lys Pro Pro Val Asp Glu Thr Gly
 645 650 655
 Lys Pro Leu Tyr Gly Asp Val Phe Gly Thr Asn Ala Ala Glu Phe Gln
 660 665 670
 Thr Lys Thr Glu Glu Glu Glu Ile Asp Arg Thr Pro Trp Gly Glu Leu
 675 680 685
 Glu Pro Ser Asp Glu Glu Ser Ser Glu Glu Glu Glu Glu Glu Ser
 690 695 700
 Asp Glu Asp Lys Pro Asp Glu Thr Gly Phe Ile Thr Pro Ala Asp Ser
 705 710 715 720
 Gly Leu Ile Thr Pro Gly Gly Phe Ser Ser Val Pro Ala Gly Met Glu
 725 730 735
 Thr Pro Glu Leu Ile Glu Leu Arg Lys Lys Lys Ile Glu Glu Ala Met
 740 745 750
 Asp Gly Ser Glu Thr Pro Gln Leu Phe Thr Val Leu Pro Glu Lys Arg
 755 760 765
 Thr Ala Thr Val Gly Gly Ala Met Met Gly Ser Thr His Ile Tyr Asp
 770 775 780
 Met Ser Thr Val Met Ser Arg Lys Gly Pro Ala Pro Glu Leu Gln Gly
 785 790 795 800
 Val Glu Val Ala Leu Ala Pro Glu Glu Leu Glu Leu Asp Pro Met Ala
 805 810 815
 Met Thr Gln Lys Tyr Glu Glu His Val Arg Glu Gln Gln Ala Gln Val
 820 825 830
 Glu Lys Glu Asp Phe Ser Asp Met Val Ala Glu His Ala Ala Lys Gln
 835 840 845
 Lys Gln Lys Lys Arg Lys Ala Gln Pro Gln Asp Ser Arg Gly Gly Ser
 850 855 860
 Lys Lys Tyr Lys Glu Phe Lys Phe
 865 870

<210> 194
 <211> 507
 <212> PRT
 <213> Homo sapiens


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<400> 194
Met Gly Cys Trp Gly Arg Asn Arg Gly Arg Leu Leu Cys Met Leu Ala
1      5      10      15

Leu Thr Phe Met Phe Met Val Leu Glu Val Val Val Ser Arg Val Thr
20      25      30

Ser Ser Leu Ala Met Leu Ser Asp Ser Phe His Met Leu Ser Asp Val
35      40      45

Leu Ala Leu Val Val Ala Leu Val Ala Glu Arg Phe Ala Arg Arg Thr
50      55      60

His Ala Thr Gln Lys Asn Thr Phe Gly Trp Ile Arg Ala Glu Val Met
65      70      75      80

Gly Ala Leu Val Asn Ala Ile Phe Leu Thr Gly Leu Cys Phe Ala Ile
85      90      95

Leu Leu Glu Ala Ile Glu Arg Phe Ile Glu Pro His Glu Met Gln Gln
100     105     110

Pro Leu Val Val Leu Gly Val Gly Val Ala Gly Leu Leu Val Asn Val
115     120     125

Leu Gly Leu Cys Leu Phe His His His Ser Gly Phe Ser Gln Asp Ser
130     135     140

Gly His Gly His Ser His Gly Gly His Gly His Gly His Gly Leu Pro
145     150     155     160

Lys Gly Pro Arg Val Lys Ser Thr Arg Pro Gly Ser Ser Asp Ile Asn
165     170     175

Val Ala Pro Gly Glu Gln Gly Pro Asp Gln Glu Glu Thr Asn Thr Leu
180     185     190

Val Ala Asn Thr Ser Asn Ser Asn Gly Leu Lys Leu Asp Pro Ala Asp
195     200     205

Pro Glu Asn Pro Arg Ser Gly Asp Thr Val Glu Val Gln Val Asn Gly
210     215     220

Asn Leu Val Arg Glu Pro Asp His Met Glu Leu Glu Glu Asp Arg Ala
225     230     235     240

Gly Gln Leu Asn Met Arg Gly Val Phe Leu His Val Leu Gly Asp Ala
245     250     255

Leu Gly Ser Val Ile Val Val Val Asn Ala Leu Val Phe Tyr Phe Ser
260     265     270

Trp Lys Gly Cys Ser Glu Gly Asp Phe Cys Val Asn Pro Cys Phe Pro
275     280     285

Asp Pro Cys Lys Ala Phe Val Glu Ile Ile Asn Ser Thr His Ala Ser
290     295     300

Val Tyr Glu Ala Gly Pro Cys Trp Val Leu Tyr Leu Asp Pro Thr Leu
305     310     315     320

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Cys Val Val Met Val Cys Ile Leu Leu Tyr Thr Thr Tyr Pro Leu Leu
 325 330 335
 Lys Glu Ser Ala Leu Ile Leu Leu Gln Thr Val Pro Lys Gln Ile Asp
 340 345 350
 Ile Arg Asn Leu Ile Lys Glu Leu Arg Asn Val Glu Gly Val Glu Glu
 355 360 365
 Val His Glu Leu His Val Trp Gln Leu Ala Gly Ser Arg Ile Ile Ala
 370 375 380
 Thr Val His Ile Lys Cys Glu Asp Pro Thr Ser Tyr Met Glu Val Ala
 385 390 395 400
 Lys Thr Ile Lys Asp Val Phe His Asn His Gly Ile His Ala Thr Thr
 405 410 415
 Ile Gln Pro Glu Phe Ala Ser Val Gly Ser Lys Ser Ser Val Val Pro
 420 425 430
 Cys Glu Leu Ala Cys Arg Thr Gln Cys Ala Leu Lys Gln Cys Cys Gly
 435 440 445
 Thr Leu Pro Gln Ala Pro Ser Gly Lys Asp Ala Glu Lys Thr Pro Ala
 450 455 460
 Val Ser Ile Ser Cys Leu Glu Leu Ser Asn Asn Leu Glu Lys Lys Pro
 465 470 475 480
 Arg Arg Thr Lys Ala Glu Asn Ile Pro Ala Val Val Ile Glu Ile Lys
 485 490 495
 Asn Met Pro Asn Lys Gln Pro Glu Ser Ser Leu
 500 505
 <210> 195
 <211> 317
 <212> PRT
 <213> Homo sapiens
 <400> 195
 Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly
 1 5 10 15
 Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile Leu
 20 25 30
 Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp
 35 40 45
 Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His
 50 55 60
 Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser
 65 70 75 80
 Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr
 85 90 95
 Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala
 100 105 110

Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr
 115 120 125
 Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp
 130 135 140
 Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser
 145 150 155 160
 Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val
 165 170 175
 Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr
 180 185 190
 Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala
 195 200 205
 Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly
 210 215 220
 Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys
 225 230 235 240
 Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile
 245 250 255
 Lys Ile Trp Asp Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln
 260 265 270
 Glu Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser
 275 280 285
 Leu Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp
 290 295 300
 Asn Leu Val Arg Val Trp Gln Val Thr Ile Gly Thr Arg
 305 310 315
 <210> 196
 <211> 662
 <212> PRT
 <213> Homo sapiens
 <400> 196
 Met Ser His Val Ala Val Glu Asn Ala Leu Gly Leu Asp Gln Gln Phe
 1 5 10 15
 Ala Gly Leu Asp Leu Asn Ser Ser Asp Asn Gln Ser Gly Gly Ser Thr
 20 25 30
 Ala Ser Lys Gly Arg Tyr Ile Pro Pro His Leu Arg Asn Arg Glu Ala
 35 40 45
 Thr Lys Gly Phe Tyr Asp Lys Asp Ser Ser Gly Trp Ser Ser Ser Lys
 50 55 60
 Asp Lys Asp Ala Tyr Ser Ser Phe Gly Ser Arg Ser Asp Ser Arg Gly
 65 70 75 80
 Lys Ser Ser Phe Phe Ser Asp Arg Gly Ser Gly Ser Arg Gly Arg Phe

				85					90					95	
Asp	Asp	Arg	Gly	Arg	Ser	Asp	Tyr	Asp	Gly	Ile	Gly	Ser	Arg	Gly	Asp
			100						105					110	
Arg	Ser	Gly	Phe	Gly	Lys	Phe	Glu	Arg	Gly	Gly	Asn	Ser	Arg	Trp	Cys
		115					120					125			
Asp	Lys	Ser	Asp	Glu	Asp	Asp	Trp	Ser	Lys	Pro	Leu	Pro	Pro	Ser	Glu
	130					135					140				
Arg	Leu	Glu	Gln	Glu	Leu	Phe	Ser	Gly	Gly	Asn	Thr	Gly	Ile	Asn	Phe
145					150					155					160
Glu	Lys	Tyr	Asp	Asp	Ile	Pro	Val	Glu	Ala	Thr	Gly	Asn	Asn	Cys	Pro
				165					170					175	
Pro	His	Ile	Glu	Ser	Phe	Ser	Asp	Val	Glu	Met	Gly	Glu	Ile	Ile	Met
			180					185					190		
Gly	Asn	Ile	Glu	Leu	Thr	Arg	Tyr	Thr	Arg	Pro	Thr	Pro	Val	Gln	Lys
		195					200					205			
His	Ala	Ile	Pro	Ile	Ile	Lys	Glu	Lys	Arg	Asp	Leu	Met	Ala	Cys	Ala
	210					215					220				
Gln	Thr	Gly	Ser	Gly	Lys	Thr	Ala	Ala	Phe	Leu	Leu	Pro	Ile	Leu	Ser
225					230					235					240
Gln	Ile	Tyr	Ser	Asp	Gly	Pro	Gly	Glu	Ala	Leu	Arg	Ala	Met	Lys	Glu
				245					250					255	
Asn	Gly	Arg	Tyr	Gly	Arg	Arg	Lys	Gln	Tyr	Pro	Ile	Ser	Leu	Val	Leu
			260					265					270		
Ala	Pro	Thr	Arg	Glu	Leu	Ala	Val	Gln	Ile	Tyr	Glu	Glu	Ala	Arg	Lys
		275					280					285			
Phe	Ser	Tyr	Arg	Ser	Arg	Val	Arg	Pro	Cys	Val	Val	Tyr	Gly	Gly	Ala
	290					295					300				
Asp	Ile	Gly	Gln	Gln	Ile	Arg	Asp	Leu	Glu	Arg	Gly	Cys	His	Leu	Leu
305					310					315					320
Val	Ala	Thr	Pro	Gly	Arg	Leu	Val	Asp	Met	Met	Glu	Arg	Gly	Lys	Ile
				325					330					335	
Gly	Leu	Asp	Phe	Cys	Lys	Tyr	Leu	Val	Leu	Asp	Glu	Ala	Asp	Arg	Met
			340					345					350		
Leu	Asp	Met	Gly	Phe	Glu	Pro	Gln	Ile	Arg	Arg	Ile	Val	Glu	Gln	Asp
		355					360					365			
Thr	Met	Pro	Pro	Lys	Gly	Val	Arg	His	Thr	Met	Met	Phe	Ser	Ala	Thr
	370					375					380				
Phe	Pro	Lys	Glu	Ile	Gln	Met	Leu	Ala	Arg	Asp	Phe	Leu	Asp	Glu	Tyr
385					390					395					400
Ile	Phe	Leu	Ala	Val	Gly	Arg	Val	Gly	Ser	Thr	Ser	Glu	Asn	Ile	Thr
				405					410					415	

Gln Lys Val Val Trp Val Glu Glu Ser Asp Lys Arg Ser Phe Leu Leu
 420 425 430
 Asp Leu Leu Asn Ala Thr Gly Lys Asp Ser Leu Thr Leu Val Phe Val
 435 440 445
 Glu Thr Lys Lys Gly Ala Asp Ser Leu Glu Asp Phe Leu Tyr His Glu
 450 455 460
 Gly Tyr Ala Cys Thr Ser Ile His Gly Asp Arg Ser Gln Arg Asp Arg
 465 470 475 480
 Glu Glu Ala Leu His Gln Phe Arg Ser Gly Lys Ser Pro Ile Leu Val
 485 490 495
 Ala Thr Ala Val Ala Ala Arg Gly Leu Asp Ile Ser Asn Val Lys His
 500 505 510
 Val Ile Asn Phe Asp Leu Pro Ser Asp Ile Glu Glu Tyr Val His Arg
 515 520 525
 Ile Gly Arg Thr Gly Arg Val Gly Asn Leu Gly Leu Ala Thr Ser Phe
 530 535 540
 Phe Asn Glu Arg Asn Ile Asn Ile Thr Lys Asp Leu Leu Asp Leu Leu
 545 550 555 560
 Val Glu Ala Lys Gln Glu Val Pro Ser Trp Leu Glu Asn Met Ala Tyr
 565 570 575
 Glu His His Tyr Lys Gly Ser Ser Arg Gly Arg Ser Lys Ser Ser Arg
 580 585 590
 Phe Ser Gly Gly Phe Gly Ala Arg Asp Tyr Arg Gln Ser Ser Gly Ala
 595 600 605
 Ser Ser Ser Ser Phe Ser Ser Ser Arg Ala Ser Ser Ser Arg Ser Gly
 610 615 620
 Gly Gly Gly His Gly Ser Ser Arg Gly Phe Gly Gly Gly Gly Tyr Gly
 625 630 635 640
 Gly Phe Tyr Asn Ser Asp Gly Tyr Gly Gly Asn Tyr Asn Ser Gln Gly
 645 650 655
 Val Asp Trp Trp Gly Asn
 660

<210> 197
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 197
 Met Ser His Val Val Val Lys Asn Asp Pro Glu Leu Asp Gln Gln Leu
 1 5 10 15
 Ala Asn Leu Asp Leu Asn Ser Glu Lys Gln Ser Gly Gly Ala Ser Thr
 20 25 30
 Ala Ser Lys Gly Arg Tyr Ile Pro Pro His Leu Arg Asn Lys Glu Ala
 35 40 45

Ser Lys Gly Phe His Asp Lys Asp Ser Ser Gly Trp Ser Cys Ser Lys
 50 55 60
 Asp Lys Asp Ala Tyr Ser Ser Phe Gly Ser Arg Asp Ser Arg Gly Lys
 65 70 75 80
 Pro Gly Tyr Phe Ser Glu Arg Gly Ser Gly Ser Arg Gly Arg Phe Asp
 85 90 95
 Asp Arg Gly Arg Ser Asp Tyr Asp Gly Ile Gly Asn Arg Glu Arg Pro
 100 105 110
 Gly Phe Gly Arg Phe Glu Arg Ser Gly His Ser Arg Trp Cys Asp Lys
 115 120 125
 Ser Val Glu Asp Asp Trp Ser Lys Pro Leu Pro Pro Ser Glu Arg Leu
 130 135 140
 Glu Gln Glu Leu Phe Ser Gly Gly Asn Thr Gly Ile Asn Phe Glu Lys
 145 150 155 160
 Tyr Asp Asp Ile Pro Val Glu Ala Thr Gly Ser Asn Cys Pro Pro His
 165 170 175
 Ile Glu Asn Phe Ser Asp Ile Asp Met Gly Glu Ile Ile Met Gly Asn
 180 185 190
 Ile Glu Leu Thr Arg Tyr Thr Arg Pro Thr Pro Val Gln Lys His Ala
 195 200 205
 Ile Pro Ile Ile Lys Gly Lys Arg Asp Leu Val Ala Cys Ala Gln Thr
 210 215 220
 Gly Ser Gly Lys Thr Ala Ala Phe Leu Leu Pro Ile Leu Ser Gln Ile
 225 230 235 240
 Tyr Thr Asp Gly Pro Gly Glu Ala Leu Lys Ala Val Lys Glu Asn Gly
 245 250 255
 Arg Tyr Gly Arg Arg Lys Gln Tyr Pro Ile Ser Leu Val Leu Ala Pro
 260 265 270
 Thr Arg Glu Leu Ala Val Gln Ile Tyr Glu Glu Ala Arg Lys Phe Ser
 275 280 285
 Tyr Arg Ser Arg Val Arg Pro Cys Val Val Tyr Gly Gly Ala Asp Ile
 290 295 300
 Gly Gln Gln Ile Arg Asp Leu Glu Arg Gly Cys His Leu Leu Val Ala
 305 310 315 320
 Thr Pro Gly Arg Leu Val Asp Met Met Glu Arg Gly Lys Ile Gly Leu
 325 330 335
 Asp Phe Cys Lys Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp
 340 345 350
 Met Gly Phe Glu Pro Gln Ile Arg Arg Ile Val Glu Gln Asp Thr Met
 355 360 365
 Pro Pro Lys Gly Val Arg His Thr Met Met Phe Ser Ala Thr Phe Pro

370 375 380
 Lys Glu Ile Gln Met Leu Ala Arg Asp Phe Leu Asp Glu Tyr Ile Phe
 385 390 395 400
 Leu Ala Val Gly Arg Val Gly Ser Thr Ser Glu Asn Ile Thr Gln Lys
 405 410 415
 Val Val Trp Val Glu Asp Leu Asp Lys Arg Ser Phe Leu Leu Asp Ile
 420 425 430
 Leu Gly Ala Thr Gly Ser Asp Ser Leu Thr Leu Val Phe Val Glu Thr
 435 440 445
 Lys Lys Gly Ala Asp Ser Leu Glu Asp Phe Leu Tyr His Glu Gly Tyr
 450 455 460
 Ala Cys Thr Ser Ile His Gly Asp Arg Ser Gln Arg Asp Arg Glu Glu
 465 470 475 480
 Ala Leu His Gln Phe Arg Ser Gly Lys Ser Pro Ile Leu Val Ala Thr
 485 490 495
 Ala Val Ala Ala Arg Gly Leu Asp Ile Ser Asn Val Arg His Val Ile
 500 505 510
 Asn Phe Asp Leu Pro Ser Asp Ile Glu Glu Tyr Val His Arg Ile Gly
 515 520 525
 Arg Thr Gly Arg Val Gly Asn Leu Gly Leu Ala Thr Ser Phe Phe Asn
 530 535 540
 Glu Lys Asn Met Asn Ile Thr Lys Asp Leu Leu Asp Leu Leu Val Glu
 545 550 555 560
 Ala Lys Gln Glu Val Pro Ser Trp Leu Glu Asn Met Ala Tyr Glu His
 565 570 575
 His Tyr Lys Gly Gly Ser Arg Gly Arg Ser Lys Ser Asn Arg Phe Ser
 580 585 590
 Gly Gly Phe Gly Ala Arg Asp Tyr Arg Gln Ser Ser Gly Ser Ser Ser
 595 600 605
 Ser Gly Phe Gly Ala Ser Arg Gly Ser Ser Ser Arg Ser Gly Gly Gly
 610 615 620
 Gly Tyr Gly Asp Ser Arg Gly Phe Gly Gly Gly Tyr Gly Gly Phe
 625 630 635 640
 Tyr Asn Ser Asp Gly Tyr Gly Gly Asn Tyr Asn Ser Gln Gly Val Asp
 645 650 655
 Trp Trp Gly Asn
 660

<210> 198
 <211> 1087
 <212> PRT
 <213> Homo sapiens
 <400> 198

Met	Ala	Asp	His	Val	Gln	Ser	Leu	Ala	Gln	Leu	Glu	Asn	Leu	Cys	Lys	1	5	10	15
Gln	Leu	Tyr	Glu	Thr	Thr	Asp	Thr	Thr	Thr	Arg	Leu	Gln	Ala	Glu	Lys	20	25	30	
Ala	Leu	Val	Glu	Phe	Thr	Asn	Ser	Pro	Asp	Cys	Leu	Ser	Lys	Cys	Gln	35	40	45	
Leu	Leu	Leu	Glu	Arg	Gly	Ser	Ser	Ser	Tyr	Ser	Gln	Leu	Leu	Ala	Ala	50	55	60	
Thr	Cys	Leu	Thr	Lys	Leu	Val	Ser	Arg	Thr	Asn	Asn	Pro	Leu	Pro	Leu	65	70	75	80
Glu	Gln	Arg	Ile	Asp	Ile	Arg	Asn	Tyr	Val	Leu	Asn	Tyr	Leu	Ala	Thr	85	90	95	
Arg	Pro	Lys	Leu	Ala	Thr	Phe	Val	Thr	Gln	Ala	Leu	Ile	Gln	Leu	Tyr	100	105	110	
Ala	Arg	Ile	Thr	Lys	Leu	Gly	Trp	Phe	Asp	Cys	Gln	Lys	Asp	Asp	Tyr	115	120	125	
Val	Phe	Arg	Asn	Ala	Ile	Thr	Asp	Val	Thr	Arg	Phe	Leu	Gln	Asp	Ser	130	135	140	
Val	Glu	Tyr	Cys	Ile	Ile	Gly	Val	Thr	Ile	Leu	Ser	Gln	Leu	Thr	Asn	145	150	155	160
Glu	Ile	Asn	Gln	Ala	Asp	Thr	Thr	His	Pro	Leu	Thr	Lys	His	Arg	Lys	165	170	175	
Ile	Ala	Ser	Ser	Phe	Arg	Asp	Ser	Ser	Leu	Phe	Asp	Ile	Phe	Thr	Leu	180	185	190	
Ser	Cys	Asn	Leu	Leu	Lys	Gln	Ala	Ser	Gly	Lys	Asn	Leu	Asn	Leu	Asn	195	200	205	
Asp	Glu	Ser	Gln	His	Gly	Leu	Leu	Met	Gln	Leu	Leu	Lys	Leu	Thr	His	210	215	220	
Asn	Cys	Leu	Asn	Phe	Asp	Phe	Ile	Gly	Thr	Ser	Thr	Asp	Glu	Ser	Ser	225	230	235	240
Asp	Asp	Leu	Cys	Thr	Val	Gln	Ile	Pro	Thr	Ser	Trp	Arg	Ser	Ala	Phe	245	250	255	
Leu	Asp	Ser	Ser	Thr	Leu	Gln	Leu	Phe	Phe	Asp	Leu	Tyr	His	Ser	Ile	260	265	270	
Pro	Pro	Ser	Phe	Ser	Pro	Leu	Val	Leu	Ser	Cys	Leu	Val	Gln	Ile	Ala	275	280	285	
Ser	Val	Arg	Arg	Ser	Leu	Phe	Asn	Asn	Ala	Glu	Arg	Ala	Lys	Phe	Leu	290	295	300	
Ser	His	Leu	Val	Asp	Gly	Val	Lys	Arg	Ile	Leu	Glu	Asn	Pro	Gln	Ser	305	310	315	320
Leu	Ser	Asp	Pro	Asn	Asn	Tyr	His	Glu	Phe	Cys	Arg	Leu	Leu	Ala	Arg	325	330	335	

Leu Lys Ser Asn Tyr Gln Leu Gly Glu Leu Val Lys Val Glu Asn Tyr
 340 345 350
 Pro Glu Val Ile Arg Leu Ile Ala Asn Phe Thr Val Thr Ser Leu Gln
 355 360 365
 His Trp Glu Phe Ala Pro Asn Ser Val His Tyr Leu Leu Ser Leu Trp
 370 375 380
 Gln Arg Leu Ala Ala Ser Val Pro Tyr Val Lys Ala Thr Glu Pro His
 385 390 395 400
 Met Leu Glu Thr Tyr Thr Pro Glu Val Thr Lys Ala Tyr Ile Thr Ser
 405 410 415
 Arg Leu Glu Ser Val His Ile Ile Leu Arg Asp Gly Leu Glu Asp Pro
 420 425 430
 Leu Glu Asp Thr Gly Leu Val Gln Gln Gln Leu Asp Gln Leu Ser Thr
 435 440 445
 Ile Gly Arg Cys Glu Tyr Glu Lys Thr Cys Ala Leu Leu Val Gln Leu
 450 455 460
 Phe Asp Gln Ser Ala Gln Ser Tyr Gln Glu Leu Leu Gln Ser Ala Ser
 465 470 475 480
 Ala Ser Pro Met Asp Ile Ala Val Gln Glu Gly Arg Leu Thr Trp Leu
 485 490 495
 Val Tyr Ile Ile Gly Ala Val Ile Gly Gly Arg Val Ser Phe Ala Ser
 500 505 510
 Thr Asp Glu Gln Asp Ala Met Asp Gly Glu Leu Val Cys Arg Val Leu
 515 520 525
 Gln Leu Met Asn Leu Thr Asp Ser Arg Leu Ala Gln Ala Gly Asn Glu
 530 535 540
 Lys Leu Glu Leu Ala Met Leu Ser Phe Phe Glu Gln Phe Arg Lys Ile
 545 550 555 560
 Tyr Ile Gly Asp Gln Val Gln Lys Ser Ser Lys Leu Tyr Arg Arg Leu
 565 570 575
 Ser Glu Val Leu Gly Leu Asn Asp Glu Thr Met Val Leu Ser Val Phe
 580 585 590
 Ile Gly Lys Ile Ile Thr Asn Leu Lys Tyr Trp Gly Arg Cys Glu Pro
 595 600 605
 Ile Thr Ser Lys Thr Leu Gln Leu Leu Asn Asp Leu Ser Ile Gly Tyr
 610 615 620
 Ser Ser Val Arg Lys Leu Val Lys Leu Ser Ala Val Gln Phe Met Leu
 625 630 635 640
 Asn Asn His Thr Ser Glu His Phe Ser Phe Leu Gly Ile Asn Asn Gln
 645 650 655
 Ser Asn Leu Thr Asp Met Arg Cys Arg Thr Thr Phe Tyr Thr Ala Leu

660										665					670				
Gly	Arg	Leu	Leu	Met	Val	Asp	Leu	Gly	Glu	Asp	Glu	Asp	Gln	Tyr	Glu				
		675						680					685						
Gln	Phe	Met	Leu	Pro	Leu	Thr	Ala	Ala	Phe	Glu	Ala	Val	Ala	Gln	Met				
		690					695					700							
Phe	Ser	Thr	Asn	Ser	Phe	Asn	Glu	Gln	Glu	Ala	Lys	Arg	Thr	Leu	Val				
		705				710					715				720				
Gly	Leu	Val	Arg	Asp	Leu	Arg	Gly	Ile	Ala	Phe	Ala	Phe	Asn	Ala	Lys				
				725					730					735					
Thr	Ser	Phe	Met	Met	Leu	Phe	Glu	Trp	Ile	Tyr	Pro	Ser	Tyr	Met	Pro				
			740					745						750					
Ile	Leu	Gln	Arg	Ala	Ile	Glu	Leu	Trp	Tyr	His	Asp	Pro	Ala	Cys	Thr				
		755					760					765							
Thr	Pro	Val	Leu	Lys	Leu	Met	Ala	Glu	Leu	Val	His	Asn	Arg	Ser	Gln				
		770				775						780							
Arg	Leu	Gln	Phe	Asp	Val	Ser	Ser	Pro	Asn	Gly	Ile	Leu	Leu	Phe	Arg				
		785			790					795					800				
Glu	Thr	Ser	Lys	Met	Ile	Thr	Met	Tyr	Gly	Asn	Arg	Ile	Leu	Thr	Leu				
				805					810					815					
Gly	Glu	Val	Pro	Lys	Asp	Gln	Val	Tyr	Ala	Leu	Lys	Leu	Lys	Gly	Ile				
			820					825					830						
Ser	Ile	Cys	Phe	Ser	Met	Leu	Lys	Ala	Ala	Leu	Ser	Gly	Ser	Tyr	Val				
		835					840					845							
Asn	Phe	Gly	Val	Phe	Arg	Leu	Tyr	Gly	Asp	Asp	Ala	Leu	Asp	Asn	Ala				
		850				855					860								
Leu	Gln	Thr	Phe	Ile	Lys	Leu	Leu	Leu	Ser	Ile	Pro	His	Ser	Asp	Leu				
		865			870					875					880				
Leu	Asp	Tyr	Pro	Lys	Leu	Ser	Gln	Ser	Tyr	Tyr	Ser	Leu	Leu	Glu	Val				
				885					890					895					
Leu	Thr	Gln	Asp	His	Met	Asn	Phe	Ile	Ala	Ser	Leu	Glu	Pro	His	Val				
			900					905					910						
Ile	Met	Tyr	Ile	Leu	Ser	Ser	Ile	Ser	Glu	Gly	Leu	Thr	Ala	Leu	Asp				
		915					920					925							
Thr	Met	Val	Cys	Thr	Gly	Cys	Cys	Ser	Cys	Leu	Asp	His	Ile	Val	Thr				
		930				935					940								
Tyr	Leu	Phe	Lys	Gln	Leu	Ser	Arg	Ser	Thr	Lys	Lys	Arg	Thr	Thr	Pro				
		945			950					955					960				
Leu	Asn	Gln	Glu	Ser	Asp	Arg	Phe	Leu	His	Ile	Met	Gln	Gln	His	Pro				
				965					970					975					
Glu	Met	Ile	Gln	Gln	Met	Leu	Ser	Thr	Val	Leu	Asn	Ile	Ile	Ile	Phe				
			980					985					990						

Glu Asp Cys Arg Asn Gln Trp Ser Met Ser Arg Pro Leu Leu Gly Leu
 995 1000 1005

Ile Leu Leu Asn Glu Lys Tyr Phe Ser Asp Leu Arg Asn Ser Ile
 1010 1015 1020

Val Asn Ser Gln Pro Pro Glu Lys Gln Gln Ala Met His Leu Cys
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Phe Glu Asn Leu Met Glu Gly Ile Glu Arg Asn Leu Leu Thr Lys
 1040 1045 1050

Asn Arg Asp Arg Phe Thr Gln Asn Leu Ser Ala Phe Arg Arg Glu
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Val Asn Asp Ser Met Lys Asn Ser Thr Tyr Gly Val Asn Ser Asn
 1070 1075 1080

Asp Met Met Ser
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His Leu Tyr Ile Gly Thr Asp Leu Thr Gln Arg Ile Glu Ala Glu Lys
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Ala Leu Leu Glu Leu Ile Asp Ser Pro Glu Cys Leu Ser Lys Cys Gln
 35 40 45

Leu Leu Leu Glu Gln Gly Thr Thr Ser Tyr Ala Gln Leu Leu Ala Ala
 50 55 60

Thr Cys Leu Ser Lys Leu Val Ser Arg Val Ser Pro Leu Pro Val Glu
 65 70 75 80

Gln Arg Met Asp Ile Arg Asn Tyr Ile Leu Asn Tyr Val Ala Ser Gln
 85 90 95

Pro Lys Leu Ala Pro Phe Val Ile Gln Ala Leu Ile Gln Val Ile Ala
 100 105 110

Lys Ile Thr Lys Leu Gly Trp Phe Glu Val Gln Lys Asp Gln Phe Val
 115 120 125

Phe Arg Glu Ile Ile Ala Asp Val Lys Lys Phe Leu Gln Gly Thr Val
 130 135 140

Glu His Cys Ile Ile Gly Val Ile Ile Leu Ser Glu Leu Thr Gln Glu
 145 150 155 160

Met Asn Leu Val Asp Tyr Ser Arg Pro Ser Ala Lys His Arg Lys Ile
 165 170 175

Ala Thr Ser Phe Arg Asp Thr Ser Leu Lys Asp Val Leu Val Leu Ala
 180 185 190

Cys Ser Leu Leu Lys Glu Val Phe Ala Lys Pro Leu Asn Leu Gln Asp
 195 200 205
 Gln Cys Gln Gln Asn Leu Val Met Gln Val Leu Lys Leu Val Leu Asn
 210 215 220
 Cys Leu Asn Phe Asp Phe Ile Gly Ser Ser Ala Asp Glu Ser Ala Asp
 225 230 235 240
 Asp Leu Cys Thr Val Gln Ile Pro Thr Thr Trp Arg Thr Ile Phe Leu
 245 250 255
 Glu Pro Glu Thr Leu Asp Leu Phe Phe Asn Leu Tyr His Ser Leu Pro
 260 265 270
 Pro Leu Leu Ser Gln Leu Ala Leu Ser Cys Leu Val Gln Phe Ala Ser
 275 280 285
 Thr Arg Arg Ser Leu Phe Asn Ser Pro Glu Arg Ala Lys Tyr Leu Gly
 290 295 300
 Asn Leu Ile Lys Gly Val Lys Arg Ile Leu Glu Asn Pro Gln Gly Leu
 305 310 315 320
 Ser Asp Pro Gly Asn Tyr His Glu Phe Cys Arg Phe Leu Ala Arg Leu
 325 330 335
 Lys Thr Asn Tyr Gln Leu Gly Glu Leu Val Met Val Lys Glu Tyr Pro
 340 345 350
 Glu Val Ile Arg Leu Ile Ala Asn Phe Thr Ile Thr Ser Leu Gln His
 355 360 365
 Trp Glu Phe Ala Pro Asn Ser Val His Tyr Leu Leu Thr Leu Trp Gln
 370 375 380
 Arg Met Val Ala Ser Val Pro Phe Val Lys Ser Thr Glu Pro His Leu
 385 390 395 400
 Leu Asp Thr Tyr Ala Pro Glu Ile Thr Lys Ala Phe Ile Thr Ser Arg
 405 410 415
 Leu Asp Ser Val Ala Ile Val Val Arg Asp His Leu Asp Asp Pro Leu
 420 425 430
 Asp Asp Thr Ala Thr Val Phe Gln Gln Leu Glu Gln Leu Cys Thr Val
 435 440 445
 Ser Arg Cys Glu Tyr Glu Lys Thr Cys Ala Leu Leu Val Gln Leu Phe
 450 455 460
 Asp Gln Asn Ala Gln Asn Tyr Gln Lys Leu Leu His Pro Tyr Ser Gly
 465 470 475 480
 Val Thr Val Asp Ile Thr Ile Gln Glu Gly Arg Leu Ala Trp Leu Val
 485 490 495
 Tyr Leu Val Gly Thr Val Val Gly Gly Arg Leu Thr Tyr Thr Ser Thr
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 Asp Glu His Asp Ala Met Asp Gly Glu Leu Ser Cys Arg Val Phe Gln

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Leu	Ile	Ser	Leu	Met	Asp	Thr	Gly	Leu	Pro	Arg	Cys	Cys	Asn	Glu	Lys
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Ile	Glu	Leu	Ala	Ile	Leu	Trp	Phe	Leu	Asp	Gln	Phe	Arg	Lys	Thr	Tyr
545					550					555					560
Val	Gly	Asp	Gln	Leu	Gln	Arg	Thr	Ser	Lys	Val	Tyr	Ala	Arg	Met	Ser
				565					570					575	
Glu	Val	Leu	Gly	Ile	Thr	Asp	Asp	Asn	His	Val	Leu	Glu	Thr	Phe	Met
			580					585					590		
Thr	Lys	Ile	Val	Thr	Asn	Leu	Lys	Tyr	Trp	Gly	Arg	Tyr	Glu	Pro	Val
		595					600					605			
Ile	Ser	Arg	Thr	Leu	Gln	Phe	Leu	Asn	Asp	Leu	Ser	Val	Gly	Tyr	Ile
	610					615					620				
Leu	Leu	Lys	Lys	Leu	Val	Lys	Ile	Asp	Ala	Val	Lys	Phe	Met	Leu	Lys
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Asn	His	Thr	Ser	Glu	His	Phe	Pro	Phe	Leu	Gly	Ile	Ser	Asp	Asn	His
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Ser	Leu	Ser	Asp	Phe	Arg	Cys	Arg	Thr	Thr	Phe	Tyr	Thr	Ala	Leu	Thr
			660					665					670		
Arg	Leu	Leu	Met	Val	Asp	Leu	Gly	Glu	Asp	Glu	Asp	Glu	Phe	Glu	Asn
			675				680					685			
Phe	Met	Leu	Pro	Leu	Thr	Val	Ala	Phe	Glu	Thr	Val	Leu	Gln	Ile	Phe
	690					695					700				
Asn	Asn	Asn	Phe	Lys	Gln	Glu	Asp	Val	Lys	Arg	Met	Leu	Ile	Gly	Leu
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Ala	Arg	Asp	Leu	Arg	Gly	Ile	Ala	Phe	Ala	Leu	Asn	Thr	Lys	Thr	Ser
				725					730					735	
Tyr	Thr	Met	Leu	Phe	Asp	Trp	Met	Tyr	Pro	Thr	Tyr	Leu	Pro	Leu	Leu
			740					745					750		
Gln	Asn	Ala	Val	Glu	Arg	Trp	Tyr	Gly	Glu	Pro	Thr	Cys	Thr	Thr	Pro
		755					760					765			
Ile	Leu	Lys	Leu	Met	Ala	Glu	Leu	Met	Gln	Asn	Arg	Ser	Gln	Arg	Leu
	770					775					780				
Asn	Phe	Asp	Val	Ser	Ser	Pro	Asn	Gly	Ile	Leu	Leu	Phe	Arg	Glu	Ala
785					790					795					800
Ser	Lys	Met	Val	Cys	Thr	Tyr	Gly	Asn	Gln	Ile	Leu	Ser	Leu	Gly	Ser
				805					810					815	
Leu	Ser	Lys	Asp	Gln	Ile	Tyr	Pro	Met	Lys	Leu	Lys	Gly	Ile	Ser	Ile
			820					825					830		
Cys	Tyr	Ser	Ala	Leu	Lys	Ser	Ala	Leu	Cys	Gly	Asn	Tyr	Val	Ser	Phe
		835					840					845			

Gly Val Phe Lys Leu Tyr Gly Asp Asn His Phe Asp Asn Val Leu Gln
 850 855 860
 Ala Phe Val Lys Met Leu Leu Ser Val Ser His Ser Asp Leu Leu Gln
 865 870 875 880
 Tyr Arg Lys Leu Ser Gln Ser Tyr Tyr Pro Leu Leu Glu Cys Leu Thr
 885 890 895
 Gln Asp His Met Ser Phe Ile Ile Asn Leu Glu Pro Pro Val Leu Met
 900 905 910
 Tyr Val Leu Thr Ser Ile Ser Glu Gly Leu Thr Thr Leu Asp Thr Val
 915 920 925
 Val Ser Ser Ser Cys Cys Thr Ser Leu Asp Tyr Ile Val Thr Tyr Leu
 930 935 940
 Phe Lys His Ile Ala Lys Glu Gly Lys Lys Pro Leu Arg Cys Arg Glu
 945 950 955 960
 Ala Thr Gln Ala Gly Gln Arg Leu Leu His Phe Met Gln Gln Asn Pro
 965 970 975
 Asp Val Leu Gln Gln Met Met Ser Val Leu Met Asn Thr Ile Val Phe
 980 985 990
 Glu Asp Cys Arg Asn Gln Trp Ser Val Ser Arg Pro Leu Leu Gly Leu
 995 1000 1005
 Ile Leu Leu Asn Glu Lys Tyr Phe Ser Glu Leu Arg Ala Ser Leu
 1010 1015 1020
 Ile Asn Ser Gln Pro Leu Pro Lys Gln Glu Val Leu Ala Gln Cys
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 Phe Arg Asn Leu Met Glu Gly Val Glu Gln Asn Leu Ser Val Lys
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 Asn Arg Asp Arg Phe Thr Gln Asn Leu Ser Val Phe Arg Arg Asp
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 Leu Asp Met Met Ser
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 Ser Ser Ser Ser Val His Glu Pro Lys Met Asp Ala Leu Ile Ile Pro
 35 40 45

Val Thr Met Glu Val Pro Cys Asp Ser Arg Gly Gln Arg Met Trp Trp
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 Ala Phe Leu Ala Ser Ser Met Val Thr Phe Phe Gly Gly Leu Phe Ile
 65 70 75 80
 Ile Leu Leu Trp Arg Thr Leu Lys Tyr Leu Trp Thr Val Cys Cys His
 85 90 95
 Cys Gly Gly Lys Thr Lys Glu Ala Gln Lys Ile Asn Asn Gly Ser Ser
 100 105 110
 Gln Ala Asp Gly Thr Leu Lys Pro Val Asp Glu Lys Glu Glu Ala Val
 115 120 125
 Ala Ala Glu Val Gly Trp Met Thr Ser Val Lys Asp Trp Ala Gly Val
 130 135 140
 Met Ile Ser Ala Gln Thr Leu Thr Gly Arg Val Leu Val Val Leu Val
 145 150 155 160
 Phe Ala Leu Ser Ile Gly Ala Leu Val Ile Tyr Phe Ile Asp Ser Ser
 165 170 175
 Asn Pro Ile Glu Ser Cys Gln Asn Phe Tyr Lys Asp Phe Thr Leu Gln
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 Ile Asp Met Ala Phe Asn Val Phe Phe Leu Leu Tyr Phe Gly Leu Arg
 195 200 205
 Phe Ile Ala Ala Asn Asp Lys Leu Trp Phe Trp Leu Glu Val Asn Ser
 210 215 220
 Val Val Asp Phe Phe Thr Val Pro Pro Val Phe Val Ser Val Tyr Leu
 225 230 235 240
 Asn Arg Ser Trp Leu Gly Leu Arg Phe Leu Arg Ala Leu Arg Leu Ile
 245 250 255
 Gln Phe Ser Glu Ile Leu Gln Phe Leu Asn Ile Leu Lys Thr Ser Asn
 260 265 270
 Ser Ile Lys Leu Val Asn Leu Leu Ser Ile Phe Ile Ser Thr Trp Leu
 275 280 285
 Thr Ala Ala Gly Phe Ile His Leu Val Glu Asn Ser Gly Asp Pro Trp
 290 295 300
 Glu Asn Phe Gln Asn Asn Gln Ala Leu Thr Tyr Trp Glu Cys Val Tyr
 305 310 315 320
 Leu Leu Met Val Thr Met Ser Thr Val Gly Tyr Gly Asp Val Tyr Ala
 325 330 335
 Lys Thr Thr Leu Gly Arg Leu Phe Met Val Phe Phe Ile Leu Gly Gly
 340 345 350
 Leu Ala Met Phe Ala Ser Tyr Val Pro Glu Ile Ile Glu Leu Ile Gly
 355 360 365
 Asn Arg Lys Lys Tyr Gly Gly Ser Tyr Ser Ala Val Ser Gly Arg Lys

370					375					380					
His	Ile	Val	Val	Cys	Gly	His	Ile	Thr	Leu	Glu	Ser	Val	Ser	Asn	Phe
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Leu	Lys	Asp	Phe	Leu	His	Lys	Asp	Arg	Asp	Asp	Val	Asn	Val	Glu	Ile
				405					410					415	
Val	Phe	Leu	His	Asn	Ile	Ser	Pro	Asn	Leu	Glu	Leu	Glu	Ala	Leu	Phe
			420					425					430		
Lys	Arg	His	Phe	Thr	Gln	Val	Glu	Phe	Tyr	Gln	Gly	Ser	Val	Leu	Asn
		435					440					445			
Pro	His	Asp	Leu	Ala	Arg	Val	Lys	Ile	Glu	Ser	Ala	Asp	Ala	Cys	Leu
		450					455					460			
Ile	Leu	Ala	Asn	Lys	Tyr	Cys	Ala	Asp	Pro	Asp	Ala	Glu	Asp	Ala	Ser
465							470					475			480
Asn	Ile	Met	Arg	Val	Ile	Ser	Ile	Lys	Asn	Tyr	His	Pro	Lys	Ile	Arg
			485						490					495	
Ile	Ile	Thr	Gln	Met	Leu	Gln	Tyr	His	Asn	Lys	Ala	His	Leu	Leu	Asn
			500					505					510		
Ile	Pro	Ser	Trp	Asn	Trp	Lys	Glu	Gly	Asp	Asp	Ala	Ile	Cys	Leu	Ala
		515					520					525			
Glu	Leu	Lys	Leu	Gly	Phe	Ile	Ala	Gln	Ser	Cys	Leu	Ala	Gln	Gly	Leu
		530					535					540			
Ser	Thr	Met	Leu	Ala	Asn	Leu	Phe	Ser	Met	Arg	Ser	Phe	Ile	Lys	Ile
545							550					555			560
Glu	Glu	Asp	Thr	Trp	Gln	Lys	Tyr	Tyr	Leu	Glu	Gly	Val	Ser	Asn	Glu
			565						570					575	
Met	Tyr	Thr	Glu	Tyr	Leu	Ser	Ser	Ala	Phe	Val	Gly	Leu	Ser	Phe	Pro
			580					585					590		
Thr	Val	Cys	Glu	Leu	Cys	Phe	Val	Lys	Leu	Lys	Leu	Leu	Met	Ile	Ala
		595					600					605			
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		610					615					620			
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625							630					635			640
Ser	Asp	Ala	Lys	Glu	Val	Lys	Arg	Ala	Phe	Phe	Tyr	Cys	Lys	Ala	Cys
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His	Asp	Asp	Ile	Thr	Asp	Pro	Lys	Arg	Ile	Lys	Lys	Cys	Gly	Cys	Lys
			660					665					670		
Arg	Leu	Glu	Asp	Glu	Gln	Pro	Ser	Thr	Leu	Ser	Pro	Lys	Lys	Lys	Gln
		675					680					685			
Arg	Asn	Gly	Gly	Met	Arg	Asn	Ser	Pro	Asn	Thr	Ser	Pro	Lys	Leu	Met
		690					695					700			

Arg His Asp Pro Leu Leu Ile Pro Gly Asn Asp Gln Ile Asp Asn Met
 705 710 715 720
 Asp Ser His Val Lys Lys Tyr Asp Ser Thr Gly Met Phe His Trp Cys
 725 730 735
 Ala Pro Lys Glu Ile Glu Lys Val Ile Leu Thr Arg Ser Glu Ala Ala
 740 745 750
 Met Thr Val Leu Ser Gly His Val Val Val Cys Ile Phe Gly Asp Val
 755 760 765
 Ser Ser Ala Leu Ile Gly Leu Arg Asn Leu Val Met Pro Leu Arg Ala
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 Ser Asn Phe His Tyr His Glu Leu Lys His Ile Val Phe Val Gly Ser
 785 790 795 800
 Ile Glu Tyr Leu Lys Arg Glu Trp Glu Thr Leu His Asn Phe Pro Lys
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 Val Ser Ile Leu Pro Gly Thr Pro Leu Ser Arg Ala Asp Leu Arg Ala
 820 825 830
 Val Asn Ile Asn Leu Cys Asp Met Cys Val Ile Leu Ser Ala Asn Gln
 835 840 845
 Asn Asn Ile Asp Asp Thr Ser Leu Gln Asp Lys Glu Cys Ile Leu Ala
 850 855 860
 Ser Leu Asn Ile Lys Ser Met Gln Phe Asp Asp Ser Ile Gly Val Leu
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 Gln Ala Asn Ser Gln Gly Phe Thr Pro Pro Gly Met Asp Arg Ser Ser
 885 890 895
 Pro Asp Asn Ser Pro Val His Gly Met Leu Arg Gln Pro Ser Ile Thr
 900 905 910
 Thr Gly Val Asn Ile Pro Ile Ile Thr Glu Leu Val Asn Asp Thr Asn
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 Val Gln Phe Leu Asp Gln Asp Asp Asp Asp Asp Pro Asp Thr Glu Leu
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 Tyr Leu Thr Gln Pro Phe Ala Cys Gly Thr Ala Phe Ala Val Ser Val
 945 950 955 960
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 980 985 990
 Leu Ile Ala Glu Glu Asn Ala Leu Arg Gly Gly Tyr Ser Thr Pro Gln
 995 1000 1005
 Thr Leu Ala Asn Arg Asp Arg Cys Arg Val Ala Gln Leu Ala Leu
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 Leu Asp Gly Pro Phe Ala Asp Leu Gly Asp Gly Gly Cys Tyr Gly
 1025 1030 1035

Asp Leu Phe Cys Lys Ala Leu Lys Thr Tyr Asn Met Leu Cys Phe
 1040 1045 1050
 Gly Ile Tyr Arg Leu Arg Asp Ala His Leu Ser Thr Pro Ser Gln
 1055 1060 1065
 Cys Thr Lys Arg Tyr Val Ile Thr Asn Pro Pro Tyr Glu Phe Glu
 1070 1075 1080
 Leu Val Pro Thr Asp Leu Ile Phe Cys Leu Met Gln Phe Asp His
 1085 1090 1095
 Asn Ala Gly Gln Ser Arg Ala Ser Leu Ser His Ser Ser His Ser
 1100 1105 1110
 Ser Gln Ser Ser Ser Lys Lys Ser Ser Ser Val His Ser Ile Pro
 1115 1120 1125
 Ser Thr Ala Asn Arg Gln Asn Arg Pro Lys Ser Arg Glu Ser Arg
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 Asp Lys Gln Lys Tyr Val Gln Glu Glu Arg Leu
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 Thr Thr His Ala Met Leu Asp Arg Glu Asn Pro Asp Pro His Glu Ala
 35 40 45
 Glu Leu Met Arg Lys Ile Val Val Ser Val Thr Asp Cys Gly Arg Pro
 50 55 60
 Pro Leu Lys Ala Thr Ser Ser Ala Thr Val Phe Val Asn Leu Leu Asp
 65 70 75 80
 Leu Asn Asp Asn Asp Pro Thr Phe Gln Asn Leu Pro Phe Val Ala Glu
 85 90 95
 Val Leu Glu Gly Ile Pro Ala Gly Val Ser Ile Tyr Gln Val Val Ala
 100 105 110
 Ile Asp Leu Asp Glu Gly Leu Asn Gly Leu Val Ser Tyr Arg Met Pro
 115 120 125
 Val Gly Met Pro Arg Met Asp Phe Leu Ile Asn Ser Ser Ser Gly Val
 130 135 140
 Val Val Thr Thr Thr Glu Leu Asp Arg Glu Arg Ile Ala Glu Tyr Gln
 145 150 155 160
 Leu Arg Val Val Ala Ser Asp Ala Gly Thr Pro Thr Lys Ser Ser Thr

165										170					175				
Ser	Thr	Leu	Thr	Ile	His	Leu	Leu	Asp	Val	Asn	Asp	Glu	Thr	Pro	Thr				
			180					185					190						
Phe	Phe	Pro	Ala	Val	Tyr	Asn	Val	Ser	Val	Ser	Glu	Asp	Val	Pro	Arg				
		195					200					205							
Glu	Phe	Arg	Val	Val	Trp	Leu	Asn	Cys	Thr	Asp	Asn	Asp	Val	Gly	Leu				
	210					215					220								
Asn	Ala	Glu	Leu	Ser	Tyr	Phe	Ile	Thr	Gly	Gly	Asn	Val	Asp	Gly	Lys				
225					230					235					240				
Phe	Ser	Val	Gly	Tyr	Arg	Asp	Ala	Val	Val	Arg	Thr	Val	Val	Gly	Leu				
				245				250						255					
Asp	Arg	Glu	Thr	Ala	Ala	Tyr	Met	Leu	Ile	Leu	Glu	Ala	Ile	Asp					
			260				265					270							
Asn	Gly	Pro	Val	Gly	Lys	Arg	His	Thr	Gly	Thr	Ala	Thr	Val	Phe	Val				
	275						280					285							
Thr	Val	Leu	Asp	Val	Asn	Asp	Asn	Arg	Pro	Ile	Phe	Leu	Gln	Ser	Ser				
	290					295					300								
Tyr	Glu	Ala	Ser	Val	Pro	Glu	Asp	Ile	Pro	Glu	Gly	His	Ser	Ile	Leu				
305					310					315					320				
Gln	Leu	Lys	Ala	Thr	Asp	Ala	Asp	Glu	Gly	Glu	Phe	Gly	Arg	Val	Trp				
				325					330					335					
Tyr	Arg	Ile	Leu	His	Gly	Asn	His	Gly	Asn	Asn	Phe	Arg	Ile	His	Val				
			340					345					350						
Ser	Asn	Gly	Leu	Leu	Met	Arg	Gly	Pro	Arg	Pro	Leu	Asp	Arg	Glu	Arg				
		355					360					365							
Asn	Ser	Ser	His	Val	Leu	Ile	Val	Glu	Ala	Tyr	Asn	His	Asp	Leu	Gly				
	370					375					380								
Pro	Met	Arg	Ser	Ser	Val	Arg	Val	Ile	Val	Tyr	Val	Glu	Asp	Ile	Asn				
385					390					395					400				
Asp	Glu	Ala	Pro	Val	Phe	Thr	Gln	Gln	Gln	Tyr	Ser	Arg	Leu	Gly	Leu				
				405					410					415					
Arg	Glu	Thr	Ala	Gly	Ile	Gly	Thr	Ser	Val	Ile	Val	Val	Gln	Ala	Thr				
			420					425					430						
Asp	Arg	Asp	Ser	Gly	Asp	Gly	Gly	Leu	Val	Asn	Tyr	Arg	Ile	Leu	Ser				
		435					440					445							
Gly	Ala	Glu	Gly	Lys	Phe	Glu	Ile	Asp	Glu	Ser	Thr	Gly	Leu	Ile	Ile				
	450					455					460								
Thr	Val	Asn	Tyr	Leu	Asp	Tyr	Glu	Thr	Lys	Thr	Ser	Tyr	Met	Met	Asn				
465					470					475					480				
Val	Ser	Ala	Thr	Asp	Gln	Ala	Pro	Pro	Phe	Asn	Gln	Gly	Phe	Cys	Ser				
				485					490					495					

Val Tyr Ile Thr Leu Leu Asn Glu Leu Asp Glu Ala Val Gln Phe Ser
 500 505 510
 Asn Ala Ser Tyr Glu Ala Ala Ile Leu Glu Asn Leu Ala Leu Gly Thr
 515 520 525
 Glu Ile Val Arg Val Gln Ala Tyr Ser Ile Asp Asn Leu Asn Gln Ile
 530 535 540
 Thr Tyr Arg Phe Asp Ala Tyr Thr Ser Thr Gln Ala Lys Ala Leu Phe
 545 550 555 560
 Lys Ile Asp Ala Ile Thr Gly Val Ile Thr Val Gln Gly Leu Val Asp
 565 570 575
 Arg Glu Lys Gly Asp Phe Tyr Thr Leu Thr Val Val Ala Asp Asp Gly
 580 585 590
 Gly Pro Lys Val Asp Ser Thr Val Val Val Tyr Ile Thr Val Leu Asp
 595 600 605
 Glu Asn Asp Asn Ser Pro Arg Phe Asp Phe Thr Ser Asp Ser Ala Val
 610 615 620
 Ser Ile Pro Glu Asp Cys Pro Val Gly Gln Arg Val Ala Thr Val Lys
 625 630 635 640
 Ala Trp Asp Pro Asp Ala Gly Ser Asn Gly Gln Val Val Phe Ser Leu
 645 650 655
 Ala Ser Gly Asn Ile Ala Gly Ala Phe Glu Ile Val Thr Thr Asn Asp
 660 665 670
 Ser Ile Gly Glu Val Phe Val Ala Arg Pro Leu Asp Arg Glu Glu Leu
 675 680 685
 Asp His Tyr Ile Leu Gln Val Val Ala Ser Asp Arg Gly Thr Pro Pro
 690 695 700
 Arg Lys Lys Asp His Ile Leu Gln Val Thr Ile Leu Asp Ile Asn Asp
 705 710 715 720
 Asn Pro Pro Val Ile Glu Ser Pro Phe Gly Tyr Asn Val Ser Val Asn
 725 730 735
 Glu Asn Val Gly Gly Gly Thr Ala Val Val Gln Val Arg Ala Thr Asp
 740 745 750
 Arg Asp Ile Gly Ile Asn Ser Val Leu Ser Tyr Tyr Ile Thr Glu Gly
 755 760 765
 Asn Lys Asp Met Thr Phe Arg Met Asp Arg Ile Ser Gly Glu Ile Ala
 770 775 780
 Thr Arg Pro Ala Pro Pro Asp Arg Glu Arg Gln Ser Phe Tyr His Leu
 785 790 795 800
 Val Ala Thr Val Glu Asp Glu Gly Thr Pro Thr Leu Ser Ala Thr Thr
 805 810 815
 His Val Tyr Val Thr Ile Val Asp Glu Asn Asp Asn Ala Pro Met Phe
 820 825 830

Gln Gln Pro His Tyr Glu Val Leu Leu Asp Glu Gly Pro Asp Thr Leu
 835 840 845
 Asn Thr Ser Leu Ile Thr Ile Gln Ala Leu Asp Leu Asp Glu Gly Pro
 850 855 860
 Asn Gly Thr Val Thr Tyr Ala Ile Val Ala Gly Asn Ile Val Asn Thr
 865 870 875 880
 Phe Arg Ile Asp Arg His Met Gly Val Ile Thr Ala Ala Lys Glu Leu
 885 890 895
 Asp Tyr Glu Ile Ser His Gly Arg Tyr Thr Leu Ile Val Thr Ala Thr
 900 905 910
 Asp Gln Cys Pro Ile Leu Ser His Arg Leu Thr Ser Thr Thr Thr Val
 915 920 925
 Leu Val Asn Val Asn Asp Ile Asn Asp Asn Val Pro Thr Phe Pro Arg
 930 935 940
 Asp Tyr Glu Gly Pro Phe Glu Val Thr Glu Gly Gln Pro Gly Pro Arg
 945 950 955 960
 Val Trp Thr Phe Leu Ala His Asp Arg Asp Ser Gly Pro Asn Gly Gln
 965 970 975
 Val Glu Tyr Ser Ile Met Asp Gly Asp Pro Leu Gly Glu Phe Val Ile
 980 985 990
 Ser Pro Val Glu Gly Val Leu Arg Val Arg Lys Asp Val Glu Leu Asp
 995 1000 1005
 Arg Glu Thr Ile Ala Phe Tyr Asn Leu Thr Ile Cys Ala Arg Asp
 1010 1015 1020
 Arg Gly Met Pro Pro Leu Ser Ser Thr Met Leu Val Gly Ile Arg
 1025 1030 1035
 Val Leu Asp Ile Asn Asp Asn Asp Pro Val Leu Leu Asn Leu Pro
 1040 1045 1050
 Met Asn Ile Thr Ile Ser Glu Asn Ser Pro Val Ser Ser Phe Val
 1055 1060 1065
 Ala His Val Leu Ala Ser Asp Ala Asp Ser Gly Cys Asn Ala Arg
 1070 1075 1080
 Leu Thr Phe Asn Ile Thr Ala Gly Asn Arg Glu Arg Ala Phe Phe
 1085 1090 1095
 Ile Asn Ala Thr Thr Gly Ile Val Thr Val Asn Arg Pro Leu Asp
 1100 1105 1110
 Arg Glu Arg Ile Pro Glu Tyr Lys Leu Thr Ile Ser Val Lys Asp
 1115 1120 1125
 Asn Pro Glu Asn Pro Arg Ile Ala Arg Arg Asp Tyr Asp Leu Leu
 1130 1135 1140
 Leu Ile Phe Leu Ser Asp Glu Asn Asp Asn His Pro Leu Phe Thr

1145	1150	1155
Lys Ser Thr Tyr Gln Ala Glu Val Met Glu Asn Ser Pro Ala Gly 1160 1165 1170		
Thr Pro Leu Thr Val Leu Asn Gly Pro Ile Leu Ala Leu Asp Ala 1175 1180 1185		
Asp Gln Asp Ile Tyr Ala Val Val Thr Tyr Gln Leu Leu Gly Ala 1190 1195 1200		
Gln Ser Gly Leu Phe Asp Ile Asn Ser Ser Thr Gly Val Val Thr 1205 1210 1215		
Val Arg Ser Gly Val Ile Ile Asp Arg Glu Ala Phe Ser Pro Pro 1220 1225 1230		
Ile Leu Glu Leu Leu Leu Leu Ala Glu Asp Ile Gly Leu Leu Asn 1235 1240 1245		
Ser Thr Ala His Leu Leu Ile Thr Ile Leu Asp Asp Asn Asp Asn 1250 1255 1260		
Arg Pro Thr Phe Ser Pro Ala Thr Leu Thr Val His Leu Leu Glu 1265 1270 1275		
Asn Cys Pro Pro Gly Phe Ser Val Leu Gln Val Thr Ala Thr Asp 1280 1285 1290		
Glu Asp Ser Gly Leu Asn Gly Glu Leu Val Tyr Arg Ile Glu Ala 1295 1300 1305		
Gly Ala Gln Asp Arg Phe Leu Ile His Leu Val Thr Gly Val Ile 1310 1315 1320		
Arg Val Gly Asn Ala Thr Ile Asp Arg Glu Glu Gln Glu Ser Tyr 1325 1330 1335		
Arg Leu Thr Val Val Ala Thr Asp Arg Gly Thr Val Pro Leu Ser 1340 1345 1350		
Gly Thr Ala Ile Val Thr Ile Leu Ile Asp Asp Ile Asn Asp Ser 1355 1360 1365		
Arg Pro Glu Phe Leu Asn Pro Ile Gln Thr Val Ser Val Leu Glu 1370 1375 1380		
Ser Ala Glu Pro Gly Thr Val Ile Ala Asn Ile Thr Ala Ile Asp 1385 1390 1395		
His Asp Leu Asn Pro Lys Leu Glu Tyr His Ile Val Gly Ile Val 1400 1405 1410		
Ala Lys Asp Asp Thr Asp Arg Leu Val Pro Asn Gln Glu Asp Ala 1415 1420 1425		
Phe Ala Val Asn Ile Asn Thr Gly Ser Val Met Val Lys Ser Pro 1430 1435 1440		
Met Asn Arg Glu Leu Val Ala Thr Tyr Glu Val Thr Leu Ser Val 1445 1450 1455		

Ile Asp 1460	Asn Ala Ser Asp 1465	Leu Pro Glu Arg Ser Val 1470	Ser Val Pro
Asn Ala 1475	Lys Leu Thr Val 1480	Asn Val Leu Asp Val 1485	Asp Asn Thr
Pro Gln 1490	Phe Lys Pro Phe 1495	Gly Ile Thr Tyr Tyr 1500	Met Glu Arg Ile
Leu Glu 1505	Gly Ala Thr Pro 1510	Gly Thr Thr Leu Ile 1515	Ala Val Ala Ala
Val Asp 1520	Pro Asp Lys Gly 1525	Leu Asn Gly Leu Val 1530	Thr Tyr Thr Leu
Leu Asp 1535	Leu Val Pro Pro 1540	Gly Tyr Val Gln Leu 1545	Glu Asp Ser Ser
Ala Gly 1550	Lys Val Ile Ala 1555	Asn Arg Thr Val Asp 1560	Tyr Glu Glu Val
His Trp 1565	Leu Asn Phe Thr 1570	Val Arg Ala Ser Asp 1575	Asn Gly Ser Pro
Pro Arg 1580	Ala Ala Glu Ile 1585	Pro Val Tyr Leu Glu 1590	Ile Val Asp Ile
Asn Asp 1595	Asn Asn Pro Ile 1600	Phe Asp Gln Pro Ser 1605	Tyr Gln Glu Ala
Val Phe 1610	Glu Asp Val Pro 1615	Val Gly Thr Ile Ile 1620	Leu Thr Val Thr
Ala Thr 1625	Asp Ala Asp Ser 1630	Gly Asn Phe Ala Leu 1635	Ile Glu Tyr Ser
Leu Gly 1640	Asp Gly Glu Ser 1645	Lys Phe Ala Ile Asn 1650	Pro Thr Thr Gly
Asp Ile 1655	Tyr Val Leu Ser 1660	Ser Leu Asp Arg Glu 1665	Lys Lys Asp His
Tyr Ile 1670	Leu Thr Ala Leu 1675	Ala Lys Asp Asn Pro 1680	Gly Asp Val Ala
Ser Asn 1685	Arg Arg Glu Asn 1690	Ser Val Gln Val Val 1695	Ile Gln Val Leu
Asp Val 1700	Asn Asp Cys Arg 1705	Pro Gln Phe Ser Lys 1710	Pro Gln Phe Ser
Thr Ser 1715	Val Tyr Glu Asn 1720	Glu Pro Ala Gly Thr 1725	Ser Val Ile Thr
Met Met 1730	Ala Thr Asp Gln 1735	Asp Glu Gly Pro Asn 1740	Gly Glu Leu Thr
Tyr Ser 1745	Leu Glu Gly Pro 1750	Gly Val Glu Ala Phe 1755	His Val Asp Met
Asp Ser 1760	Gly Leu Val Thr 1765	Thr Gln Arg Pro Leu 1770	Gln Ser Tyr Glu

Lys	Phe	Ser	Leu	Thr	Val	Val	Ala	Thr	Asp	Gly	Gly	Glu	Pro	Pro
1775						1780					1785			
Leu	Trp	Gly	Thr	Thr	Met	Leu	Leu	Val	Glu	Val	Ile	Asp	Val	Asn
1790						1795					1800			
Asp	Asn	Arg	Pro	Val	Phe	Val	Arg	Pro	Pro	Asn	Gly	Thr	Ile	Leu
1805						1810					1815			
His	Ile	Arg	Glu	Glu	Ile	Pro	Leu	Arg	Ser	Asn	Val	Tyr	Glu	Val
1820						1825					1830			
Tyr	Ala	Thr	Asp	Lys	Asp	Glu	Gly	Leu	Asn	Gly	Ala	Val	Arg	Tyr
1835						1840					1845			
Ser	Phe	Leu	Lys	Thr	Ala	Gly	Asn	Arg	Asp	Trp	Glu	Phe	Phe	Ile
1850						1855					1860			
Ile	Asp	Pro	Ile	Ser	Gly	Leu	Ile	Gln	Thr	Ala	Gln	Arg	Leu	Asp
1865						1870					1875			
Arg	Glu	Ser	Gln	Ala	Val	Tyr	Ser	Leu	Ile	Leu	Val	Ala	Ser	Asp
1880						1885					1890			
Leu	Gly	Gln	Pro	Val	Pro	Tyr	Glu	Thr	Met	Gln	Pro	Leu	Gln	Val
1895						1900					1905			
Ala	Leu	Glu	Asp	Ile	Asp	Asp	Asn	Glu	Pro	Leu	Phe	Val	Arg	Pro
1910						1915					1920			
Pro	Lys	Gly	Ser	Pro	Gln	Tyr	Gln	Leu	Leu	Thr	Val	Pro	Glu	His
1925						1930					1935			
Ser	Pro	Arg	Gly	Thr	Leu	Val	Gly	Asn	Val	Thr	Gly	Ala	Val	Asp
1940						1945					1950			
Ala	Asp	Glu	Gly	Pro	Asn	Ala	Ile	Val	Tyr	Tyr	Phe	Ile	Ala	Ala
1955						1960					1965			
Gly	Asn	Glu	Glu	Lys	Asn	Phe	His	Leu	Gln	Pro	Asp	Gly	Cys	Leu
1970						1975					1980			
Leu	Val	Leu	Arg	Asp	Leu	Asp	Arg	Glu	Arg	Glu	Ala	Ile	Phe	Ser
1985						1990					1995			
Phe	Ile	Val	Lys	Ala	Ser	Ser	Asn	Arg	Ser	Trp	Thr	Pro	Pro	Arg
2000						2005					2010			
Gly	Pro	Ser	Pro	Thr	Leu	Asp	Leu	Val	Ala	Asp	Leu	Thr	Leu	Gln
2015						2020					2025			
Glu	Val	Arg	Val	Val	Leu	Glu	Asp	Ile	Asn	Asp	Gln	Pro	Pro	Arg
2030						2035					2040			
Phe	Thr	Lys	Ala	Glu	Tyr	Thr	Ala	Gly	Val	Ala	Thr	Asp	Ala	Lys
2045						2050					2055			
Val	Gly	Ser	Glu	Leu	Ile	Gln	Val	Leu	Ala	Leu	Asp	Ala	Asp	Ile
2060						2065					2070			
Gly	Asn	Asn	Ser	Leu	Val	Phe	Tyr	Ser	Ile	Leu	Ala	Ile	His	Tyr

2075	2080	2085
Phe Arg Ala Leu Ala Asn Asp 2090	Ser Glu Asp Val Gly 2095	Gln Val Phe 2100
Thr Met Gly Ser Met Asp Gly 2105	Ile Leu Arg Thr Phe 2110	Asp Leu Phe 2115
Met Ala Tyr Ser Pro Gly Tyr 2120	Phe Val Val Asp Ile 2125	Val Ala Arg 2130
Asp Leu Ala Gly His Asn Asp 2135	Thr Ala Ile Ile Gly 2140	Ile Tyr Ile 2145
Leu Arg Asp Asp Gln Arg Val 2150	Lys Ile Val Ile Asn 2155	Glu Ile Pro 2160
Asp Arg Val Arg Gly Phe Glu 2165	Glu Glu Phe Ile His 2170	Leu Leu Ser 2175
Asn Ile Thr Gly Ala Ile Val 2180	Asn Thr Asp Asn Val 2185	Gln Phe His 2190
Val Asp Lys Lys Gly Arg Val 2195	Asn Phe Ala Gln Thr 2200	Glu Leu Leu 2205
Ile His Val Val Asn Arg Asp 2210	Thr Asn Arg Ile Leu 2215	Asp Val Asp 2220
Arg Val Ile Gln Met Ile Asp 2225	Glu Asn Lys Glu Gln 2230	Leu Arg Asn 2235
Leu Phe Arg Asn Tyr Asn Val 2240	Leu Asp Val Gln Pro 2245	Ala Ile Ser 2250
Val Arg Leu Pro Asp Asp Met 2255	Ser Ala Leu Gln Met 2260	Ala Ile Ile 2265
Val Leu Ala Ile Leu Leu Phe 2270	Leu Ala Ala Met Leu 2275	Phe Val Leu 2280
Met Asn Trp Tyr Tyr Arg Thr 2285	Val His Lys Arg Lys 2290	Leu Lys Ala 2295
Ile Val Ala Gly Ser Ala Gly 2300	Asn Arg Gly Phe Ile 2305	Asp Ile Met 2310
Asp Met Pro Asn Thr Asn Lys 2315	Tyr Ser Phe Asp Gly 2320	Ala Asn Pro 2325
Val Trp Leu Asp Pro Phe Cys 2330	Arg Asn Leu Glu Leu 2335	Ala Ala Gln 2340
Ala Glu His Glu Asp Asp Leu 2345	Pro Glu Asn Leu Ser 2350	Glu Ile Ala 2355
Asp Leu Trp Asn Ser Pro Thr 2360	Arg Thr His Gly Thr 2365	Phe Gly Arg 2370
Glu Pro Ala Ala Val Lys Pro 2375	Asp Asp Asp Arg Tyr 2380	Leu Arg Ala 2385

Ala Ile Gln Glu Tyr Asp Asn Ile Ala Lys Leu Gly Gln Ile Ile
 2390 2395 2400
 Arg Glu Gly Pro Ile Lys Gly Ser Leu Leu Lys Val Val Leu Glu
 2405 2410 2415
 Asp Tyr Leu Arg Leu Lys Lys Leu Phe Ala Gln Arg Met Val Gln
 2420 2425 2430
 Lys Ala Ser Ser Cys His Ser Ser Ile Ser Glu Leu Ile Gln Thr
 2435 2440 2445
 Glu Leu Asp Glu Glu Pro Gly Asp His Ser Pro Gly Gln Gly Ser
 2450 2455 2460
 Leu Arg Phe Arg His Lys Pro Pro Val Glu Leu Lys Gly Pro Asp
 2465 2470 2475
 Gly Ile His Val Val His Gly Ser Thr Gly Thr Leu Leu Ala Thr
 2480 2485 2490
 Asp Leu Asn Ser Leu Pro Glu Glu Asp Gln Lys Gly Leu Gly Arg
 2495 2500 2505
 Ser Leu Glu Thr Leu Thr Ala Ala Glu Ala Thr Ala Phe Glu Arg
 2510 2515 2520
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 2540 2545 2550
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 20 25 30
 Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu His
 35 40 45
 Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg Asn
 50 55 60
 His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His Ser
 65 70 75 80
 Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu Gly
 85 90 95
 Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu Ser
 100 105 110
 Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr Ile
 115 120 125

Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro Leu
 130 135 140
 Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile Ser
 145 150 155 160
 Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val Thr
 165 170 175
 Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys Asn
 180 185 190
 Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln Ile
 195 200 205
 Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly Lys
 210 215 220
 Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr Ala
 225 230 235 240
 Phe Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
 245 250 255
 Arg Met Leu Leu Val Ala Leu Thr Met Pro Gly Val Leu Cys Val Ala
 260 265 270
 Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Gly
 275 280 285
 Arg Phe Glu Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ala Asn
 290 295 300
 Gly Ile Val Val Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln Asp
 305 310 315 320
 Leu Ser Ser Lys Lys Gln Gln Ser His Asn Ile Leu Asp Leu Leu Arg
 325 330 335
 Thr Trp Asn Ile Arg Met Val Thr Ile Met Ser Ile Met Leu Trp Met
 340 345 350
 Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu
 355 360 365
 His Gly Asp Ile Phe Val Asn Cys Phe Leu Ser Ala Met Val Glu Val
 370 375 380
 Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg Arg
 385 390 395 400
 Tyr Ser Met Ala Thr Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe
 405 410 415
 Met Gln Leu Val Pro Pro Asp Leu Tyr Tyr Leu Ala Thr Val Leu Val
 420 425 430
 Met Val Gly Lys Phe Gly Val Thr Ala Ala Phe Ser Met Val Tyr Val
 435 440 445
 Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly

450 455 460
 Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe
 465 470 475 480
 Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly
 485 490 495
 Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Leu Pro Glu Ser
 500 505 510
 Phe Gly Thr Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys
 515 520 525
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 Asn Ile Leu Thr Arg His Leu Asp Leu Asp Pro Leu Asp His Arg Asn
 35 40 45
 Phe Tyr Ser Lys Leu Lys Ser Lys Val Thr Thr Trp Lys Ala Lys Ala
 50 55 60
 Leu Trp Tyr Lys Leu Asp Lys Arg Gly Ser His Lys Glu Tyr Lys Arg
 65 70 75 80
 Gly Lys Ser Cys Thr Asn Thr Lys Cys Leu Ile Val Gly Gly Gly Pro
 85 90 95
 Cys Gly Leu Arg Thr Ala Ile Glu Leu Ala Tyr Leu Gly Ala Lys Val
 100 105 110
 Val Val Val Glu Lys Arg Asp Ser Phe Ser Arg Asn Asn Val Leu His
 115 120 125
 Leu Trp Pro Phe Thr Ile His Asp Leu Arg Gly Leu Gly Ala Lys Lys
 130 135 140
 Phe Tyr Gly Lys Phe Cys Ala Gly Ser Ile Asp His Ile Ser Ile Arg
 145 150 155 160
 Gln Leu Gln Leu Ile Leu Phe Lys Val Ala Leu Met Leu Gly Val Glu
 165 170 175
 Ile His Val Asn Val Glu Phe Val Lys Val Leu Glu Pro Pro Glu Asp
 180 185 190

Gln Glu Asn Gln Lys Ile Gly Trp Arg Ala Glu Phe Leu Pro Thr Asp
 195 200 205
 His Ser Leu Ser Glu Phe Glu Phe Asp Val Ile Ile Gly Ala Asp Gly
 210 215 220
 Arg Arg Asn Thr Leu Glu Gly Phe Arg Arg Lys Glu Phe Arg Gly Lys
 225 230 235 240
 Leu Ala Ile Ala Ile Thr Ala Asn Phe Ile Asn Arg Asn Ser Thr Ala
 245 250 255
 Glu Ala Lys Val Glu Glu Ile Ser Gly Val Ala Phe Ile Phe Asn Gln
 260 265 270
 Lys Phe Phe Gln Asp Leu Lys Glu Glu Thr Gly Ile Asp Leu Glu Asn
 275 280 285
 Ile Val Tyr Tyr Lys Asp Cys Thr His Tyr Phe Val Met Thr Ala Lys
 290 295 300
 Lys Gln Ser Leu Leu Asp Lys Gly Val Ile Ile Asn Asp Tyr Ile Asp
 305 310 315 320
 Thr Glu Met Leu Leu Cys Ala Glu Asn Val Asn Gln Asp Asn Leu Leu
 325 330 335
 Ser Tyr Ala Arg Glu Ala Ala Asp Phe Ala Thr Asn Tyr Gln Leu Pro
 340 345 350
 Ser Leu Asp Phe Ala Met Asn His Tyr Gly Gln Pro Asp Val Ala Met
 355 360 365
 Phe Asp Phe Thr Cys Met Tyr Ala Ser Glu Asn Ala Ala Leu Val Arg
 370 375 380
 Glu Arg Gln Ala His Gln Leu Leu Val Ala Leu Val Gly Asp Ser Leu
 385 390 395 400
 Leu Glu Pro Phe Trp Pro Met Gly Thr Gly Cys Ala Arg Gly Phe Leu
 405 410 415
 Ala Ala Phe Asp Thr Ala Trp Met Val Lys Ser Trp Asn Gln Gly Thr
 420 425 430
 Pro Pro Leu Glu Leu Leu Ala Glu Arg Glu Ser Leu Tyr Arg Leu Leu
 435 440 445
 Pro Gln Thr Thr Pro Glu Asn Ile Asn Lys Asn Phe Glu Gln Tyr Thr
 450 455 460
 Leu Asp Pro Gly Thr Arg Tyr Pro Asn Leu Asn Ser His Cys Val Arg
 465 470 475 480
 Pro His Gln Val Lys His Leu Tyr Ile Thr Lys Glu Leu Glu His Tyr
 485 490 495
 Pro Leu Glu Arg Leu Gly Ser Val Arg Arg Ser Val Asn Leu Ser Arg
 500 505 510
 Lys Glu Ser Asp Ile Arg Pro Ser Lys Leu Leu Thr Trp Cys Gln Gln
 515 520 525

Gln Thr Glu Gly Tyr Gln His Val Asn Val Thr Asp Leu Thr Thr Ser
 530 535 540
 Trp Arg Ser Gly Leu Ala Leu Cys Ala Ile Ile His Arg Phe Arg Pro
 545 550 555 560
 Glu Leu Ile Asn Phe Asp Ser Leu Asn Glu Asp Asp Ala Val Glu Asn
 565 570 575
 Asn Gln Leu Ala Phe Asp Val Ala Glu Arg Glu Phe Gly Ile Pro Pro
 580 585 590
 Val Thr Thr Gly Lys Glu Met Ala Ser Ala Gln Glu Pro Asp Lys Leu
 595 600 605
 Ser Met Val Met Tyr Leu Ser Lys Phe Tyr Glu Leu Phe Arg Gly Thr
 610 615 620
 Pro Leu Arg Pro Val Asp Ser Trp Arg Lys Asn Tyr Gly Glu Asn Ala
 625 630 635 640
 Asp Leu Ser Leu Ala Lys Ser Ser Ile Ser Asn Asn Tyr Leu Asn Leu
 645 650 655
 Thr Phe Pro Arg Lys Arg Thr Pro Arg Val Asp Gly Gln Thr Gly Glu
 660 665 670
 Asn Asp Met Asn Lys Arg Arg Arg Lys Gly Phe Thr Asn Leu Asp Glu
 675 680 685
 Pro Ser Asn Phe Ser Ser Arg Ser Leu Gly Ser Asn Gln Glu Cys Gly
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 Ser Ser Lys Glu Gly Gly Asn Gln Asn Lys Val Lys Ser Met Ala Asn
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 Gln Leu Leu Ala Lys Phe Glu Glu Ser Thr Arg Asn Pro Ser Leu Met
 725 730 735
 Lys Gln Glu Arg Arg Val Ser Gly Ile Gly Lys Pro Val Leu Cys Ser
 740 745 750
 Ser Ser Gly Pro Pro Val His Ser Cys Cys Pro Lys Pro Glu Glu Ala
 755 760 765
 Thr Pro Ser Pro Ser Pro Pro Leu Lys Arg Gln Phe Pro Ser Val Val
 770 775 780
 Val Thr Gly His Val Leu Arg Glu Leu Lys Gln Val Ser Ala Gly Ser
 785 790 795 800
 Glu Cys Leu Ser Arg Pro Trp Arg Ala Arg Ala Lys Ser Asp Leu Gln
 805 810 815
 Leu Gly Gly Thr Glu Asn Phe Ala Thr Leu Pro Ser Thr Arg Pro Arg
 820 825 830
 Ala Gln Ala Leu Ser Gly Val Leu Trp Arg Leu Gln Gln Val Glu Glu
 835 840 845
 Lys Ile Leu Gln Lys Arg Ala Gln Asn Leu Ala Asn Arg Glu Phe His

850	855	860
Thr Lys Asn Ile Lys Glu Lys Ala Ala His Leu Ala Ser Met Phe Gly 865 870 875 880		
His Gly Asp Phe Pro Gln Asn Lys Leu Leu Ser Lys Gly Leu Ser His 885 890 895		
Thr His Pro Pro Ser Pro Pro Ser Arg Leu Pro Ser Pro Asp Pro Ala 900 905 910		
Ala Ser Ser Ser Pro Ser Thr Val Asp Ser Ala Ser Pro Ala Arg Lys 915 920 925		
Glu Lys Lys Ser Pro Ser Gly Phe His Phe His Pro Ser His Leu Arg 930 935 940		
Thr Val His Pro Gln Leu Thr Val Gly Lys Val Ser Ser Gly Ile Gly 945 950 955 960		
Ala Ala Ala Glu Val Leu Val Asn Leu Tyr Met Asn Asp His Arg Pro 965 970 975		
Lys Ala Gln Ala Thr Ser Pro Asp Leu Glu Ser Met Arg Lys Ser Phe 980 985 990		
Pro Leu Asn Leu Gly Gly Ser Asp Thr Cys Tyr Phe Cys Lys Lys Arg 995 1000 1005		
Val Tyr Val Met Glu Arg Leu Ser Ala Glu Gly His Phe Phe His 1010 1015 1020		
Arg Glu Cys Phe Arg Cys Ser Ile Cys Ala Thr Thr Leu Arg Leu 1025 1030 1035		
Ala Ala Tyr Thr Phe Asp Cys Asp Glu Gly Lys Phe Tyr Cys Lys 1040 1045 1050		
Pro His Phe Ile His Cys Lys Thr Asn Ser Lys Gln Arg Lys Arg 1055 1060 1065		
Arg Ala Glu Leu Lys Gln Gln Arg Glu Glu Glu Ala Thr Trp Gln 1070 1075 1080		
Glu Gln Glu Ala Pro Arg Arg Asp Thr Pro Thr Glu Ser Ser Cys 1085 1090 1095		
Ala Val Ala Ala Ile Gly Thr Leu Glu Gly Ser Pro Pro Val His 1100 1105 1110		
Phe Ser Leu Pro Val Leu His Pro Leu Leu Gly 1115 1120		
<210> 204		
<211> 395		
<212> PRT		
<213> Homo sapiens		
<400> 204		
Met Asn Gly Pro Val Asp Gly Leu Cys Asp His Ser Leu Ser Glu Gly 1 5 10 15		

Val Phe Met Phe Thr Ser Glu Ser Val Gly Glu Gly His Pro Asp Lys
 20 25 30
 Ile Cys Asp Gln Ile Ser Asp Ala Val Leu Asp Ala His Leu Lys Gln
 35 40 45
 Asp Pro Asn Ala Lys Val Ala Cys Glu Thr Val Cys Lys Thr Gly Met
 50 55 60
 Val Leu Leu Cys Gly Glu Ile Thr Ser Met Ala Met Val Asp Tyr Gln
 65 70 75 80
 Arg Val Val Arg Asp Thr Ile Lys His Ile Gly Tyr Asp Asp Ser Ala
 85 90 95
 Lys Gly Phe Asp Phe Lys Thr Cys Asn Val Leu Val Ala Leu Glu Gln
 100 105 110
 Gln Ser Pro Asp Ile Ala Gln Cys Val His Leu Asp Arg Asn Glu Glu
 115 120 125
 Asp Val Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asp
 130 135 140
 Glu Thr Glu Glu Cys Met Pro Leu Thr Ile Ile Leu Ala His Lys Leu
 145 150 155 160
 Asn Ala Arg Met Ala Asp Leu Arg Arg Ser Gly Leu Leu Pro Trp Leu
 165 170 175
 Arg Pro Asp Ser Lys Thr Gln Val Thr Val Gln Tyr Met Gln Asp Asn
 180 185 190
 Gly Ala Val Ile Pro Val Arg Ile His Thr Ile Val Ile Ser Val Gln
 195 200 205
 His Asn Glu Asp Ile Thr Leu Glu Glu Met Arg Arg Ala Leu Lys Glu
 210 215 220
 Gln Val Ile Arg Ala Val Val Pro Ala Lys Tyr Leu Asp Glu Asp Thr
 225 230 235 240
 Val Tyr His Leu Gln Pro Ser Gly Arg Phe Val Ile Gly Gly Pro Gln
 245 250 255
 Gly Asp Ala Gly Val Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly
 260 265 270
 Gly Trp Gly Ala His Gly Gly Gly Ala Phe Ser Gly Lys Asp Tyr Thr
 275 280 285
 Lys Val Asp Arg Ser Ala Ala Tyr Ala Ala Arg Trp Val Ala Lys Ser
 290 295 300
 Leu Val Lys Ala Gly Leu Cys Arg Arg Val Leu Val Gln Val Ser Tyr
 305 310 315 320
 Ala Ile Gly Val Ala Glu Pro Leu Ser Ile Ser Ile Phe Thr Tyr Gly
 325 330 335
 Thr Ser Gln Lys Thr Glu Arg Glu Leu Leu Asp Val Val His Lys Asn
 340 345 350

Phe Asp Leu Arg Pro Gly Val Ile Val Arg Asp Leu Asp Leu Lys Lys
 355 360 365

Pro Ile Tyr Gln Lys Thr Ala Cys Tyr Gly His Phe Gly Arg Ser Glu
 370 375 380

Phe Pro Trp Glu Val Pro Arg Lys Leu Val Phe
 385 390 395

<210> 205

<211> 1207

<212> PRT

<213> Homo sapiens

<400> 205

Ser Glu Lys Glu Lys Glu Glu Leu Glu Arg Leu Gln Lys Glu Glu Glu
 1 5 10 15

Glu Arg Lys Lys Arg Leu Gln Leu Tyr Val Phe Val Met Arg Cys Ile
 20 25 30

Ala Tyr Pro Phe Asn Ala Lys Gln Pro Thr Asp Met Ala Arg Arg Gln
 35 40 45

Gln Lys Ile Ser Lys Gln Gln Leu Gln Thr Val Lys Asp Arg Phe Gln
 50 55 60

Ala Phe Leu Asn Gly Glu Thr Gln Ile Met Ala Asp Glu Ala Phe Met
 65 70 75 80

Asn Ala Val Gln Ser Tyr Tyr Glu Val Phe Leu Lys Ser Asp Arg Val
 85 90 95

Ala Arg Met Val Gln Ser Gly Gly Cys Ser Ala Asn Asp Ser Arg Glu
 100 105 110

Val Phe Lys Lys His Ile Glu Lys Arg Val Arg Ser Leu Pro Glu Ile
 115 120 125

Asp Gly Leu Ser Lys Glu Thr Val Leu Ser Ser Trp Met Ala Lys Phe
 130 135 140

Asp Ala Ile Tyr Arg Gly Glu Glu Asp Pro Arg Lys Gln Gln Ala Arg
 145 150 155 160

Met Thr Ala Ser Ala Ala Ser Glu Leu Ile Leu Ser Lys Glu Gln Leu
 165 170 175

Tyr Glu Met Phe Gln Asn Ile Leu Gly Ile Lys Lys Phe Glu His Gln
 180 185 190

Leu Leu Tyr Asn Ala Cys Gln Leu Asp Asn Pro Asp Glu Gln Ala Ala
 195 200 205

Gln Ile Arg Arg Glu Leu Asp Gly Arg Leu Gln Met Ala Asp Gln Ile
 210 215 220

Ala Arg Glu Arg Lys Phe Pro Lys Phe Val Ser Lys Glu Met Glu Asn
 225 230 235 240

Met Tyr Ile Glu Glu Leu Lys Ser Ser Val Asn Leu Leu Met Ala Asn

431

Ser Ser Asn Pro Cys Asn Phe Asp His Ala Ser Leu Phe Glu Met Val
 580 585 590
 Gln Arg Leu Thr Leu Asp His Arg Leu Asn Asp Ser Tyr Ser Cys Leu
 595 600 605
 Gly Trp Phe Ser Pro Gly Gln Val Phe Val Leu Asp Glu Tyr Cys Ala
 610 615 620
 Arg Asn Gly Val Arg Gly Cys His Arg His Leu Cys Tyr Leu Arg Asp
 625 630 635 640
 Leu Leu Glu Arg Ala Glu Asn Gly Ala Met Ile Asp Pro Thr Leu Leu
 645 650 655
 His Tyr Ser Phe Ala Phe Cys Ala Ser His Val His Gly Asn Arg Pro
 660 665 670
 Asp Gly Ile Gly Thr Val Thr Val Glu Glu Lys Glu Arg Phe Glu Glu
 675 680 685
 Ile Lys Glu Arg Leu Arg Val Leu Leu Glu Asn Gln Ile Thr His Phe
 690 695 700
 Arg Tyr Cys Phe Pro Phe Gly Arg Pro Glu Gly Ala Leu Lys Ala Thr
 705 710 715 720
 Leu Ser Leu Leu Glu Arg Val Leu Met Lys Asp Ile Val Thr Pro Val
 725 730 735
 Pro Gln Glu Glu Val Lys Thr Val Ile Arg Lys Cys Leu Glu Gln Ala
 740 745 750
 Ala Leu Val Asn Tyr Ser Arg Leu Ser Glu Tyr Ala Lys Ile Glu Glu
 755 760 765
 Asn Gln Lys Asp Ala Glu Asn Val Gly Arg Leu Ile Thr Pro Ala Lys
 770 775 780
 Lys Leu Glu Asp Thr Ile Arg Leu Ala Glu Leu Val Ile Glu Val Leu
 785 790 795 800
 Gln Gln Asn Glu Glu His His Ala Glu Gly Lys Glu Ala Phe Ala Trp
 805 810 815
 Trp Ser Asp Leu Met Val Glu His Ala Glu Thr Phe Leu Ser Leu Phe
 820 825 830
 Ala Val Asp Met Asp Ala Ala Leu Glu Val Gln Pro Pro Asp Thr Trp
 835 840 845
 Asp Ser Phe Pro Leu Phe Gln Leu Leu Asn Asp Phe Leu Arg Thr Asp
 850 855 860
 Tyr Asn Leu Cys Asn Gly Lys Phe His Lys His Leu Gln Asp Leu Phe
 865 870 875 880
 Ala Pro Leu Val Val Arg Tyr Val Asp Leu Met Glu Ser Ser Ile Ala
 885 890 895
 Gln Ser Ile His Arg Gly Phe Glu Arg Glu Ser Trp Glu Pro Val Asn
 900 905 910

Asn Gly Ser Gly Thr Ser Glu Asp Leu Phe Trp Lys Leu Asp Ala Leu
 915 920 925
 Gln Thr Phe Ile Arg Asp Leu His Trp Pro Glu Glu Glu Phe Gly Lys
 930 935 940
 His Leu Glu Gln Arg Leu Lys Leu Met Ala Ser Asp Met Ile Glu Ser
 945 950 955 960
 Cys Val Lys Arg Thr Arg Ile Ala Phe Glu Val Lys Leu Gln Lys Thr
 965 970 975
 Ser Arg Ser Thr Asp Phe Arg Val Pro Gln Ser Ile Cys Thr Met Phe
 980 985 990
 Asn Val Met Val Asp Ala Lys Ala Gln Ser Thr Lys Leu Cys Ser Met
 995 1000 1005
 Glu Met Gly Gln Glu His Gln Tyr His Ser Lys Ile Asp Glu Leu
 1010 1015 1020
 Ile Glu Glu Thr Val Lys Glu Met Ile Thr Leu Leu Val Ala Lys
 1025 1030 1035
 Phe Val Thr Ile Leu Glu Gly Val Leu Ala Lys Leu Ser Arg Tyr
 1040 1045 1050
 Asp Glu Gly Thr Leu Phe Ser Ser Phe Leu Ser Phe Thr Val Lys
 1055 1060 1065
 Ala Ala Ser Lys Tyr Val Asp Val Pro Lys Pro Gly Met Asp Val
 1070 1075 1080
 Ala Asp Ala Tyr Val Thr Phe Val Arg His Ser Gln Asp Val Leu
 1085 1090 1095
 Arg Asp Lys Val Asn Glu Glu Met Tyr Ile Glu Arg Leu Phe Asp
 1100 1105 1110
 Gln Trp Tyr Asn Ser Ser Met Asn Val Ile Cys Thr Trp Leu Thr
 1115 1120 1125
 Asp Arg Met Asp Leu Gln Leu His Ile Tyr Gln Leu Lys Thr Leu
 1130 1135 1140
 Ile Arg Met Val Lys Lys Thr Tyr Arg Asp Phe Arg Leu Gln Gly
 1145 1150 1155
 Val Leu Asp Ser Thr Leu Asn Ser Lys Thr Tyr Glu Thr Ile Arg
 1160 1165 1170
 Asn Arg Leu Thr Val Glu Glu Ala Thr Ala Ser Val Ser Glu Gly
 1175 1180 1185
 Gly Gly Leu Gln Gly Ile Ser Met Lys Asp Ser Asp Glu Glu Asp
 1190 1195 1200
 Glu Glu Asp Asp
 1205
 <210> 206

<211> 1018
 <212> PRT
 <213> Homo sapiens

<400> 206
 Gln Leu Tyr Glu Met Phe Gln Gln Ile Leu Gly Ile Lys Lys Leu Glu
 1 5 10 15
 His Gln Leu Leu Tyr Asn Ala Cys Gln Leu Asp Asn Ala Asp Glu Gln
 20 25 30
 Ala Ala Gln Ile Arg Arg Glu Leu Asp Gly Arg Leu Gln Leu Ala Asp
 35 40 45
 Lys Met Ala Lys Glu Arg Lys Phe Pro Lys Phe Ile Ala Lys Asp Met
 50 55 60
 Glu Asn Met Tyr Ile Glu Glu Leu Arg Ser Ser Val Asn Leu Leu Met
 65 70 75 80
 Ala Asn Leu Glu Ser Leu Pro Val Ser Lys Gly Gly Pro Glu Phe Lys
 85 90 95
 Leu Gln Lys Leu Lys Arg Ser Gln Asn Ser Ala Phe Leu Asp Ile Gly
 100 105 110
 Asp Glu Asn Glu Ile Gln Leu Ser Lys Ser Asp Val Val Leu Ser Phe
 115 120 125
 Thr Leu Glu Ile Val Ile Met Glu Val Gln Gly Leu Lys Ser Val Ala
 130 135 140
 Pro Asn Arg Ile Val Tyr Cys Thr Met Glu Val Glu Gly Glu Lys Leu
 145 150 155 160
 Gln Thr Asp Gln Ala Glu Ala Ser Arg Pro Gln Trp Gly Thr Gln Gly
 165 170 175
 Asp Phe Thr Thr Thr His Pro Arg Pro Val Val Lys Val Lys Leu Phe
 180 185 190
 Thr Glu Ser Thr Gly Val Leu Ala Leu Glu Asp Lys Glu Leu Gly Arg
 195 200 205
 Val Ile Leu Tyr Pro Thr Ser Asn Ser Ser Lys Ser Ala Glu Leu His
 210 215 220
 Arg Met Val Val Pro Lys Asn Ser Gln Asp Ser Asp Leu Lys Ile Lys
 225 230 235 240
 Leu Ala Val Arg Met Asp Lys Pro Ala His Met Lys His Ser Gly Tyr
 245 250 255
 Leu Tyr Ala Leu Gly Gln Lys Val Trp Lys Arg Trp Lys Lys Arg Tyr
 260 265 270
 Phe Val Leu Val Gln Val Ser Gln Tyr Thr Phe Ala Met Cys Ser Tyr
 275 280 285
 Arg Glu Lys Lys Ser Glu Pro Gln Glu Leu Met Gln Leu Glu Gly Tyr
 290 295 300

Thr Val Asp Tyr Thr Asp Pro His Pro Gly Leu Gln Gly Gly Cys Met
 305 310 315 320
 Phe Phe Asn Ala Val Lys Glu Gly Asp Thr Val Ile Phe Ala Ser Asp
 325 330 335
 Asp Glu Gln Asp Arg Ile Leu Trp Val Gln Ala Met Tyr Arg Ala Thr
 340 345 350
 Gly Gln Ser Tyr Lys Pro Val Pro Ala Ile Gln Thr Gln Lys Leu Asn
 355 360 365
 Pro Lys Gly Gly Thr Leu His Ala Asp Ala Gln Leu Tyr Ala Asp Arg
 370 375 380
 Phe Gln Lys His Gly Met Asp Glu Phe Ile Ser Ala Asn Pro Cys Lys
 385 390 395 400
 Leu Asp His Ala Phe Leu Phe Arg Ile Leu Gln Arg Gln Thr Leu Asp
 405 410 415
 His Arg Leu Asn Asp Ser Tyr Ser Cys Leu Gly Trp Phe Ser Pro Gly
 420 425 430
 Gln Val Phe Val Leu Asp Glu Tyr Cys Ala Arg Tyr Gly Val Arg Gly
 435 440 445
 Cys His Arg His Leu Cys Tyr Leu Ala Glu Leu Met Glu His Ser Glu
 450 455 460
 Asn Gly Ala Val Ile Asp Pro Thr Leu Leu His Tyr Ser Phe Ala Phe
 465 470 475 480
 Cys Ala Ser His Val His Gly Asn Arg Pro Asp Gly Ile Gly Thr Val
 485 490 495
 Ser Val Glu Glu Lys Glu Arg Phe Glu Glu Ile Lys Glu Arg Leu Ser
 500 505 510
 Ser Leu Leu Glu Asn Gln Ile Ser His Phe Arg Tyr Cys Phe Pro Phe
 515 520 525
 Gly Arg Pro Glu Gly Ala Leu Lys Ala Thr Leu Ser Leu Leu Glu Arg
 530 535 540
 Val Leu Met Lys Asp Ile Ala Thr Pro Ile Pro Ala Glu Glu Val Lys
 545 550 555 560
 Lys Val Val Arg Lys Cys Leu Glu Lys Ala Ala Leu Ile Asn Tyr Thr
 565 570 575
 Arg Leu Thr Glu Tyr Ala Lys Ile Glu Glu Thr Met Asn Gln Ala Ser
 580 585 590
 Pro Ala Arg Lys Leu Glu Glu Ile Leu His Leu Ala Glu Leu Cys Ile
 595 600 605
 Glu Val Leu Gln Gln Asn Glu Glu His His Ala Glu Ala Phe Ala Trp
 610 615 620
 Trp Pro Asp Leu Leu Ala Glu His Ala Glu Lys Phe Trp Ala Leu Phe
 625 630 635 640

Thr Val Asp Met Asp Thr Ala Leu Glu Ala Gln Pro Gln Asp Ser Trp
 645 650 655
 Asp Ser Phe Pro Leu Phe Gln Leu Leu Asn Asn Phe Leu Arg Asn Asp
 660 665 670
 Thr Leu Leu Cys Asn Gly Lys Phe His Lys His Leu Gln Glu Ile Phe
 675 680 685
 Val Pro Leu Val Val Arg Tyr Val Asp Leu Met Glu Ser Ser Ile Ala
 690 695 700
 Gln Ser Ile His Arg Gly Phe Glu Gln Glu Thr Trp Gln Pro Val Asn
 705 710 715 720
 Asn Gly Ser Ala Thr Ser Glu Asp Leu Phe Trp Lys Leu Asp Ala Leu
 725 730 735
 Gln Met Phe Val Phe Asp Leu His Trp Pro Glu Gln Glu Phe Ala His
 740 745 750
 His Leu Glu Gln Arg Leu Lys Leu Met Ala Ser Asp Met Leu Glu Ala
 755 760 765
 Cys Val Lys Arg Thr Arg Thr Ala Phe Glu Leu Lys Leu Gln Lys Ala
 770 775 780
 Ser Lys Thr Thr Asp Leu Arg Ile Pro Ala Ser Val Cys Thr Met Phe
 785 790 795 800
 Asn Val Leu Val Asp Ala Lys Lys Gln Ser Thr Lys Leu Cys Ala Leu
 805 810 815
 Asp Gly Gly Gln Glu Phe Gly Ser Gln Trp Gln Gln Tyr His Ser Lys
 820 825 830
 Ile Asp Asp Leu Ile Asp Asn Ser Val Lys Glu Ile Ile Ser Leu Leu
 835 840 845
 Val Ser Lys Phe Val Ser Val Leu Glu Gly Val Leu Ser Lys Leu Ser
 850 855 860
 Arg Tyr Asp Glu Gly Thr Phe Phe Ser Ser Ile Leu Ser Phe Thr Val
 865 870 875 880
 Lys Ala Ala Ala Lys Tyr Val Asp Val Pro Lys Pro Gly Met Asp Leu
 885 890 895
 Ala Asp Thr Tyr Ile Met Phe Val Arg Gln Asn Gln Asp Ile Leu Arg
 900 905 910
 Glu Lys Val Asn Glu Glu Met Tyr Ile Glu Lys Leu Phe Asp Gln Trp
 915 920 925
 Tyr Ser Ser Ser Met Lys Val Ile Cys Val Trp Leu Thr Asp Arg Leu
 930 935 940
 Asp Leu Gln Leu His Ile Tyr Gln Leu Lys Thr Leu Ile Lys Ile Val
 945 950 955 960
 Lys Lys Thr Tyr Arg Asp Phe Arg Leu Gln Gly Val Leu Glu Gly Thr

965 970 975
 Leu Asn Ser Lys Thr Tyr Asp Thr Val His Arg Arg Leu Thr Val Glu
 980 985 990
 Glu Ala Thr Ala Ser Val Ser Glu Gly Gly Gly Leu Gln Gly Ile Thr
 995 1000 1005
 Met Lys Asp Ser Asp Glu Glu Glu Glu Gly
 1010 1015
 <210> 207
 <211> 591
 <212> PRT
 <213> Homo sapiens
 <400> 207
 Met Ser Ser Leu Ser Ala Leu Phe Ser Val Ser Asp Lys Thr Gly Leu
 1 5 10 15
 Val Glu Phe Ala Arg Asn Leu Thr Ala Leu Gly Leu Asn Leu Val Ala
 20 25 30
 Ser Gly Gly Thr Ala Lys Ala Leu Arg Asp Ala Gly Leu Ala Val Arg
 35 40 45
 Asp Val Ser Glu Leu Thr Gly Phe Pro Glu Met Leu Gly Gly Arg Val
 50 55 60
 Lys Thr Leu His Pro Ala Val His Ala Gly Ile Leu Ala Arg Asn Ile
 65 70 75 80
 Pro Glu Asp Asn Ala Asp Met Ala Arg Leu Asp Phe Asn Leu Ile Arg
 85 90 95
 Val Val Ala Cys Asn Leu Tyr Pro Phe Val Lys Thr Val Ala Ser Pro
 100 105 110
 Gly Val Thr Val Glu Glu Ala Val Glu Gln Ile Asp Ile Gly Gly Val
 115 120 125
 Thr Leu Leu Arg Ala Ala Ala Lys Asn His Ala Arg Val Thr Val Val
 130 135 140
 Cys Glu Pro Glu Asp Tyr Val Val Val Ser Thr Glu Met Gln Ser Ser
 145 150 155 160
 Glu Ser Lys Gly Thr Ser Leu Glu Thr Arg Arg Gln Leu Ala Leu Lys
 165 170 175
 Ala Phe Thr His Thr Ala Gln Tyr Asp Glu Ala Ile Ser Asp Tyr Phe
 180 185 190
 Arg Lys Gln Tyr Ser Lys Gly Val Ser Gln Met Pro Leu Arg Tyr Gly
 195 200 205
 Met Asn Pro His Gln Thr Pro Ala Gln Leu Tyr Thr Leu Gln Pro Lys
 210 215 220
 Leu Pro Ile Thr Val Leu Asn Gly Ala Pro Gly Phe Ile Asn Leu Cys
 225 230 235 240

Asp Ala Leu Asn Ala Trp Gln Leu Val Lys Glu Leu Lys Glu Ala Leu
 245 250 255
 Gly Ile Pro Ala Ala Ala Ser Phe Lys His Val Ser Pro Ala Gly Ala
 260 265 270
 Ala Val Gly Ile Pro Leu Ser Glu Asp Glu Ala Lys Val Cys Met Val
 275 280 285
 Tyr Asp Leu Tyr Lys Thr Leu Thr Pro Ile Ser Ala Ala Tyr Ala Arg
 290 295 300
 Ala Arg Gly Ala Asp Arg Met Ser Ser Phe Gly Asp Phe Val Ala Leu
 305 310 315 320
 Ser Asp Val Cys Asp Val Pro Thr Ala Lys Ile Ile Ser Arg Glu Val
 325 330 335
 Ser Asp Gly Ile Ile Ala Pro Gly Tyr Glu Glu Glu Ala Leu Thr Ile
 340 345 350
 Leu Ser Lys Lys Lys Asn Gly Asn Tyr Cys Val Leu Gln Met Asp Gln
 355 360 365
 Ser Tyr Lys Pro Asp Glu Asn Glu Val Arg Thr Leu Phe Gly Leu His
 370 375 380
 Leu Ser Gln Lys Arg Asn Asn Gly Val Val Asp Lys Ser Leu Phe Ser
 385 390 395 400
 Asn Val Val Thr Lys Asn Lys Asp Leu Pro Glu Ser Ala Leu Arg Asp
 405 410 415
 Leu Ile Val Ala Thr Ile Ala Val Lys Tyr Thr Gln Ser Asn Ser Val
 420 425 430
 Cys Tyr Ala Lys Asn Gly Gln Val Ile Gly Ile Gly Ala Gly Gln Gln
 435 440 445
 Ser Arg Ile His Cys Thr Arg Leu Ala Gly Asp Lys Ala Asn Tyr Trp
 450 455 460
 Trp Leu Arg His His Pro Gln Val Leu Ser Met Lys Phe Lys Thr Gly
 465 470 475 480
 Val Lys Arg Ala Glu Ile Ser Asn Ala Ile Asp Gln Tyr Val Thr Gly
 485 490 495
 Thr Ile Gly Glu Asp Glu Asp Leu Ile Lys Trp Lys Ala Leu Phe Glu
 500 505 510
 Glu Val Pro Glu Leu Leu Thr Glu Ala Glu Lys Lys Glu Trp Val Glu
 515 520 525
 Lys Leu Thr Glu Val Ser Ile Ser Ser Asp Ala Phe Phe Pro Phe Arg
 530 535 540
 Asp Asn Val Asp Arg Ala Lys Arg Ser Gly Val Ala Tyr Ile Ala Ala
 545 550 555 560
 Pro Ser Gly Ser Ala Ala Asp Lys Val Val Ile Glu Ala Cys Asp Glu
 565 570 575

Leu Gly Ile Ile Leu Ala His Thr Asn Leu Arg Leu Phe His His
 580 585 590

<210> 208
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 208
 Ala Pro Ala Leu Leu Ile Pro Ala Ala Leu Ala Ser Phe Ile Leu
 1 5 10 15
 Ala Phe Gly Thr Gly Val Glu Phe Val Arg Phe Thr Ser Leu Arg Pro
 20 25 30
 Leu Leu Gly Gly Ile Pro Glu Ser Gly Gly Pro Asp Ala Arg Gln Gly
 35 40 45
 Trp Leu Ala Ala Leu Gln Asp Arg Ser Ile Leu Ala Pro Leu Ala Trp
 50 55 60
 Asp Leu Gly Leu Leu Leu Leu Phe Val Gly Gln His Ser Leu Met Ala
 65 70 75 80
 Ala Glu Arg Val Lys Ala Trp Thr Ser Arg Tyr Phe Gly Val Leu Gln
 85 90 95
 Arg Ser Leu Tyr Val Ala Cys Thr Ala Leu Ala Leu Gln Leu Val Met
 100 105 110
 Arg Tyr Trp Glu Pro Ile Pro Lys Gly Pro Val Leu Trp Glu Ala Arg
 115 120 125
 Ala Glu Pro Trp Ala Thr Trp Val Pro Leu Leu Cys Phe Val Leu His
 130 135 140
 Val Ile Ser Trp Leu Leu Ile Phe Ser Ile Leu Leu Val Phe Asp Tyr
 145 150 155 160
 Ala Glu Leu Met Gly Leu Lys Gln Val Tyr Tyr His Val Leu Gly Leu
 165 170 175
 Gly Glu Pro Leu Ala Leu Lys Ser Pro Arg Ala Leu Arg Leu Phe Ser
 180 185 190
 His Leu Arg His Pro Val Cys Val Glu Leu Leu Thr Val Leu Trp Val
 195 200 205
 Val Pro Thr Leu Gly Thr Asp Arg Leu Leu Leu Ala Phe Leu Leu Thr
 210 215 220
 Leu Tyr Leu Gly Leu Ala His Gly Leu Asp Gln Gln Asp Leu Arg Tyr
 225 230 235 240
 Leu Arg Ala Gln Leu Gln Arg Lys Leu His Leu Leu Ser Arg Pro Gln
 245 250 255
 Asp Gly Glu Ala Glu
 260

<210> 209

<211> 623
 <212> PRT
 <213> Homo sapiens

<400> 209

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Met Glu Ser Tyr His Lys Pro Asp Gln Gln Lys Leu Gln Ala Leu Lys
1      5      10      15

Asp Thr Ala Asn Arg Leu Arg Ile Ser Ser Ile Gln Ala Thr Thr Ala
      20      25      30

Ala Gly Ser Gly His Pro Thr Ser Cys Cys Ser Ala Ala Glu Ile Met
      35      40      45

Ala Val Leu Phe Phe His Thr Met Arg Tyr Lys Ser Gln Asp Pro Arg
      50      55      60

Asn Pro His Asn Asp Arg Phe Val Leu Ser Lys Gly His Ala Ala Pro
      65      70      75      80

Ile Leu Tyr Ala Val Trp Ala Glu Ala Gly Phe Leu Ala Glu Ala Glu
      85      90      95

Leu Leu Asn Leu Arg Lys Ile Ser Ser Asp Leu Asp Gly His Pro Val
      100      105      110

Pro Lys Gln Ala Phe Thr Asp Val Ala Thr Gly Ser Leu Gly Gln Gly
      115      120      125

Leu Gly Ala Ala Cys Gly Met Ala Tyr Thr Gly Lys Tyr Phe Asp Lys
      130      135      140

Ala Ser Tyr Arg Val Tyr Cys Leu Leu Gly Asp Gly Glu Leu Ser Glu
      145      150      155      160

Gly Ser Val Trp Glu Ala Met Ala Phe Ala Ser Ile Tyr Lys Leu Asp
      165      170      175

Asn Leu Val Ala Ile Leu Asp Ile Asn Arg Leu Gly Gln Ser Asp Pro
      180      185      190

Ala Pro Leu Gln His Gln Met Asp Ile Tyr Gln Lys Arg Cys Glu Ala
      195      200      205

Phe Gly Trp His Ala Ile Ile Val Asp Gly His Ser Val Glu Glu Leu
      210      215      220

Cys Lys Ala Phe Gly Gln Ala Lys His Gln Pro Thr Ala Ile Ile Ala
      225      230      235      240

Lys Thr Phe Lys Gly Arg Gly Ile Thr Gly Val Glu Asp Lys Glu Ser
      245      250      255

Trp His Gly Lys Pro Leu Pro Lys Asn Met Ala Glu Gln Ile Ile Gln
      260      265      270

Glu Ile Tyr Ser Gln Ile Gln Ser Lys Lys Lys Ile Leu Ala Thr Pro
      275      280      285

Pro Gln Glu Asp Ala Pro Ser Val Asp Ile Ala Asn Ile Arg Met Pro
      290      295      300

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Ser Leu Pro Ser Tyr Lys Val Gly Asp Lys Ile Ala Thr Arg Lys Ala
 305 310 315 320
 Tyr Gly Gln Ala Leu Ala Lys Leu Gly His Ala Ser Asp Arg Ile Ile
 325 330 335
 Ala Leu Asp Gly Asp Thr Lys Asn Ser Thr Phe Ser Glu Ile Phe Lys
 340 345 350
 Lys Glu His Pro Asp Arg Phe Ile Glu Cys Tyr Ile Ala Glu Gln Asn
 355 360 365
 Met Val Ser Ile Ala Val Gly Cys Ala Thr Arg Asn Arg Thr Val Pro
 370 375 380
 Phe Cys Ser Thr Phe Ala Ala Phe Phe Thr Arg Ala Phe Asp Gln Ile
 385 390 395 400
 Arg Met Ala Ala Ile Ser Glu Ser Asn Ile Asn Leu Cys Gly Ser His
 405 410 415
 Cys Gly Val Ser Ile Gly Glu Asp Gly Pro Ser Gln Met Ala Leu Glu
 420 425 430
 Asp Leu Ala Met Phe Arg Ser Val Pro Thr Ser Thr Val Phe Tyr Pro
 435 440 445
 Ser Asp Gly Val Ala Thr Glu Lys Ala Val Glu Leu Ala Ala Asn Thr
 450 455 460
 Lys Gly Ile Cys Phe Ile Arg Thr Ser Arg Pro Glu Asn Ala Ile Ile
 465 470 475 480
 Tyr Asn Asn Asn Glu Asp Phe Gln Val Gly Gln Ala Lys Val Val Leu
 485 490 495
 Lys Ser Lys Asp Asp Gln Val Thr Val Ile Gly Ala Gly Val Thr Leu
 500 505 510
 His Glu Ala Leu Ala Ala Ala Glu Leu Leu Lys Lys Glu Lys Ile Asn
 515 520 525
 Ile Arg Val Leu Asp Pro Phe Thr Ile Lys Pro Leu Asp Arg Lys Leu
 530 535 540
 Ile Leu Asp Ser Ala Arg Ala Thr Lys Gly Arg Ile Leu Thr Val Glu
 545 550 555 560
 Asp His Tyr Tyr Glu Gly Gly Ile Gly Glu Ala Val Ser Ser Ala Val
 565 570 575
 Val Gly Glu Pro Gly Ile Thr Val Thr His Leu Ala Val Asn Arg Val
 580 585 590
 Pro Arg Ser Gly Lys Pro Ala Glu Leu Leu Lys Met Phe Gly Ile Asp
 595 600 605
 Arg Asp Ala Ile Ala Gln Ala Val Arg Gly Leu Ile Thr Lys Ala
 610 615 620
 <210> 210
 <211> 772

<212> PRT

<213> Homo sapiens

<400> 210

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Leu Cys Pro Tyr Leu Ser Pro Asp Ala Thr Gly Pro Ser Gly Leu Arg
1          5          10          15

Val Leu Pro Gln Gly Tyr Gly Trp Asn Leu Leu Tyr Gly Ser Leu Leu
20          25          30

Leu Gly Leu Val Gly Gly Val Cys Thr Leu Gly Ala Gly Leu Tyr Ala
35          40          45

Arg Ala Ser Phe Leu Thr Phe Leu Leu Val Ser Gly Ser Leu Ala Ser
50          55          60

Val Leu Ile Ser Phe Val Ala Val Gly Pro Arg Asp Ile Arg Leu Thr
65          70          75          80

Pro Arg Pro Gly Pro Asn Gly Ser Ser Leu Pro Pro Arg Phe Gly His
85          90          95

Phe Thr Gly Phe Asn Ser Ser Thr Leu Lys Asp Asn Leu Gly Ala Gly
100         105         110

Tyr Ala Glu Asp Tyr Thr Thr Gly Ala Val Met Asn Phe Ala Ser Val
115         120         125

Phe Ala Val Leu Phe Asn Gly Cys Thr Gly Ile Met Ala Gly Ala Asn
130         135         140

Met Ser Gly Glu Leu Lys Asp Pro Ser Arg Ala Ile Pro Leu Gly Thr
145         150         155         160

Ile Val Ala Val Ala Tyr Thr Phe Phe Val Tyr Val Leu Leu Phe Phe
165         170         175

Leu Ser Ser Phe Thr Cys Asp Arg Thr Leu Leu Gln Glu Asp Tyr Gly
180         185         190

Phe Phe Arg Ala Ile Ser Leu Trp Pro Pro Leu Val Leu Ile Gly Ile
195         200         205

Tyr Ala Thr Ala Leu Ser Ala Ser Met Ser Ser Leu Ile Gly Ala Ser
210         215         220

Arg Ile Leu His Ala Leu Ala Arg Asp Asp Leu Phe Gly Val Ile Leu
225         230         235         240

Ala Pro Ala Lys Val Val Ser Arg Gly Gly Asn Pro Trp Ala Ala Val
245         250         255

Leu Tyr Ser Trp Gly Leu Val Gln Leu Val Leu Leu Ala Gly Lys Leu
260         265         270

Asn Thr Leu Ala Ala Val Val Thr Val Phe Tyr Leu Val Ala Tyr Ala
275         280         285

Ala Val Asp Leu Ser Cys Leu Ser Leu Glu Trp Ala Ser Ala Pro Asn
290         295         300

Phe Arg Pro Thr Phe Ser Leu Phe Ser Trp His Thr Cys Leu Leu Gly

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305		310		315		320									
Val	Ala	Ser	Cys	Leu	Leu	Met	Met	Phe	Leu	Ile	Ser	Pro	Gly	Ala	Ala
				325					330					335	
Gly	Gly	Ser	Leu	Leu	Leu	Met	Gly	Leu	Leu	Ala	Ala	Leu	Leu	Thr	Ala
			340					345					350		
Arg	Gly	Gly	Pro	Ser	Ser	Trp	Gly	Tyr	Val	Ser	Gln	Ala	Leu	Leu	Phe
		355					360					365			
His	Gln	Val	Arg	Lys	Tyr	Leu	Leu	Arg	Leu	Asp	Val	Arg	Lys	Asp	His
	370					375					380				
Val	Lys	Phe	Trp	Arg	Pro	Gln	Leu	Leu	Leu	Val	Gly	Asn	Pro	Arg	
385					390				395					400	
Gly	Ala	Leu	Pro	Leu	Leu	Arg	Leu	Ala	Asn	Gln	Leu	Lys	Lys	Gly	Gly
			405					410						415	
Leu	Tyr	Val	Leu	Gly	His	Val	Thr	Leu	Gly	Asp	Leu	Asp	Ser	Leu	Pro
			420					425					430		
Ser	Asp	Pro	Val	Gln	Pro	Gln	Tyr	Gly	Ala	Trp	Leu	Ser	Leu	Val	Asp
		435					440					445			
Arg	Ala	Gln	Val	Lys	Ala	Phe	Val	Asp	Leu	Thr	Leu	Ser	Pro	Ser	Val
	450					455					460				
Arg	Gln	Gly	Ala	Gln	His	Leu	Leu	Arg	Ile	Ser	Gly	Leu	Gly	Gly	Met
465					470				475						480
Lys	Pro	Asn	Thr	Leu	Val	Leu	Gly	Phe	Tyr	Asp	Asp	Ala	Pro	Pro	Gln
			485					490						495	
Asp	His	Phe	Leu	Thr	Asp	Pro	Ala	Phe	Ser	Glu	Pro	Ala	Asp	Ser	Thr
			500					505					510		
Arg	Glu	Gly	Ser	Ser	Pro	Ala	Leu	Ser	Thr	Leu	Phe	Pro	Pro	Pro	Arg
		515					520					525			
Ala	Pro	Gly	Ser	Pro	Arg	Ala	Leu	Asn	Pro	Gln	Asp	Tyr	Val	Ala	Thr
	530					535					540				
Val	Ala	Asp	Ala	Leu	Lys	Met	Asn	Lys	Asn	Val	Val	Leu	Ala	Arg	Ala
545					550					555					560
Ser	Gly	Ala	Leu	Pro	Pro	Glu	Arg	Leu	Ser	Arg	Gly	Ser	Gly	Gly	Thr
			565					570					575		
Ser	Gln	Leu	His	His	Val	Asp	Val	Trp	Pro	Leu	Asn	Leu	Leu	Arg	Pro
			580					585					590		
Arg	Gly	Gly	Pro	Gly	Tyr	Val	Asp	Val	Cys	Gly	Leu	Phe	Leu	Leu	Gln
		595					600					605			
Met	Ala	Thr	Ile	Leu	Gly	Met	Val	Pro	Ala	Trp	His	Ser	Ala	Arg	Leu
	610					615					620				
Arg	Ile	Phe	Leu	Cys	Leu	Gly	Pro	Arg	Glu	Ala	Pro	Gly	Ala	Ala	Glu
625					630					635					640

Gly Arg Leu Arg Ala Leu Leu Ser Gln Leu Arg Ile Arg Ala Glu Val
 645 650 655
 Gln Glu Val Val Trp Gly Glu Gly Ala Gly Ala Gly Glu Pro Glu Ala
 660 665 670
 Glu Glu Glu Gly Asp Phe Val Asn Ser Gly Arg Gly Asp Ala Glu Ala
 675 680 685
 Glu Ala Leu Ala Arg Ser Ala Asn Ala Leu Val Arg Ala Gln Gln Gly
 690 695 700
 Arg Gly Thr Gly Gly Gly Pro Gly Gly Pro Glu Gly Gly Asp Ala Glu
 705 710 715 720
 Gly Pro Ile Thr Ala Leu Thr Phe Leu Tyr Leu Pro Arg Pro Pro Ala
 725 730 735
 Asp Pro Ala Arg Tyr Pro Arg Tyr Leu Ala Leu Leu Glu Thr Leu Thr
 740 745 750
 Arg Asp Leu Gly Pro Thr Leu Leu Val His Gly Val Thr Pro Val Thr
 755 760 765
 Cys Thr Asp Leu
 770

<210> 211
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 <212> PRT
 <213> Homo sapiens

<400> 211
 Met Ala Gly Glu Leu Ala Asp Lys Lys Asp Arg Asp Ala Ser Pro Ser
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 Lys Glu Glu Arg Lys Arg Ser Arg Thr Pro Asp Arg Glu Arg Asp Arg
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 Asp Arg Asp Arg Lys Ser Ser Pro Ser Lys Asp Arg Lys Arg His Arg
 35 40 45
 Ser Arg Asp Arg Arg Arg Gly Gly Ser Arg Ser Arg Ser Arg Ser Arg
 50 55 60
 Ser Lys Ser Ala Glu Arg Glu Arg Arg His Lys Glu Arg Glu Arg Asp
 65 70 75 80
 Lys Glu Arg Asp Arg Asn Lys Lys Asp Arg Asp Arg Asp Lys Asp Gly
 85 90 95
 His Arg Arg Asp Lys Asp Arg Lys Arg Ser Ser Leu Ser Pro Gly Arg
 100 105 110
 Gly Lys Asp Phe Lys Ser Arg Lys Asp Arg Asp Ser Lys Lys Asp Glu
 115 120 125
 Glu Asp Glu His Gly Asp Lys Lys Pro Lys Ala Gln Pro Leu Ser Leu
 130 135 140
 Glu Glu Leu Leu Ala Lys Lys Lys Ala Glu Glu Glu Ala Glu Ala Lys
 145 150 155 160

Pro Lys Phe Leu Ser Lys Ala Glu Arg Glu Ala Glu Ala Leu Lys Arg
 165 170 175
 Arg Gln Gln Glu Val Glu Glu Arg Gln Arg Met Leu Glu Glu Glu Arg
 180 185 190
 Lys Lys Arg Lys Gln Phe Gln Asp Leu Gly Arg Lys Met Leu Glu Asp
 195 200 205
 Pro Gln Glu Arg Glu Arg Arg Glu Arg Arg Glu Arg Met Glu Arg Glu
 210 215 220
 Thr Asn Gly Asn Glu Asp Glu Glu Gly Arg Gln Lys Ile Arg Glu Glu
 225 230 235 240
 Lys Asp Lys Ser Lys Glu Leu His Ala Ile Lys Glu Arg Tyr Leu Gly
 245 250 255
 Gly Ile Lys Lys Arg Arg Arg Thr Arg His Leu Asn Asp Arg Lys Phe
 260 265 270
 Val Phe Glu Trp Asp Ala Ser Glu Asp Thr Ser Ile Asp Tyr Asn Pro
 275 280 285
 Leu Tyr Lys Glu Arg His Gln Val Gln Leu Leu Gly Arg Gly Phe Ile
 290 295 300
 Ala Gly Ile Asp Leu Lys Gln Gln Lys Arg Glu Gln Ser Arg Phe Tyr
 305 310 315 320
 Gly Asp Leu Met Glu Lys Arg Arg Thr Leu Glu Glu Lys Glu Gln Glu
 325 330 335
 Glu Ala Arg Leu Arg Lys Leu Arg Lys Lys Glu Ala Lys Gln Arg Trp
 340 345 350
 Asp Asp Arg His Trp Ser Gln Lys Lys Leu Asp Glu Met Thr Asp Arg
 355 360 365
 Asp Trp Arg Ile Phe Arg Glu Asp Tyr Ser Ile Thr Thr Lys Gly Gly
 370 375 380
 Lys Ile Pro Asn Pro Ile Arg Ser Trp Lys Asp Ser Ser Leu Pro Pro
 385 390 395 400
 His Ile Leu Glu Val Ile Asp Lys Cys Gly Tyr Lys Glu Pro Thr Pro
 405 410 415
 Ile Gln Arg Gln Ala Ile Pro Ile Gly Leu Gln Asn Arg Asp Ile Ile
 420 425 430
 Gly Val Ala Glu Thr Gly Ser Gly Lys Thr Ala Ala Phe Leu Ile Pro
 435 440 445
 Leu Leu Val Trp Ile Thr Thr Leu Pro Lys Ile Asp Arg Ile Glu Glu
 450 455 460
 Ser Asp Gln Gly Pro Tyr Ala Ile Ile Leu Ala Pro Thr Arg Glu Leu
 465 470 475 480
 Ala Gln Gln Ile Glu Glu Glu Thr Ile Lys Phe Gly Lys Pro Leu Gly

485										490					495				
Ile	Arg	Thr	Val	Ala	Val	Ile	Gly	Gly	Ile	Ser	Arg	Glu	Asp	Gln	Gly				
			500					505					510						
Phe	Arg	Leu	Arg	Met	Gly	Cys	Glu	Ile	Val	Ile	Ala	Thr	Pro	Gly	Arg				
		515					520					525							
Leu	Ile	Asp	Val	Leu	Glu	Asn	Arg	Tyr	Leu	Val	Leu	Ser	Arg	Cys	Thr				
	530					535						540							
Tyr	Val	Val	Leu	Asp	Glu	Ala	Asp	Arg	Met	Ile	Asp	Met	Gly	Phe	Glu				
545					550					555					560				
Pro	Asp	Val	Gln	Lys	Ile	Leu	Glu	His	Met	Pro	Val	Ser	Asn	Gln	Lys				
				565					570					575					
Pro	Asp	Thr	Asp	Glu	Ala	Glu	Asp	Pro	Glu	Lys	Met	Leu	Ala	Asn	Phe				
			580					585					590						
Glu	Ser	Gly	Lys	His	Lys	Tyr	Arg	Gln	Thr	Val	Met	Phe	Thr	Ala	Thr				
		595					600					605							
Met	Pro	Pro	Ala	Val	Glu	Arg	Leu	Ala	Arg	Ser	Tyr	Leu	Arg	Arg	Pro				
	610					615					620								
Ala	Val	Val	Tyr	Ile	Gly	Ser	Ala	Gly	Lys	Pro	His	Glu	Arg	Val	Glu				
625					630					635					640				
Gln	Lys	Val	Phe	Leu	Met	Ser	Glu	Ser	Glu	Lys	Arg	Lys	Lys	Leu	Leu				
				645					650					655					
Ala	Ile	Leu	Glu	Gln	Gly	Phe	Asp	Pro	Pro	Ile	Ile	Ile	Phe	Val	Asn				
			660					665					670						
Gln	Lys	Lys	Gly	Cys	Asp	Val	Leu	Ala	Lys	Ser	Leu	Glu	Lys	Met	Gly				
		675					680					685							
Tyr	Asn	Ala	Cys	Thr	Leu	His	Gly	Gly	Lys	Gly	Gln	Glu	Gln	Arg	Glu				
	690					695					700								
Phe	Ala	Leu	Ser	Asn	Leu	Lys	Ala	Gly	Ala	Lys	Asp	Ile	Leu	Val	Ala				
705					710					715					720				
Thr	Asp	Val	Ala	Gly	Arg	Gly	Ile	Asp	Ile	Gln	Asp	Val	Ser	Met	Val				
				725					730					735					
Val	Asn	Tyr	Asp	Met	Ala	Lys	Asn	Ile	Glu	Asp	Tyr	Ile	His	Arg	Ile				
			740					745					750						
Gly	Arg	Thr	Gly	Arg	Ala	Gly	Lys	Ser	Gly	Val	Ala	Ile	Thr	Phe	Leu				
		755					760					765							
Thr	Lys	Glu	Asp	Ser	Ala	Val	Phe	Tyr	Glu	Leu	Lys	Gln	Ala	Ile	Leu				
	770					775					780								
Glu	Ser	Pro	Val	Ser	Ser	Cys	Pro	Pro	Glu	Leu	Ala	Asn	His	Pro	Asp				
785					790					795					800				
Ala	Gln	His	Lys	Pro	Gly	Thr	Ile	Leu	Thr	Lys	Lys	Arg	Arg	Glu	Glu				
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Thr Ile Phe Ala
820

<210> 212
<211> 1032
<212> PRT
<213> Homo sapiens

<400> 212

Met Gly Arg Glu Ser Arg His Tyr Arg Lys Arg Ser Ala Ser Arg Gly
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Arg Ser Gly Ser Arg Ser Arg Ser Arg Ser Pro Ser Asp Lys Arg Ser
20 25 30
Lys Arg Gly Asp Asp Arg Arg Ser Arg Ser Arg Asp Arg Asp Arg Arg
35 40 45
Arg Glu Arg Ser Arg Ser Arg Asp Lys Arg Arg Ser Arg Ser Arg Asp
50 55 60
Arg Lys Arg Leu Arg Arg Ser Arg Ser Arg Glu Arg Asp Arg Ser Arg
65 70 75 80
Glu Arg Arg Arg Ser Arg Ser Arg Asp Arg Arg Arg Ser Arg Ser Arg
85 90 95
Ser Arg Gly Arg Arg Ser Arg Ser Ser Ser Pro Gly Asn Lys Ser Lys
100 105 110
Lys Thr Glu Asn Arg Ser Arg Ser Lys Glu Lys Thr Asp Gly Gly Glu
115 120 125
Ser Ser Lys Glu Lys Lys Lys Asp Lys Asp Asp Lys Glu Asp Glu Lys
130 135 140
Glu Lys Asp Ala Gly Asn Phe Asp Gln Asn Lys Leu Glu Glu Glu Met
145 150 155 160
Arg Lys Arg Lys Glu Arg Val Glu Lys Trp Arg Glu Glu Gln Arg Lys
165 170 175
Lys Ala Met Glu Asn Ile Gly Glu Leu Lys Lys Glu Ile Glu Glu Met
180 185 190
Lys Gln Gly Lys Lys Trp Ser Leu Glu Asp Asp Asp Asp Asp Glu Asp
195 200 205
Asp Pro Ala Glu Ala Glu Lys Glu Gly Asn Glu Met Glu Gly Glu Glu
210 215 220
Leu Asp Pro Leu Asp Ala Tyr Met Glu Glu Val Lys Glu Glu Val Lys
225 230 235 240
Lys Phe Asn Met Arg Ser Val Lys Gly Gly Gly Gly Asn Glu Lys Lys
245 250 255
Ser Gly Pro Thr Val Thr Lys Val Val Thr Val Val Thr Thr Lys Lys
260 265 270
Ala Val Val Asp Ser Asp Lys Lys Lys Gly Glu Leu Met Glu Asn Asp
275 280 285

Gln Asp Ala Met Glu Tyr Ser Ser Glu Glu Glu Glu Val Asp Leu Gln
 290 295 300
 Thr Ala Leu Thr Gly Tyr Gln Thr Lys Gln Arg Lys Leu Leu Glu Pro
 305 310 315 320
 Val Asp His Gly Lys Ile Glu Tyr Glu Pro Phe Arg Lys Asn Phe Tyr
 325 330 335
 Val Glu Val Pro Glu Leu Ala Lys Met Ser Gln Glu Glu Val Asn Val
 340 345 350
 Phe Arg Leu Glu Met Glu Gly Ile Thr Val Lys Gly Lys Gly Cys Pro
 355 360 365
 Lys Pro Ile Lys Ser Trp Val Gln Cys Gly Ile Ser Met Lys Ile Leu
 370 375 380
 Asn Ser Leu Lys Lys His Gly Tyr Glu Lys Pro Thr Pro Ile Gln Thr
 385 390 395 400
 Gln Ala Ile Pro Ala Ile Met Ser Gly Arg Asp Leu Ile Gly Ile Ala
 405 410 415
 Lys Thr Gly Ser Gly Lys Thr Ile Ala Phe Leu Leu Pro Met Phe Arg
 420 425 430
 His Ile Met Asp Gln Arg Ser Leu Glu Glu Gly Glu Gly Pro Ile Ala
 435 440 445
 Val Ile Met Thr Pro Thr Arg Glu Leu Ala Leu Gln Ile Thr Lys Glu
 450 455 460
 Cys Lys Lys Phe Ser Lys Thr Leu Gly Leu Arg Val Val Cys Val Tyr
 465 470 475 480
 Gly Gly Thr Gly Ile Ser Glu Gln Ile Ala Glu Leu Lys Arg Gly Ala
 485 490 495
 Glu Ile Ile Val Cys Thr Pro Gly Arg Met Ile Asp Met Leu Ala Ala
 500 505 510
 Asn Ser Gly Arg Val Thr Asn Leu Arg Arg Val Thr Tyr Val Val Leu
 515 520 525
 Asp Glu Ala Asp Arg Met Phe Asp Met Gly Phe Glu Pro Gln Val Met
 530 535 540
 Arg Ile Val Asp Asn Val Arg Pro Asp Arg Gln Thr Val Met Phe Ser
 545 550 555 560
 Ala Thr Phe Pro Arg Ala Met Glu Ala Leu Ala Arg Arg Ile Leu Ser
 565 570 575
 Lys Pro Ile Glu Val Gln Val Gly Gly Arg Ser Val Val Cys Ser Asp
 580 585 590
 Val Glu Gln Gln Val Ile Val Ile Glu Glu Glu Lys Lys Phe Leu Lys
 595 600 605
 Leu Leu Glu Leu Leu Gly His Tyr Gln Glu Ser Gly Ser Val Ile Ile

610					615					620					
Phe	Val	Asp	Lys	Gln	Glu	His	Ala	Asp	Gly	Leu	Leu	Lys	Asp	Leu	Met
625					630					635					640
Arg	Ala	Ser	Tyr	Pro	Cys	Met	Ser	Leu	His	Gly	Gly	Ile	Asp	Gln	Tyr
				645					650					655	
Asp	Arg	Asp	Ser	Ile	Ile	Asn	Asp	Phe	Lys	Asn	Gly	Thr	Cys	Lys	Leu
			660					665					670		
Leu	Val	Ala	Thr	Ser	Val	Ala	Ala	Arg	Gly	Leu	Asp	Val	Lys	His	Leu
		675					680					685			
Ile	Leu	Val	Val	Asn	Tyr	Ser	Cys	Pro	Asn	His	Tyr	Glu	Asp	Tyr	Val
	690					695					700				
His	Arg	Ala	Gly	Arg	Thr	Gly	Arg	Ala	Gly	Asn	Lys	Gly	Tyr	Ala	Tyr
705					710					715					720
Thr	Phe	Ile	Thr	Glu	Asp	Gln	Ala	Arg	Tyr	Ala	Gly	Asp	Ile	Ile	Lys
				725					730					735	
Ala	Leu	Glu	Leu	Ser	Gly	Thr	Ala	Val	Pro	Pro	Asp	Leu	Glu	Lys	Leu
			740					745				750			
Trp	Ser	Asp	Phe	Lys	Asp	Gln	Gln	Lys	Ala	Glu	Gly	Lys	Ile	Ile	Lys
		755					760					765			
Lys	Ser	Ser	Gly	Phe	Ser	Gly	Lys	Gly	Phe	Lys	Phe	Asp	Glu	Thr	Glu
		770				775					780				
Gln	Ala	Leu	Ala	Asn	Glu	Arg	Lys	Lys	Leu	Gln	Lys	Ala	Ala	Leu	Gly
785					790					795					800
Leu	Gln	Asp	Ser	Asp	Asp	Glu	Asp	Ala	Ala	Val	Asp	Ile	Asp	Glu	Gln
				805					810					815	
Ile	Glu	Ser	Met	Phe	Asn	Ser	Lys	Lys	Arg	Val	Lys	Asp	Met	Ala	Ala
			820					825					830		
Pro	Gly	Thr	Ser	Ser	Val	Pro	Ala	Pro	Thr	Ala	Gly	Asn	Ala	Glu	Lys
		835					840					845			
Leu	Glu	Ile	Ala	Lys	Arg	Leu	Ala	Leu	Arg	Ile	Asn	Ala	Gln	Lys	Asn
	850					855					860				
Leu	Gly	Ile	Glu	Ser	Gln	Val	Asp	Val	Met	Gln	Gln	Ala	Thr	Asn	Ala
865					870					875					880
Ile	Leu	Arg	Gly	Gly	Thr	Ile	Leu	Ala	Pro	Thr	Val	Ser	Ala	Lys	Thr
				885					890					895	
Ile	Ala	Glu	Gln	Leu	Ala	Glu	Lys	Ile	Asn	Ala	Lys	Leu	Asn	Tyr	Val
			900					905					910		
Pro	Leu	Glu	Lys	Gln	Glu	Glu	Glu	Arg	Gln	Asp	Gly	Gly	Gln	Asn	Glu
		915					920					925			
Ser	Phe	Lys	Arg	Tyr	Glu	Glu	Glu	Leu	Glu	Ile	Asn	Asp	Phe	Pro	Gln
	930					935					940				

Thr Ala Arg Trp Lys Val Thr Ser Lys Glu Ala Leu Gln Arg Ile Ser
 945 950 955 960
 Glu Tyr Ser Glu Ala Ala Ile Thr Ile Arg Gly Thr Tyr Phe Pro Pro
 965 970 975
 Gly Lys Glu Pro Lys Glu Gly Glu Arg Lys Ile Tyr Leu Ala Ile Glu
 980 985 990
 Ser Ala Asn Glu Leu Ala Val Gln Lys Ala Lys Ala Glu Ile Thr Arg
 995 1000 1005
 Leu Ile Lys Glu Glu Leu Ile Arg Leu Gln Asn Ser Tyr Gln Pro
 1010 1015 1020
 Thr Asn Lys Gly Arg Tyr Lys Val Leu
 1025 1030
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 <211> 437
 <212> PRT
 <213> Homo sapiens
 <400> 213
 Met Ala Thr Arg Ser Cys Arg Glu Lys Ala Gln Lys Leu Asn Glu Gln
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 His Gln Leu Ile Leu Ser Lys Leu Leu Arg Glu Glu Asp Asn Lys Tyr
 20 25 30
 Cys Ala Asp Cys Glu Ala Lys Gly Pro Arg Trp Ala Ser Trp Asn Ile
 35 40 45
 Gly Val Phe Ile Cys Ile Arg Cys Ala Gly Ile His Arg Asn Leu Gly
 50 55 60
 Val His Ile Ser Arg Val Lys Ser Val Asn Leu Asp Gln Trp Thr Ala
 65 70 75 80
 Glu Gln Ile Gln Cys Met Gln Asp Met Gly Asn Thr Lys Ala Arg Leu
 85 90 95
 Leu Tyr Glu Ala Asn Leu Pro Glu Asn Phe Arg Arg Pro Gln Thr Asp
 100 105 110
 Gln Ala Val Glu Phe Phe Ile Arg Asp Lys Tyr Glu Lys Lys Lys Tyr
 115 120 125
 Tyr Asp Lys Asn Ala Ile Ala Ile Thr Asn Lys Glu Lys Glu Lys Lys
 130 135 140
 Lys Glu Glu Lys Lys Arg Glu Lys Glu Pro Glu Lys Pro Ala Lys Pro
 145 150 155 160
 Leu Thr Ala Glu Lys Leu Gln Lys Lys Asp Gln Gln Leu Glu Pro Lys
 165 170 175
 Lys Ser Thr Ser Pro Lys Lys Ala Ala Glu Pro Thr Val Asp Leu Leu
 180 185 190
 Gly Leu Asp Gly Pro Ala Val Ala Pro Val Thr Asn Gly Asn Thr Thr
 195 200 205

Val Pro Pro Leu Asn Asp Asp Leu Asp Ile Phe Gly Pro Met Ile Ser
 210 215 220
 Asn Pro Leu Pro Ala Thr Val Met Pro Pro Ala Gln Gly Thr Pro Ser
 225 230 235 240
 Ala Pro Ala Ala Ala Thr Leu Ser Thr Val Thr Ser Gly Asp Leu Asp
 245 250 255
 Leu Phe Thr Glu Gln Thr Thr Lys Ser Glu Glu Val Ala Lys Lys Gln
 260 265 270
 Leu Ser Lys Asp Ser Ile Leu Ser Leu Tyr Gly Thr Gly Thr Ile Gln
 275 280 285
 Gln Gln Ser Thr Pro Gly Val Phe Met Gly Pro Thr Asn Ile Pro Phe
 290 295 300
 Thr Ser Gln Ala Pro Ala Ala Phe Gln Gly Phe Pro Ser Met Gly Val
 305 310 315 320
 Pro Val Pro Ala Ala Pro Gly Leu Ile Gly Asn Val Met Gly Gln Ser
 325 330 335
 Pro Ser Met Met Val Gly Met Pro Met Pro Asn Gly Phe Met Gly Asn
 340 345 350
 Ala Gln Thr Gly Val Met Pro Leu Pro Gln Asn Val Val Gly Pro Gln
 355 360 365
 Gly Gly Met Val Gly Gln Met Gly Ala Pro Gln Ser Lys Phe Gly Leu
 370 375 380
 Pro Gln Ala Gln Gln Pro Gln Trp Ser Leu Ser Gln Ile Met Gln Lys
 385 390 395 400
 Gly Asp Ala Val Leu Gln His Ser Ile Ile Ser Ala Ile Tyr Trp Pro
 405 410 415
 Thr Thr Arg Trp Leu Lys Cys Pro Leu Val Asp Glu Ser Ala Asp Gly
 420 425 430
 Trp His Glu Tyr Gln
 435
 <210> 214
 <211> 409
 <212> PRT
 <213> Homo sapiens
 <400> 214
 Leu Glu Glu Asp Asn Lys Phe Cys Ala Asp Cys Gln Ser Lys Gly Pro
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 Arg Trp Ala Ser Trp Asn Ile Gly Val Phe Ile Cys Ile Arg Cys Ala
 20 25 30
 Gly Ile His Arg Asn Leu Gly Val His Ile Ser Arg Val Lys Ser Val
 35 40 45
 Asn Leu Asp Gln Trp Thr Gln Glu Gln Ile Gln Cys Met Gln Glu Met

50	55	60
Gly Asn Gly Lys Ala Asn Arg Leu Tyr Glu Ala Tyr Leu Pro Glu Thr 65 70 75 80		
Phe Arg Arg Pro Gln Ile Asp Pro Ala Val Glu Gly Phe Ile Arg Asp 85 90 95		
Lys Tyr Glu Lys Lys Lys Tyr Met Asp Arg Ser Leu Asp Ile Asn Ala 100 105 110		
Phe Arg Lys Glu Lys Asp Asp Lys Trp Lys Arg Gly Ser Glu Pro Val 115 120 125		
Pro Glu Lys Lys Leu Glu Pro Val Val Phe Glu Lys Val Lys Met Pro 130 135 140		
Gln Lys Lys Glu Asp Pro Gln Leu Pro Arg Lys Ser Ser Pro Lys Ser 145 150 155 160		
Thr Ala Pro Val Met Asp Leu Leu Gly Leu Asp Ala Pro Val Ala Cys 165 170 175		
Ser Ile Ala Asn Ser Lys Thr Ser Asn Thr Leu Glu Lys Asp Leu Asp 180 185 190		
Leu Leu Ala Ser Val Pro Ser Pro Ser Ser Ser Gly Ser Arg Lys Val 195 200 205		
Val Gly Ser Met Pro Thr Ala Gly Ser Ala Gly Ser Val Pro Glu Asn 210 215 220		
Leu Asn Leu Phe Pro Glu Pro Gly Ser Lys Ser Glu Glu Ile Gly Lys 225 230 235 240		
Lys Gln Leu Ser Lys Asp Ser Ile Leu Ser Leu Tyr Gly Ser Gln Thr 245 250 255		
Pro Gln Met Pro Thr Gln Ala Met Phe Met Ala Pro Ala Gln Met Ala 260 265 270		
Tyr Pro Thr Ala Tyr Pro Ser Phe Pro Gly Val Thr Pro Pro Asn Ser 275 280 285		
Ile Met Gly Ser Met Met Pro Pro Pro Val Gly Met Val Ala Gln Pro 290 295 300		
Gly Ala Ser Gly Met Val Ala Pro Met Ala Met Pro Ala Gly Tyr Met 305 310 315 320		
Gly Gly Met Gln Ala Ser Met Met Gly Val Pro Asn Gly Met Met Thr 325 330 335		
Thr Gln Gln Ala Gly Tyr Met Ala Gly Met Ala Ala Met Pro Gln Thr 340 345 350		
Val Tyr Gly Val Gln Pro Ala Gln Gln Leu Gln Trp Asn Leu Thr Gln 355 360 365		
Met Thr Gln Gln Met Ala Gly Met Asn Phe Tyr Gly Ala Asn Gly Met 370 375 380		

Met Asn Tyr Gly Gln Ser Met Ser Gly Gly Asn Gly Gln Ala Ala Asn
 385 390 395 400

Gln Thr Leu Ser Pro Gln Met Trp Lys
 405

<210> 215
 <211> 473
 <212> PRT
 <213> Homo sapiens

<400> 215
 Met Ser Thr Glu Leu Phe Ser Ser Thr Arg Glu Glu Gly Ser Ser Gly
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Ser Gly Pro Ser Phe Arg Ser Asn Gln Arg Lys Met Leu Asn Leu Leu
 20 25 30

Leu Glu Arg Asp Thr Ser Phe Thr Val Cys Pro Asp Val Pro Arg Thr
 35 40 45

Pro Val Gly Lys Phe Leu Gly Asp Ser Ala Asn Leu Ser Ile Leu Ser
 50 55 60

Gly Gly Thr Pro Lys Cys Cys Leu Asp Leu Ser Asn Leu Ser Ser Gly
 65 70 75 80

Glu Ile Thr Ala Thr Gln Leu Thr Thr Ser Ala Asp Leu Asp Glu Thr
 85 90 95

Gly His Leu Asp Ser Ser Gly Leu Gln Glu Val His Leu Ala Gly Met
 100 105 110

Asn His Asp Gln His Leu Met Lys Cys Ser Pro Ala Gln Leu Leu Cys
 115 120 125

Ser Thr Pro Asn Gly Leu Asp Arg Gly His Arg Lys Arg Asp Ala Met
 130 135 140

Cys Ser Ser Ser Ala Asn Lys Glu Asn Asp Asn Gly Asn Leu Val Asp
 145 150 155 160

Ser Glu Met Lys Tyr Leu Gly Ser Pro Ile Thr Thr Val Pro Lys Leu
 165 170 175

Asp Lys Asn Pro Asn Leu Gly Glu Asp Gln Ala Glu Glu Ile Ser Asp
 180 185 190

Glu Leu Met Glu Phe Ser Leu Lys Asp Gln Glu Ala Lys Val Ser Arg
 195 200 205

Ser Gly Leu Tyr Arg Ser Pro Ser Met Pro Glu Asn Leu Asn Arg Pro
 210 215 220

Arg Leu Lys Gln Val Glu Lys Phe Lys Asp Asn Thr Ile Pro Asp Lys
 225 230 235 240

Val Lys Lys Lys Tyr Phe Ser Gly Gln Gly Lys Leu Arg Lys Gly Leu
 245 250 255

Cys Leu Lys Lys Thr Val Ser Leu Cys Asp Ile Thr Ile Thr Gln Met
 260 265 270

Leu Glu Glu Asp Ser Asn Gln Gly His Leu Ile Gly Asp Phe Ser Lys
 275 280 285
 Val Cys Ala Leu Pro Thr Val Ser Gly Lys His Gln Asp Leu Lys Tyr
 290 295 300
 Val Asn Pro Glu Thr Val Ala Ala Leu Leu Ser Gly Lys Phe Gln Gly
 305 310 315 320
 Leu Ile Glu Lys Phe Tyr Val Ile Asp Cys Arg Tyr Pro Tyr Glu Tyr
 325 330 335
 Leu Gly Gly His Ile Gln Gly Ala Leu Asn Leu Tyr Ser Gln Glu Glu
 340 345 350
 Leu Phe Asn Phe Phe Leu Lys Lys Pro Ile Val Pro Leu Asp Thr Gln
 355 360 365
 Lys Arg Ile Ile Ile Val Phe His Cys Glu Phe Ser Ser Glu Arg Gly
 370 375 380
 Pro Arg Met Cys Arg Cys Leu Arg Glu Glu Asp Arg Ser Leu Asn Gln
 385 390 395 400
 Tyr Pro Ala Leu Tyr Tyr Pro Glu Leu Tyr Ile Leu Lys Gly Gly Tyr
 405 410 415
 Arg Asp Phe Phe Pro Glu Tyr Met Glu Leu Cys Glu Pro Gln Ser Tyr
 420 425 430
 Cys Pro Met His His Gln Asp His Lys Thr Glu Leu Leu Arg Cys Arg
 435 440 445
 Ser Gln Ser Lys Val Gln Glu Gly Glu Arg Gln Leu Arg Glu Gln Ile
 450 455 460
 Ala Leu Leu Val Lys Asp Met Ser Pro
 465 470
 <210> 216
 <211> 601
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 <213> Homo sapiens
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 Met Glu Val Pro Gln Pro Glu Pro Ala Pro Gly Ser Ala Leu Ser Pro
 1 5 10 15
 Ala Gly Val Cys Gly Gly Ala Gln Arg Pro Gly His Leu Pro Gly Leu
 20 25 30
 Leu Leu Gly Ser His Gly Leu Leu Gly Ser Pro Val Arg Ala Ala Ala
 35 40 45
 Ser Ser Pro Val Thr Thr Leu Thr Gln Thr Met His Asp Leu Ala Gly
 50 55 60
 Leu Gly Ser Arg Ser Arg Leu Thr His Leu Ser Leu Ser Arg Arg Ala
 65 70 75 80
 Ser Glu Ser Ser Leu Ser Ser Glu Ser Ser Glu Ser Ser Asp Ala Gly

85										90					95				
Leu	Cys	Met	Asp	Ser	Pro	Ser	Pro	Met	Asp	Pro	His	Met	Ala	Glu	Gln				
			100						105					110					
Thr	Phe	Glu	Gln	Ala	Ile	Gln	Ala	Ala	Ser	Arg	Ile	Ile	Arg	Asn	Glu				
			115						120					125					
Gln	Phe	Ala	Ile	Arg	Arg	Phe	Gln	Ser	Met	Pro	Val	Arg	Leu	Leu	Gly				
			130						135					140					
His	Ser	Pro	Val	Leu	Arg	Asn	Ile	Thr	Asn	Ser	Gln	Ala	Pro	Asp	Gly				
						150								160					
Arg	Arg	Lys	Ser	Glu	Ala	Gly	Ser	Gly	Ala	Ala	Ser	Ser	Ser	Gly	Glu				
						165								175					
Asp	Lys	Glu	Asn	Val	Arg	Phe	Trp	Lys	Ala	Gly	Val	Gly	Ala	Leu	Arg				
									185					190					
Glu	Glu	Glu	Gly	Ala	Cys	Trp	Gly	Gly	Ser	Leu	Ala	Cys	Glu	Asp	Pro				
									200					205					
Pro	Leu	Pro	Ser	Trp	Leu	Gln	Asp	Gly	Phe	Val	Phe	Lys	Met	Pro	Trp				
									215					220					
Lys	Pro	Thr	His	Pro	Ser	Ser	Thr	His	Ala	Leu	Ala	Glu	Trp	Ala	Ser				
									235					240					
Arg	Arg	Glu	Ala	Phe	Ala	Gln	Arg	Pro	Ser	Ser	Ala	Pro	Asp	Leu	Met				
									250					255					
Cys	Leu	Ser	Pro	Asp	Arg	Lys	Met	Glu	Val	Glu	Glu	Leu	Ser	Pro	Leu				
									265					270					
Ala	Leu	Gly	Arg	Phe	Ser	Leu	Thr	Pro	Ala	Glu	Gly	Asp	Thr	Glu	Glu				
									280					285					
Asp	Asp	Gly	Phe	Val	Asp	Ile	Leu	Glu	Ser	Asp	Leu	Lys	Asp	Asp	Asp				
									295					300					
Ala	Val	Pro	Pro	Gly	Met	Glu	Ser	Leu	Ile	Ser	Ala	Pro	Leu	Val	Lys				
									315					320					
Thr	Leu	Glu	Lys	Glu	Glu	Glu	Lys	Asp	Leu	Val	Met	Tyr	Ser	Lys	Cys				
									330					335					
Gln	Arg	Leu	Phe	Arg	Ser	Pro	Ser	Met	Pro	Cys	Ser	Val	Ile	Arg	Pro				
									345					350					
Ile	Leu	Lys	Arg	Leu	Glu	Arg	Pro	Gln	Asp	Arg	Asp	Thr	Pro	Val	Gln				
									360					365					
Asn	Lys	Arg	Arg	Arg	Ser	Val	Thr	Pro	Pro	Glu	Glu	Gln	Gln	Glu	Ala				
									375					380					
Glu	Glu	Pro	Lys	Ala	Arg	Val	Leu	Arg	Ser	Lys	Ser	Leu	Cys	His	Asp				
									395					400					
Glu	Ile	Glu	Asn	Leu	Leu	Asp	Ser	Asp	His	Arg	Glu	Leu	Ile	Gly	Asp				
									410					415					

Tyr Ser Lys Ala Phe Leu Leu Gln Thr Val Asp Gly Lys His Gln Asp
 420 425 430
 Leu Lys Tyr Ile Ser Pro Glu Thr Met Val Ala Leu Leu Thr Gly Lys
 435 440 445
 Phe Ser Asn Ile Val Asp Lys Phe Val Ile Val Asp Cys Arg Tyr Pro
 450 455 460
 Tyr Glu Tyr Glu Gly Gly His Ile Lys Thr Ala Val Asn Leu Pro Leu
 465 470 475 480
 Glu Arg Asp Ala Glu Ser Phe Leu Leu Lys Ser Pro Ile Ala Pro Cys
 485 490 495
 Ser Leu Asp Lys Arg Val Ile Leu Ile Phe His Cys Glu Phe Ser Ser
 500 505 510
 Glu Arg Gly Pro Arg Met Cys Arg Phe Ile Arg Glu Arg Asp Arg Ala
 515 520 525
 Val Asn Asp Tyr Pro Ser Leu Tyr Tyr Pro Glu Met Tyr Ile Leu Lys
 530 535 540
 Gly Gly Tyr Lys Glu Phe Phe Pro Gln His Pro Asn Phe Cys Glu Pro
 545 550 555 560
 Gln Asp Tyr Arg Pro Met Asn His Glu Ala Phe Lys Asp Glu Leu Lys
 565 570 575
 Thr Phe Arg Leu Lys Thr Arg Ser Trp Ala Gly Glu Arg Ser Arg Arg
 580 585 590
 Glu Leu Cys Ser Arg Leu Gln Asp Gln
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 <212> PRT
 <213> Homo sapiens
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 Ser Ala Ala Gly Gly Leu Ser Pro Val Thr Asn Leu Thr Val Thr Met
 35 40 45
 Asp Gln Leu Gln Gly Leu Gly Ser Asp Tyr Glu Gln Pro Leu Glu Val
 50 55 60
 Lys Asn Asn Ser Asn Leu Gln Arg Met Gly Ser Ser Glu Ser Thr Asp
 65 70 75 80
 Ser Gly Phe Cys Leu Asp Ser Pro Gly Pro Leu Asp Ser Lys Glu Asn
 85 90 95
 Leu Glu Asn Pro Met Arg Arg Ile His Ser Leu Pro Gln Lys Leu Leu
 100 105 110

Gly Cys Ser Pro Ala Leu Lys Arg Ser His Ser Asp Ser Leu Asp His
 115 120 125
 Asp Ile Phe Gln Leu Ile Asp Pro Asp Glu Asn Lys Glu Asn Glu Ala
 130 135 140
 Phe Glu Phe Lys Lys Pro Val Arg Pro Val Ser Arg Gly Cys Leu His
 145 150 155 160
 Ser His Gly Leu Gln Glu Gly Lys Asp Leu Phe Thr Gln Arg Gln Asn
 165 170 175
 Ser Ala Gln Leu Gly Met Leu Ser Ser Asn Glu Arg Asp Ser Ser Glu
 180 185 190
 Pro Gly Asn Phe Ile Pro Leu Phe Thr Pro Gln Ser Pro Val Thr Ala
 195 200 205
 Thr Leu Ser Asp Glu Asp Asp Gly Phe Val Asp Leu Leu Asp Gly Glu
 210 215 220
 Asn Leu Lys Asn Glu Glu Glu Thr Pro Ser Cys Met Ala Ser Leu Trp
 225 230 235 240
 Thr Ala Pro Leu Val Met Arg Thr Thr Asn Leu Asp Asn Arg Cys Lys
 245 250 255
 Leu Phe Asp Ser Pro Ser Leu Cys Ser Ser Ser Thr Arg Ser Val Leu
 260 265 270
 Lys Arg Pro Glu Arg Ser Gln Glu Glu Ser Pro Pro Gly Ser Thr Lys
 275 280 285
 Arg Arg Lys Ser Met Ser Gly Ala Ser Pro Lys Glu Ser Thr Asn Pro
 290 295 300
 Glu Lys Ala His Glu Thr Leu His Gln Ser Leu Ser Leu Ala Ser Ser
 305 310 315 320
 Pro Lys Gly Thr Ile Glu Asn Ile Leu Asp Asn Asp Pro Arg Asp Leu
 325 330 335
 Ile Gly Asp Phe Ser Lys Gly Tyr Leu Phe His Thr Val Ala Gly Lys
 340 345 350
 His Gln Asp Leu Lys Tyr Ile Ser Pro Glu Ile Met Ala Ser Val Leu
 355 360 365
 Asn Gly Lys Phe Ala Asn Leu Ile Lys Glu Phe Val Ile Ile Asp Cys
 370 375 380
 Arg Tyr Pro Tyr Glu Tyr Glu Gly Gly His Ile Lys Gly Ala Val Asn
 385 390 395 400
 Leu His Met Glu Glu Glu Val Glu Asp Phe Leu Leu Lys Lys Pro Ile
 405 410 415
 Val Pro Thr Asp Gly Lys Arg Val Ile Val Val Phe His Cys Glu Phe
 420 425 430
 Ser Ser Glu Arg Gly Pro Arg Met Cys Arg Tyr Val Arg Glu Arg Asp

435 440 445
 Arg Leu Gly Asn Glu Tyr Pro Lys Leu His Tyr Pro Glu Leu Tyr Val
 450 455 460
 Leu Lys Gly Gly Tyr Lys Glu Phe Phe Met Lys Cys Gln Ser Tyr Cys
 465 470 475 480
 Glu Pro Pro Ser Tyr Arg Pro Met His His Glu Asp Phe Lys Glu Asp
 485 490 495
 Leu Lys Lys Phe Arg Thr Lys Ser Arg Thr Trp Ala Gly Glu Lys Ser
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 Lys Arg Glu Met Tyr Ser Arg Leu Lys Lys Leu
 515 520

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 35 40 45
 Asp Gly Asp Val Phe Arg Phe Pro Gly Leu Cys Asp Tyr Asn Phe Ala
 50 55 60
 Ser Asp Cys Arg Gly Ser Tyr Lys Glu Phe Ala Val His Leu Lys Arg
 65 70 75 80
 Gly Pro Gly Gln Ala Glu Ala Pro Ala Gly Val Glu Ser Ile Leu Leu
 85 90 95
 Thr Ile Lys Asp Asp Thr Ile Tyr Leu Thr Arg His Leu Ala Val Leu
 100 105 110
 Asn Gly Ala Val Val Ser Thr Pro His Tyr Ser Pro Gly Leu Leu Ile
 115 120 125
 Glu Lys Ser Asp Ala Tyr Thr Lys Val Tyr Ser Arg Ala Gly Leu Thr
 130 135 140
 Leu Met Trp Asn Arg Glu Asp Ala Leu Met Leu Glu Leu Asp Thr Lys
 145 150 155 160
 Phe Arg Asn His Thr Cys Gly Leu Cys Gly Asp Tyr Asn Gly Leu Gln
 165 170 175
 Ser Tyr Ser Glu Phe Leu Ser Asp Gly Val Leu Phe Ser Pro Leu Glu
 180 185 190
 Phe Gly Asn Met Gln Lys Ile Asn Gln Pro Asp Val Val Cys Glu Asp
 195 200 205

Pro Glu Glu Glu Val Ala Pro Ala Ser Cys Ser Glu His Arg Ala Glu
 210 215 220
 Cys Glu Arg Leu Leu Thr Ala Glu Ala Phe Ala Asp Cys Gln Asp Leu
 225 230 235 240
 Val Pro Leu Glu Pro Tyr Leu Arg Ala Cys Gln Gln Asp Arg Cys Arg
 245 250 255
 Cys Pro Gly Gly Asp Thr Cys Val Cys Ser Thr Val Ala Glu Phe Ser
 260 265 270
 Arg Gln Cys Ser His Ala Gly Gly Arg Pro Gly Asn Trp Arg Thr Ala
 275 280 285
 Thr Leu Cys Pro Lys Thr Cys Pro Gly Asn Leu Val Tyr Leu Glu Ser
 290 295 300
 Gly Ser Pro Cys Met Asp Thr Cys Ser His Leu Glu Val Ser Ser Leu
 305 310 315 320
 Cys Glu Glu His Arg Met Asp Gly Cys Phe Cys Pro Glu Gly Thr Val
 325 330 335
 Tyr Asp Asp Ile Gly Asp Ser Gly Cys Val Pro Val Ser Gln Cys His
 340 345 350
 Cys Arg Leu His Gly His Leu Tyr Thr Pro Gly Gln Glu Ile Thr Asn
 355 360 365
 Asp Cys Glu Gln Cys Val Cys Asn Ala Gly Arg Trp Val Cys Lys Asp
 370 375 380
 Leu Pro Cys Pro Gly Thr Cys Ala Leu Glu Gly Gly Ser His Ile Thr
 385 390 395 400
 Thr Phe Asp Gly Lys Thr Tyr Thr Phe His Gly Asp Cys Tyr Tyr Val
 405 410 415
 Leu Ala Lys Gly Asp His Asn Asp Ser Tyr Ala Leu Leu Gly Glu Leu
 420 425 430
 Ala Pro Cys Gly Ser Thr Asp Lys Gln Thr Cys Leu Lys Thr Val Val
 435 440 445
 Leu Leu Ala Asp Lys Lys Lys Asn Ala Val Val Phe Lys Ser Asp Gly
 450 455 460
 Ser Val Leu Leu Asn Gln Leu Gln Val Asn Leu Pro His Val Thr Ala
 465 470 475 480
 Ser Phe Ser Val Phe Arg Pro Ser Ser Tyr His Ile Met Val Ser Met
 485 490 495
 Ala Ile Gly Val Arg Leu Gln Val Gln Leu Ala Pro Val Met Gln Leu
 500 505 510
 Phe Val Thr Leu Asp Gln Ala Ser Gln Gly Gln Val Gln Gly Leu Cys
 515 520 525
 Gly Asn Phe Asn Gly Leu Glu Gly Asp Asp Phe Lys Thr Ala Ser Gly
 530 535 540

Leu Val Glu Ala Thr Gly Ala Gly Phe Ala Asn Thr Trp Lys Ala Gln
 545 550 555 560
 Ser Thr Cys His Asp Lys Leu Asp Trp Leu Asp Asp Pro Cys Ser Leu
 565 570 575
 Asn Ile Glu Ser Ala Asn Tyr Ala Glu His Trp Cys Ser Leu Leu Lys
 580 585 590
 Lys Thr Glu Thr Pro Phe Gly Arg Cys His Ser Ala Val Asp Pro Ala
 595 600 605
 Glu Tyr Tyr Lys Arg Cys Lys Tyr Asp Thr Cys Asn Cys Gln Asn Asn
 610 615 620
 Glu Asp Cys Leu Cys Ala Ala Leu Ser Ser Tyr Ala Arg Ala Cys Thr
 625 630 635 640
 Ala Lys Gly Val Met Leu Trp Gly Trp Arg Glu His Val Cys Asn Lys
 645 650 655
 Asp Val Gly Ser Cys Pro Asn Ser Gln Val Phe Leu Tyr Asn Leu Thr
 660 665 670
 Thr Cys Gln Gln Thr Cys Arg Ser Leu Ser Glu Ala Asp Ser His Cys
 675 680 685
 Leu Glu Gly Phe Ala Pro Val Asp Gly Cys Gly Cys Pro Asp His Thr
 690 695 700
 Phe Leu Asp Glu Lys Gly Arg Cys Val Pro Leu Ala Lys Cys Ser Cys
 705 710 715 720
 Tyr His Arg Gly Leu Tyr Leu Glu Ala Gly Asp Val Val Val Arg Gln
 725 730 735
 Glu Glu Arg Cys Val Cys Arg Asp Gly Arg Leu His Cys Arg Gln Ile
 740 745 750
 Arg Leu Ile Gly Gln Ser Cys Thr Ala Pro Lys Ile His Met Asp Cys
 755 760 765
 Ser Asn Leu Thr Ala Leu Ala Thr Ser Lys Pro Arg Ala Leu Ser Cys
 770 775 780
 Gln Thr Leu Ala Ala Gly Tyr Tyr His Thr Glu Cys Val Ser Gly Cys
 785 790 795 800
 Val Cys Pro Asp Gly Leu Met Asp Asp Gly Arg Gly Gly Cys Val Val
 805 810 815
 Glu Lys Glu Cys Pro Cys Val His Asn Asn Asp Leu Tyr Ser Ser Gly
 820 825 830
 Ala Lys Ile Lys Val Asp Cys Asn Thr Cys Thr Cys Lys Arg Gly Arg
 835 840 845
 Trp Val Cys Thr Gln Ala Val Cys His Gly Thr Cys Ser Ile Tyr Gly
 850 855 860
 Ser Gly His Tyr Ile Thr Phe Asp Gly Lys Tyr Tyr Asp Phe Asp Gly

865		870		875		880
His Cys Ser Tyr Val Ala Val Gln Asp Tyr Cys Gly Gln Asn Ser Ser						
		885		890		895
Leu Gly Ser Phe Ser Ile Ile Thr Glu Asn Val Pro Cys Gly Thr Thr						
		900		905		910
Gly Val Thr Cys Ser Lys Ala Ile Lys Ile Phe Met Gly Arg Thr Glu						
		915		920		925
Leu Lys Leu Glu Asp Lys His Arg Val Val Ile Gln Arg Asp Glu Gly						
		930		935		940
His His Val Ala Tyr Thr Thr Arg Glu Val Gly Gln Tyr Leu Val Val						
		945		950		955
						960
Glu Ser Ser Thr Gly Ile Ile Val Ile Trp Asp Lys Arg Thr Thr Val						
		965		970		975
Phe Ile Lys Leu Ala Pro Ser Tyr Lys Gly Thr Val Cys Gly Leu Cys						
		980		985		990
Gly Asn Phe Asp His Arg Ser Asn Asn Asp Phe Thr Thr Arg Asp His						
		995		1000		1005
Met Val Val Ser Ser Glu Leu Asp Phe Gly Asn Ser Trp Lys Glu						
		1010		1015		1020
Ala Pro Thr Cys Pro Asp Val Ser Thr Asn Pro Glu Pro Cys Ser						
		1025		1030		1035
Leu Asn Pro His Arg Arg Ser Trp Ala Glu Lys Gln Cys Ser Ile						
		1040		1045		1050
Leu Lys Ser Ser Val Phe Ser Ile Cys His Ser Lys Val Asp Pro						
		1055		1060		1065
Lys Pro Phe Tyr Glu Ala Cys Val His Asp Ser Cys Ser Cys Asp						
		1070		1075		1080
Thr Gly Gly Asp Cys Glu Cys Phe Cys Ser Ala Val Ala Ser Tyr						
		1085		1090		1095
Ala Gln Glu Cys Thr Lys Glu Gly Ala Cys Val Phe Trp Arg Thr						
		1100		1105		1110
Pro Asp Leu Cys Pro Ile Phe Cys Asp Tyr Tyr Asn Pro Pro His						
		1115		1120		1125
Glu Cys Glu Trp His Tyr Glu Pro Cys Gly Asn Arg Ser Phe Glu						
		1130		1135		1140
Thr Cys Arg Thr Ile Asn Gly Ile His Ser Asn Ile Ser Val Ser						
		1145		1150		1155
Tyr Leu Glu Gly Cys Tyr Pro Arg Cys Pro Lys Asp Arg Pro Ile						
		1160		1165		1170
Tyr Glu Glu Asp Leu Lys Lys Cys Val Thr Ala Asp Lys Cys Gly						
		1175		1180		1185

Cys Tyr	Val Glu Asp Thr	His Tyr	Pro Pro Gly	Ala	Ser Val Pro
1190		1195		1200	
Thr Glu	Glu Thr Cys Lys	Ser Cys	Val Cys Thr	Asn	Ser Ser Gln
1205		1210		1215	
Val Val	Cys Arg Pro Glu	Glu Gly	Lys Ile Leu	Asn	Gln Thr Gln
1220		1225		1230	
Asp Gly	Ala Phe Cys Tyr	Trp Glu	Ile Cys Gly	Pro	Asn Gly Thr
1235		1240		1245	
Val Glu	Lys His Phe Asn	Ile Cys	Ser Ile Thr	Thr	Arg Pro Ser
1250		1255		1260	
Thr Leu	Thr Thr Phe Thr	Thr Ile	Thr Leu Pro	Thr	Thr Pro Thr
1265		1270		1275	
Ser Phe	Thr Thr Thr Thr	Thr Thr	Thr Thr Pro	Thr	Ser Ser Thr
1280		1285		1290	
Val Leu	Ser Thr Thr Pro	Lys Leu	Cys Cys Leu	Trp	Ser Asp Trp
1295		1300		1305	
Ile Asn	Glu Asp His Pro	Ser Ser	Gly Ser Asp	Asp	Gly Asp Arg
1310		1315		1320	
Glu Pro	Phe Asp Gly Val	Cys Gly	Ala Pro Glu	Asp	Ile Glu Cys
1325		1330		1335	
Arg Ser	Val Lys Asp Pro	His Leu	Ser Leu Glu	Gln	His Gly Gln
1340		1345		1350	
Lys Val	Gln Cys Asp Val	Ser Val	Gly Phe Ile	Cys	Lys Asn Glu
1355		1360		1365	
Asp Gln	Phe Gly Asn Gly	Pro Phe	Gly Leu Cys	Tyr	Asp Tyr Lys
1370		1375		1380	
Ile Arg	Val Asn Cys Cys	Trp Pro	Met Asp Lys	Cys	Ile Thr Thr
1385		1390		1395	
Pro Ser	Pro Pro Thr Thr	Thr Pro	Ser Pro Pro	Pro	Thr Thr Thr
1400		1405		1410	
Thr Thr	Leu Pro Pro Thr	Thr Thr	Pro Ser Pro	Pro	Thr Thr Thr
1415		1420		1425	
Thr Thr	Thr Pro Pro Pro	Thr Thr	Pro Ser Pro	Pro	Pro Ile Thr
1430		1435		1440	
Thr Thr	Thr Thr Pro Leu	Pro Thr	Thr Thr Pro	Ser	Pro Pro Ile
1445		1450		1455	
Ser Thr	Thr Thr Thr Pro	Pro Pro	Thr Thr Thr	Pro	Ser Pro Pro
1460		1465		1470	
Thr Thr	Thr Pro Ser Pro	Pro Thr	Thr Thr Pro	Ser	Pro Pro Thr
1475		1480		1485	
Thr Thr	Thr Thr Thr Pro	Pro Pro	Thr Thr Thr	Pro	Ser Pro Pro
1490		1495		1500	

Met	Thr	Thr	Pro	Ile	Thr	Pro	Pro	Ala	Ser	Thr	Thr	Thr	Leu	Pro
1505						1510					1515			
Pro	Thr	Thr	Thr	Pro	Ser	Pro	Pro	Thr	Thr	Thr	Thr	Thr	Thr	Pro
1520						1525					1530			
Pro	Pro	Thr	Thr	Thr	Pro	Ser	Pro	Pro	Thr	Thr	Thr	Pro	Ile	Thr
1535						1540					1545			
Pro	Pro	Thr	Ser	Thr	Thr	Thr	Leu	Pro	Pro	Thr	Thr	Thr	Pro	Ser
1550						1555					1560			
Pro	Pro	Pro	Thr	Thr	Thr	Thr	Thr	Pro	Pro	Pro	Thr	Thr	Thr	Pro
1565						1570					1575			
Ser	Pro	Pro	Thr	Thr	Thr	Thr	Pro	Ser	Pro	Pro	Thr	Ile	Thr	Thr
1580						1585					1590			
Thr	Thr	Pro	Pro	Pro	Thr	Thr	Thr	Pro	Ser	Pro	Pro	Thr	Thr	Thr
1595						1600					1605			
Thr	Thr	Thr	Pro	Pro	Pro	Thr	Thr	Thr	Pro	Ser	Pro	Pro	Thr	Thr
1610						1615					1620			
Thr	Pro	Ile	Thr	Pro	Pro	Thr	Ser	Thr	Thr	Thr	Leu	Pro	Pro	Thr
1625						1630					1635			
Thr	Thr	Pro	Ser	Pro	Pro	Pro	Thr	Thr	Thr	Thr	Thr	Pro	Pro	Pro
1640						1645					1650			
Thr	Thr	Thr	Pro	Ser	Pro	Pro	Thr	Thr	Thr	Thr	Pro	Ser	Pro	Pro
1655						1660					1665			
Ile	Thr	Thr	Thr	Thr	Thr	Pro	Pro	Pro	Thr	Thr	Thr	Pro	Ser	Ser
1670						1675					1680			
Pro	Ile	Thr	Thr	Thr	Pro	Ser	Pro	Pro	Thr	Thr	Thr	Met	Thr	Thr
1685						1690					1695			
Pro	Ser	Pro	Thr	Thr	Thr	Pro	Ser	Ser	Pro	Ile	Thr	Thr	Thr	Thr
1700						1705					1710			
Thr	Pro	Ser	Ser	Thr	Thr	Thr	Pro	Ser	Pro	Pro	Pro	Thr	Thr	Met
1715						1720					1725			
Thr	Thr	Pro	Ser	Pro	Thr	Thr	Thr	Pro	Ser	Pro	Pro	Thr	Thr	Thr
1730						1735					1740			
Met	Thr	Thr	Leu	Pro	Pro	Thr	Thr	Thr	Ser	Ser	Pro	Leu	Thr	Thr
1745						1750					1755			
Thr	Pro	Leu	Pro	Pro	Ser	Ile	Thr	Pro	Pro	Thr	Phe	Ser	Pro	Phe
1760						1765					1770			
Ser	Thr	Thr	Thr	Pro	Thr	Thr	Pro	Cys	Val	Pro	Leu	Cys	Asn	Trp
1775						1780					1785			
Thr	Gly	Trp	Leu	Asp	Ser	Gly	Lys	Pro	Asn	Phe	His	Lys	Pro	Gly
1790						1795					1800			
Gly	Asp	Thr	Glu	Leu	Ile	Gly	Asp	Val	Cys	Gly	Pro	Gly	Trp	Ala

1805	1810	1815
Ala Asn Ile Ser Cys Arg 1820	Ala Thr Met Tyr Pro 1825	Asp Val Pro Ile 1830
Gly Gln Leu Gly Gln Thr 1835	Val Val Cys Asp Val 1840	Ser Val Gly Leu 1845
Ile Cys Lys Asn Glu Asp 1850	Gln Lys Pro Gly Gly 1855	Val Ile Pro Met 1860
Ala Phe Cys Leu Asn Tyr 1865	Glu Ile Asn Val Gln 1870	Cys Cys Glu Cys 1875
Val Thr Gln Pro Thr Thr 1880	Met Thr Thr Thr Thr 1885	Thr Glu Asn Pro 1890
Thr Pro Pro Thr Thr Thr 1895	Pro Ile Thr Thr Thr 1900	Thr Thr Val Thr 1905
Pro Thr Pro Thr Pro Thr 1910	Gly Thr Gln Thr Pro 1915	Thr Thr Thr Pro 1920
Ile Thr Thr Thr Thr Thr 1925	Val Thr Pro Thr Pro 1930	Thr Pro Thr Gly 1935
Thr Gln Thr Pro Thr Thr 1940	Thr Pro Ile Thr Thr 1945	Thr Thr Val 1950
Thr Pro Thr Pro Thr Pro 1955	Thr Gly Thr Gln Thr 1960	Pro Thr Thr Thr 1965
Pro Ile Thr Thr Thr Thr 1970	Thr Val Thr Pro Thr 1975	Pro Thr Pro Thr 1980
Gly Thr Gln Thr Pro Thr 1985	Thr Thr Pro Ile Thr 1990	Thr Thr Thr 1995
Val Thr Pro Thr Pro Thr 2000	Pro Thr Gly Thr Gln 2005	Thr Pro Thr Thr 2010
Thr Pro Ile Thr Thr Thr 2015	Thr Thr Val Thr Pro 2020	Thr Pro Thr Pro 2025
Thr Gly Thr Gln Thr Pro 2030	Thr Thr Pro Thr Thr 2035	Thr Thr Thr 2040
Thr Val Thr Pro Thr Pro 2045	Thr Pro Thr Gly Thr 2050	Gln Thr Pro Thr 2055
Thr Thr Pro Ile Thr Thr 2060	Thr Thr Val Thr Thr 2065	Pro Thr Pro Thr 2070
Pro Thr Gly Thr Gln Thr 2075	Pro Thr Thr Thr Pro 2080	Ile Thr Thr Thr 2085
Thr Thr Val Thr Pro Thr 2090	Pro Thr Pro Thr Gly 2095	Thr Gln Thr Pro 2100
Thr Thr Thr Pro Ile Thr 2105	Thr Thr Thr Val Thr 2110	Thr Pro Thr Pro 2115

Thr 2120	Pro	Thr Gly	Thr Gln	Thr 2125	Pro	Thr	Thr	Thr	Pro 2130	Ile	Thr	Thr
Thr 2135	Thr	Thr Val	Thr Pro	Thr 2140	Pro	Thr	Pro	Thr	Gly 2145	Thr	Gln	Thr
Pro 2150	Thr	Thr Thr	Pro Ile	Thr 2155	Thr	Thr	Thr	Thr	Val 2160	Thr	Pro	Thr
Pro 2165	Thr	Pro Thr	Gly Thr	Gln 2170	Thr	Pro	Thr	Thr	Thr 2175	Pro	Ile	Thr
Thr 2180	Thr	Thr Thr	Val Thr	Pro 2185	Thr	Pro	Thr	Pro	Thr 2190	Gly	Thr	Gln
Thr 2195	Pro	Thr Thr	Thr Pro	Ile 2200	Thr	Thr	Thr	Thr	Thr 2205	Val	Thr	Pro
Thr 2210	Pro	Thr Pro	Thr Gly	Thr 2215	Gln	Thr	Pro	Thr	Thr 2220	Thr	Pro	Ile
Thr 2225	Thr	Thr Thr	Thr Val	Thr 2230	Pro	Thr	Pro	Thr	Pro 2235	Thr	Gly	Thr
Gln 2240	Thr	Pro Thr	Thr Thr	Pro 2245	Ile	Thr	Thr	Thr	Thr 2250	Thr	Val	Thr
Pro 2255	Thr	Pro Thr	Pro Thr	Gly 2260	Thr	Gln	Thr	Pro	Thr 2265	Thr	Thr	Pro
Ile 2270	Thr	Thr Thr	Thr Thr	Val 2275	Thr	Pro	Thr	Pro	Thr 2280	Pro	Thr	Gly
Thr 2285	Gln	Thr Pro	Thr Thr	Thr 2290	Pro	Ile	Thr	Thr	Thr 2295	Thr	Thr	Val
Thr 2300	Pro	Thr Pro	Thr Pro	Thr 2305	Gly	Thr	Gln	Thr	Pro 2310	Thr	Thr	Thr
Pro 2315	Ile	Thr Thr	Thr Thr	Thr 2320	Val	Thr	Pro	Thr	Pro 2325	Thr	Pro	Thr
Gly 2330	Thr	Gln Thr	Pro Thr	Thr 2335	Thr	Pro	Ile	Thr	Thr 2340	Thr	Thr	Thr
Val 2345	Thr	Pro Thr	Pro Thr	Pro 2350	Thr	Gly	Thr	Gln	Thr 2355	Pro	Thr	Thr
Thr 2360	Pro	Ile Thr	Thr Thr	Thr 2365	Thr	Val	Thr	Pro	Thr 2370	Pro	Thr	Pro
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Thr 2390	Val	Thr Pro	Thr Pro	Thr 2395	Pro	Thr	Gly	Thr	Gln 2400	Thr	Pro	Thr
Thr 2405	Thr	Pro Ile	Thr Thr	Thr 2410	Thr	Thr	Val	Thr	Pro 2415	Thr	Pro	Thr
Pro 2420	Thr	Gly Thr	Gln Thr	Pro 2425	Thr	Thr	Thr	Pro	Ile 2430	Thr	Thr	Thr

Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro	2435	2440	2445
Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro	2450	2455	2460
Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Thr Pro Ile Thr Thr	2465	2470	2475
Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr	2480	2485	2490
Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr	2495	2500	2505
Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Thr Pro Ile Thr	2510	2515	2520
Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln	2525	2530	2535
Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro	2540	2545	2550
Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Thr Pro Ile	2555	2560	2565
Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr	2570	2575	2580
Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Thr Val Thr	2585	2590	2595
Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr Thr Pro	2600	2605	2610
Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly	2615	2620	2625
Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr Thr Val	2630	2635	2640
Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr Thr	2645	2650	2655
Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr	2660	2665	2670
Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr	2675	2680	2685
Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr	2690	2695	2700
Thr Pro Ile Thr Thr Thr Thr Thr Val Thr Pro Thr Pro Thr Pro	2705	2710	2715
Thr Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr	2720	2725	2730
Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr			

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Thr Thr Thr Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr		
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Gly Thr Gln Thr Pro Thr Thr Thr Pro Ile Thr Thr Thr Thr Thr		
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Val Thr Pro Thr Pro Thr Pro Thr Gly Thr Gln Thr Pro Thr Thr		
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Thr	Val	Thr	Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr
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Thr	Thr	Pro	Ile	Thr	Thr	Thr	Thr	Thr	Val	Thr	Pro	Thr	Pro	Thr
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Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro	Ile	Thr	Thr	Thr
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Pro	Thr	Pro	Thr	Pro	Thr	Gly	Thr	Gln	Thr	Pro	Thr	Thr	Thr	Pro
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Gly Thr	Gln Thr	Pro Thr	Thr Thr	Pro Ile
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Val Thr	Pro Thr	Pro Thr	Pro Thr	Gln Thr
3725		3730		3735
Thr Pro	Ile Thr	Thr Thr	Thr Thr	Val Thr
3740		3745		3750
Thr Gly	Thr Gln	Thr Pro	Thr Thr	Pro Ile
3755		3760		3765
Thr Val	Thr Pro	Thr Pro	Thr Thr	Gly Thr
3770		3775		3780
Thr Thr	Pro Ile	Thr Thr	Thr Thr	Val Thr
3785		3790		3795
Pro Thr	Gly Thr	Gln Thr	Pro Thr	Ile Thr
3800		3805		3810
Thr Thr	Val Thr	Pro Thr	Thr Thr	Gly Thr
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Thr Thr	Thr Pro	Ile Thr	Thr Thr	Thr Val
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3845		3850		3855
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Pro Thr	Thr Thr	Pro Ile	Thr Thr	Thr Thr
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Pro Thr	Pro Thr	Gly Thr	Gln Thr	Thr Thr
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Gln Thr	Pro Thr	Thr Thr	Pro Thr	Ile Thr
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Pro Thr 3980	Pro Thr Pro Thr 3985	Gly Thr Gln Thr Pro Thr 3990	Thr Thr Pro
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Ser Thr 4220	Pro Gln Thr Ser Arg 4225	Ser Thr Ser Ser Pro 4230	Leu Thr Glu
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Ser Thr 4250	Ala Pro Pro Ser Thr 4255	Pro Thr Ala Pro Thr 4260	Thr Thr Ser
Gly Gly 4265	His Thr Leu Ser Pro 4270	Pro Pro Ser Thr Thr 4275	Thr Ser Pro
Pro Gly 4280	Thr Pro Thr Arg Gly 4285	Thr Thr Thr Gly Ser 4290	Ser Ser Ala

Pro Thr 4295	Pro Ser Thr Val 4300	Gln Thr Thr Thr Thr 4305	Ser Ala Trp Thr
Pro Thr 4310	Pro Thr Pro Leu Ser 4315	Thr Pro Ser Ile Ile 4320	Arg Thr Thr
Gly Leu 4325	Arg Pro Tyr Pro Ser 4330	Ser Val Leu Ile Cys 4335	Cys Val Leu
Asn Asp 4340	Thr Tyr Tyr Ala Pro 4345	Gly Glu Glu Val Tyr 4350	Asn Gly Thr
Tyr Gly 4355	Asp Thr Cys Tyr Phe 4360	Val Asn Cys Ser Leu 4365	Ser Cys Thr
Leu Glu 4370	Phe Tyr Asn Trp Ser 4375	Cys Pro Ser Thr Pro 4380	Ser Pro Thr
Pro Thr 4385	Pro Ser Lys Ser Thr 4390	Pro Thr Pro Ser Lys 4395	Pro Ser Ser
Thr Pro 4400	Ser Lys Pro Thr Pro 4405	Gly Thr Lys Pro Pro 4410	Glu Cys Pro
Asp Phe 4415	Asp Pro Pro Arg Gln 4420	Glu Asn Glu Thr Trp 4425	Trp Leu Cys
Asp Cys 4430	Phe Met Ala Thr Cys 4435	Lys Tyr Asn Asn Thr 4440	Val Glu Ile
Val Lys 4445	Val Glu Cys Glu Pro 4450	Pro Pro Met Pro Thr 4455	Cys Ser Asn
Gly Leu 4460	Gln Pro Val Arg Val 4465	Glu Asp Pro Asp Gly 4470	Cys Cys Trp
His Trp 4475	Glu Cys Asp Cys Tyr 4480	Cys Thr Gly Trp Gly 4485	Asp Pro His
Tyr Val 4490	Thr Phe Asp Gly Leu 4495	Tyr Tyr Ser Tyr Gln 4500	Gly Asn Cys
Thr Tyr 4505	Val Leu Val Glu Glu 4510	Ile Ser Pro Ser Val 4515	Asp Asn Phe
Gly Val 4520	Tyr Ile Asp Asn Tyr 4525	His Cys Asp Pro Asn 4530	Asp Lys Val
Ser Cys 4535	Pro Arg Thr Leu Ile 4540	Val Arg His Glu Thr 4545	Gln Glu Val
Leu Ile 4550	Lys Thr Val His Met 4555	Met Pro Met Gln Val 4560	Gln Val Gln
Val Asn 4565	Arg Gln Ala Val Ala 4570	Leu Pro Tyr Lys Lys 4575	Tyr Gly Leu
Glu Val 4580	Tyr Gln Ser Gly Ile 4585	Asn Tyr Val Val Asp 4590	Ile Pro Glu
Leu Gly	Val Leu Val Ser Tyr	Asn Gly Leu Ser Phe	Ser Val Arg

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Leu Pro Tyr His Arg Phe Gly	Asn Asn Thr Lys Gly	Gln Cys Gly
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Thr Cys Thr Asn Thr Thr Ser	Asp Asp Cys Ile Leu	Pro Ser Gly
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Glu Ile Val Ser Asn Cys Glu	Ala Ala Ala Asp Gln	Trp Leu Val
4640	4645	4650
Asn Asp Pro Ser Lys Pro His	Cys Pro His Ser Ser	Ser Thr Thr
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Lys Arg Pro Ala Val Thr Val	Pro Gly Gly Gly Lys	Thr Thr Pro
4670	4675	4680
His Lys Asp Cys Thr Pro Ser	Pro Leu Cys Gln Leu	Ile Lys Asp
4685	4690	4695
Ser Leu Phe Ala Gln Cys His	Ala Leu Val Pro Pro	Gln His Tyr
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Tyr Asp Ala Cys Val Phe Asp	Ser Cys Phe Met Pro	Gly Ser Ser
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Leu Glu Cys Ala Ser Leu Gln	Ala Tyr Ala Ala Leu	Cys Ala Gln
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Gln Asn Ile Cys Leu Asp Trp	Arg Asn His Thr His	Gly Ala Cys
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Leu Val Glu Cys Pro Ser His	Arg Glu Tyr Gln Ala	Cys Gly Pro
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Ala Glu Glu Pro Thr Cys Lys	Ser Ser Ser Ser Gln	Gln Asn Asn
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Cys Gln Pro Lys Arg Cys Ser	Gln Lys Pro Val Thr	His Cys Val
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Glu Asp Gly Thr Tyr Leu Ala	Thr Glu Val Asn Pro	Ala Asp Thr
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Glu Lys Pro Ser Val Cys Pro	Leu Gly Phe Glu Val	Lys Ser Lys
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Cys	Asn	Thr	Ser	Cys	Ser	Pro	Gly	Phe	Glu	Leu	Met	Glu	Ala	Pro
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Gly	Glu	Cys	Cys	Lys	Lys	Cys	Glu	Gln	Thr	His	Cys	Ile	Ile	Lys
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Arg	Pro	Asp	Asn	Gln	His	Val	Ile	Leu	Lys	Pro	Gly	Asp	Phe	Lys
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Ser	Asp	Pro	Lys	Asn	Asn	Cys	Thr	Phe	Phe	Ser	Cys	Val	Lys	Ile
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His	Asn	Gln	Leu	Ile	Ser	Ser	Val	Ser	Asn	Ile	Thr	Cys	Pro	Asn
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Gly

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 <211> 2911
 <212> PRT
 <213> Homo sapiens

<400> 219

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Met Gly Arg Arg Arg Arg Leu Cys Leu Gln Leu Tyr Phe Leu Trp Leu
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Gly Cys Val Val Leu Trp Ala Gln Gly Thr Ala Gly Gln Pro Gln Pro
20          25          30

Pro Pro Pro Lys Pro Pro Arg Pro Gln Pro Pro Pro Gln Gln Val Arg
35          40          45

Ser Ala Thr Ala Gly Ser Glu Gly Gly Phe Leu Ala Pro Glu Tyr Arg
50          55          60

Glu Glu Gly Ala Ala Val Ala Ser Arg Val Arg Arg Arg Gly Gln Gln
65          70          75          80

Asp Val Leu Arg Gly Pro Asn Val Cys Gly Ser Arg Phe His Ser Tyr
85          90          95

Cys Cys Pro Gly Trp Lys Thr Leu Pro Gly Gly Asn Gln Cys Ile Val
100         105         110

Pro Ile Cys Arg Asn Ser Cys Gly Asp Gly Phe Cys Ser Arg Pro Asn
115         120         125

Met Cys Thr Cys Ser Ser Gly Gln Ile Ser Ser Thr Cys Gly Ser Lys
130         135         140

Ser Ile Gln Gln Cys Ser Val Arg Cys Met Asn Gly Gly Thr Cys Ala
145         150         155         160

Asp Asp His Cys Gln Cys Gln Lys Gly Tyr Ile Gly Thr Tyr Cys Gly
165         170         175

Gln Pro Val Cys Glu Asn Gly Cys Gln Asn Gly Gly Arg Cys Ile Ala
180         185         190

Gln Pro Cys Ala Cys Val Tyr Gly Phe Thr Gly Pro Gln Cys Glu Arg
195         200         205

Asp Tyr Arg Thr Gly Pro Cys Phe Thr Gln Val Asn Asn Gln Met Cys
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Gln Gly Gln Leu Thr Gly Ile Val Cys Thr Lys Thr Leu Cys Cys Ala
225         230         235         240

Thr Thr Gly Arg Ala Trp Gly His Pro Cys Glu Met Cys Pro Ala Gln
245         250         255

Pro Gln Pro Cys Arg Arg Gly Phe Ile Pro Asn Ile Arg Thr Gly Ala
260         265         270

Cys Gln Asp Val Asp Glu Cys Gln Ala Ile Pro Gly Ile Cys Gln Gly
275         280         285

Gly Asn Cys Ile Asn Thr Val Gly Ser Phe Glu Cys Arg Cys Pro Ala
290         295         300

Gly His Lys Gln Ser Glu Thr Thr Gln Lys Cys Glu Asp Ile Asp Glu
305         310         315         320

Cys Ser Ile Ile Pro Gly Ile Cys Glu Thr Gly Glu Cys Ser Asn Thr

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Leu Val Asn Gly Arg Cys Ala Gln Glu Leu Pro Gly Arg Met Thr Lys	370		375		380
Met Gln Cys Cys Cys Glu Pro Gly Arg Cys Trp Gly Ile Gly Thr Ile	385		390		395
Pro Glu Ala Cys Pro Val Arg Gly Ser Glu Glu Tyr Arg Arg Leu Cys	405		410		415
Met Asp Gly Leu Pro Met Gly Gly Ile Pro Gly Ser Ala Gly Ser Arg	420		425		430
Pro Gly Gly Thr Gly Gly Asn Gly Phe Ala Pro Ser Gly Asn Gly Asn	435		440		445
Gly Tyr Gly Pro Gly Gly Thr Gly Phe Ile Pro Ile Pro Gly Gly Asn	450		455		460
Gly Phe Ser Pro Gly Val Gly Gly Ala Gly Val Gly Ala Gly Gly Gln	465		470		475
Gly Pro Ile Ile Thr Gly Leu Thr Ile Leu Asn Gln Thr Ile Asp Ile	485		490		495
Cys Lys His His Ala Asn Leu Cys Leu Asn Gly Arg Cys Ile Pro Thr	500		505		510
Val Ser Ser Tyr Arg Cys Glu Cys Asn Met Gly Tyr Lys Gln Asp Ala	515		520		525
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Glu Cys Ile Gln Asn Gly Val Leu Cys Lys Asn Gly Arg Cys Val Asn	580		585		590
Ser Asp Gly Ser Phe Gln Cys Ile Cys Asn Ala Gly Phe Glu Leu Thr	595		600		605
Thr Asp Gly Lys Asn Cys Val Asp His Asp Glu Cys Thr Thr Thr Asn	610		615		620
Met Cys Leu Asn Gly Met Cys Ile Asn Glu Asp Gly Ser Phe Lys Cys	625		630		635
Ile Cys Lys Pro Gly Phe Val Leu Ala Pro Asn Gly Arg Tyr Cys Thr	645		650		655

Asp Val Asp Glu Cys Gln Thr Pro Gly Ile Cys Met Asn Gly His Cys
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 Ile Asn Ser Glu Gly Ser Phe Arg Cys Asp Cys Pro Pro Gly Leu Ala
 675 680 685
 Val Gly Met Asp Gly Arg Val Cys Val Asp Thr His Met Arg Ser Thr
 690 695 700
 Cys Tyr Gly Gly Ile Lys Lys Gly Val Cys Val Arg Pro Phe Pro Gly
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 Ala Val Thr Lys Ser Glu Cys Cys Cys Ala Asn Pro Asp Tyr Gly Phe
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 Asp Ala Ser Gly Arg Asn Cys Ile Asp Ile Asp Glu Cys Leu Val Asn
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 Ser Cys Thr Cys Pro Pro Gly Tyr Val Phe Arg Thr Glu Thr Glu Thr
 835 840 845
 Cys Glu Asp Ile Asn Glu Cys Glu Ser Asn Pro Cys Val Asn Gly Ala
 850 855 860
 Cys Arg Asn Asn Leu Gly Ser Phe Asn Cys Glu Cys Ser Pro Gly Ser
 865 870 875 880
 Lys Leu Ser Ser Thr Gly Leu Ile Cys Ile Asp Ser Leu Lys Gly Thr
 885 890 895
 Cys Trp Leu Asn Ile Gln Asp Ser Arg Cys Glu Val Asn Ile Asn Gly
 900 905 910
 Ala Thr Leu Lys Ser Glu Cys Cys Ala Thr Leu Gly Ala Ala Trp Gly
 915 920 925
 Ser Pro Cys Glu Arg Cys Glu Leu Asp Thr Ala Cys Pro Arg Gly Leu
 930 935 940
 Ala Arg Ile Lys Gly Val Thr Cys Glu Asp Val Asn Glu Cys Glu Val
 945 950 955 960
 Phe Pro Gly Val Cys Pro Asn Gly Arg Cys Val Asn Ser Lys Gly Ser
 965 970 975
 Phe His Cys Glu Cys Pro Glu Gly Leu Thr Leu Asp Gly Thr Gly Arg
 980 985 990

Val	Cys	Leu	Asp	Ile	Arg	Met	Glu	Gln	Cys	Tyr	Leu	Lys	Trp	Asp	Glu
	995						1000					1005			
Asp	Glu	Cys	Ile	His	Pro	Val	Pro	Gly	Lys	Phe	Arg	Met	Asp	Ala	
	1010					1015					1020				
Cys	Cys	Cys	Ala	Val	Gly	Ala	Ala	Trp	Gly	Thr	Glu	Cys	Glu	Glu	
	1025					1030					1035				
Cys	Pro	Lys	Pro	Gly	Thr	Lys	Glu	Tyr	Glu	Thr	Leu	Cys	Pro	Arg	
	1040					1045					1050				
Gly	Ala	Gly	Phe	Ala	Asn	Arg	Gly	Asp	Val	Leu	Thr	Gly	Arg	Pro	
	1055					1060					1065				
Phe	Tyr	Lys	Asp	Ile	Asn	Glu	Cys	Lys	Ala	Phe	Pro	Gly	Met	Cys	
	1070					1075					1080				
Thr	Tyr	Gly	Lys	Cys	Arg	Asn	Thr	Ile	Gly	Ser	Phe	Lys	Cys	Arg	
	1085					1090					1095				
Cys	Asn	Ser	Gly	Phe	Ala	Leu	Asp	Met	Glu	Glu	Arg	Asn	Cys	Thr	
	1100					1105					1110				
Asp	Ile	Asp	Glu	Cys	Arg	Ile	Ser	Pro	Asp	Leu	Cys	Gly	Ser	Gly	
	1115					1120					1125				
Ile	Cys	Val	Asn	Thr	Pro	Gly	Ser	Phe	Glu	Cys	Glu	Cys	Phe	Glu	
	1130					1135					1140				
Gly	Tyr	Glu	Ser	Gly	Phe	Met	Met	Met	Lys	Asn	Cys	Met	Asp	Ile	
	1145					1150					1155				
Asp	Gly	Cys	Glu	Arg	Asn	Pro	Leu	Leu	Cys	Arg	Gly	Gly	Thr	Cys	
	1160					1165					1170				
Val	Asn	Thr	Glu	Gly	Ser	Phe	Gln	Cys	Asp	Cys	Pro	Leu	Gly	His	
	1175					1180					1185				
Glu	Leu	Ser	Pro	Ser	Arg	Glu	Asp	Cys	Val	Asp	Ile	Asn	Glu	Cys	
	1190					1195					1200				
Ser	Leu	Ser	Asp	Asn	Leu	Cys	Arg	Asn	Gly	Lys	Cys	Val	Asn	Met	
	1205					1210					1215				
Ile	Gly	Thr	Tyr	Gln	Cys	Ser	Cys	Asn	Pro	Gly	Tyr	Gln	Ala	Thr	
	1220					1225					1230				
Pro	Asp	Arg	Gln	Gly	Cys	Thr	Asp	Ile	Asp	Glu	Cys	Met	Ile	Met	
	1235					1240					1245				
Asn	Gly	Gly	Cys	Asp	Thr	Gln	Cys	Thr	Asn	Ser	Glu	Gly	Ser	Tyr	
	1250					1255					1260				
Glu	Cys	Ser	Cys	Ser	Glu	Gly	Tyr	Ala	Leu	Met	Pro	Asp	Gly	Arg	
	1265					1270					1275				
Ser	Cys	Ala	Asp	Ile	Asp	Glu	Cys	Glu	Asn	Asn	Pro	Asp	Ile	Cys	
	1280					1285					1290				
Asp	Gly	Gly	Gln	Cys	Thr	Asn	Ile	Pro	Gly	Glu	Tyr	Arg	Cys	Leu	

1295	1300	1305
Cys Tyr Asp Gly Phe Met Ala 1310	Ser Met Asp Met Lys Thr Cys Ile 1315	
Asp Val Asn Glu Cys Asp Leu 1325	Asn Ser Asn Ile Cys Met Phe Gly 1330	
Glu Cys Glu Asn Thr Lys Gly 1340	Ser Phe Ile Cys His Cys Gln Leu 1345	
Gly Tyr Ser Val Lys Lys Gly 1355	Thr Thr Gly Cys Thr Asp Val Asp 1360	
Glu Cys Glu Ile Gly Ala His 1370	Asn Cys Asp Met His Ala Ser Cys 1375	
Leu Asn Ile Pro Gly Ser Phe 1385	Lys Cys Ser Cys Arg Glu Gly Trp 1390	
Ile Gly Asn Gly Ile Lys Cys 1400	Ile Asp Leu Asp Glu Cys Ser Asn 1405	
Gly Thr His Gln Cys Ser Ile 1415	Asn Ala Gln Cys Val Asn Thr Pro 1420	
Gly Ser Tyr Arg Cys Ala Cys 1430	Ser Glu Gly Phe Thr Gly Asp Gly 1435	
Phe Thr Cys Ser Asp Val Asp 1445	Glu Cys Ala Glu Asn Ile Asn Leu 1450	
Cys Glu Asn Gly Gln Cys Leu 1460	Asn Val Pro Gly Ala Tyr Arg Cys 1465	
Glu Cys Glu Met Gly Phe Thr 1475	Pro Ala Ser Asp Ser Arg Ser Cys 1480	
Gln Asp Ile Asp Glu Cys Ser 1490	Phe Gln Asn Ile Cys Val Ser Gly 1495	
Thr Cys Asn Asn Leu Pro Gly 1505	Met Phe His Cys Ile Cys Asp Asp 1510	
Gly Tyr Glu Leu Asp Arg Thr 1520	Gly Gly Asn Cys Thr Asp Ile Asp 1525	
Glu Cys Ala Asp Pro Ile Asn 1535	Cys Val Asn Gly Leu Cys Val Asn 1540	
Thr Pro Gly Arg Tyr Glu Cys 1550	Asn Cys Pro Pro Asp Phe Gln Leu 1555	
Asn Pro Thr Gly Val Gly Cys 1565	Val Asp Asn Arg Val Gly Asn Cys 1570	
Tyr Leu Lys Phe Gly Pro Arg 1580	Gly Asp Gly Ser Leu Ser Cys Asn 1585	
Thr Glu Ile Gly Val Gly Val 1595	Ser Arg Ser Ser Cys Cys Cys Ser 1600	

Leu Gly 1610	Lys Ala Trp Gly Asn 1615	Pro Cys Glu Thr Cys 1620	Pro Pro Val
Asn Ser 1625	Thr Glu Tyr Tyr Thr 1630	Leu Cys Pro Gly Gly 1635	Glu Gly Phe
Arg Pro 1640	Asn Pro Ile Thr Ile 1645	Ile Leu Glu Asp Ile 1650	Asp Glu Cys
Gln Glu 1655	Leu Pro Gly Leu Cys 1660	Gln Gly Gly Asn Cys 1665	Ile Asn Thr
Phe Gly 1670	Ser Phe Gln Cys Glu 1675	Cys Pro Gln Gly Tyr 1680	Tyr Leu Ser
Glu Asp 1685	Thr Arg Ile Cys Glu 1690	Asp Ile Asp Glu Cys 1695	Phe Ala His
Pro Gly 1700	Val Cys Gly Pro Gly 1705	Thr Cys Tyr Asn Thr 1710	Leu Gly Asn
Tyr Thr 1715	Cys Ile Cys Pro Pro 1720	Glu Tyr Met Gln Val 1725	Asn Gly Gly
His Asn 1730	Cys Met Asp Met Arg 1735	Lys Ser Phe Cys Tyr 1740	Arg Ser Tyr
Asn Gly 1745	Thr Thr Cys Glu Asn 1750	Glu Leu Pro Phe Asn 1755	Val Thr Lys
Arg Met 1760	Cys Cys Cys Thr Tyr 1765	Asn Val Gly Lys Ala 1770	Gly Asn Lys
Pro Cys 1775	Glu Pro Cys Pro Thr 1780	Pro Gly Thr Ala Asp 1785	Phe Lys Thr
Ile Cys 1790	Gly Asn Ile Pro Gly 1795	Phe Thr Phe Asp Ile 1800	His Thr Gly
Lys Ala 1805	Val Asp Ile Asp Glu 1810	Cys Lys Glu Ile Pro 1815	Gly Ile Cys
Ala Asn 1820	Gly Val Cys Ile Asn 1825	Gln Ile Gly Ser Phe 1830	Arg Cys Glu
Cys Pro 1835	Thr Gly Phe Ser Tyr 1840	Asn Asp Leu Leu Leu 1845	Val Cys Glu
Asp Ile 1850	Asp Glu Cys Ser Asn 1855	Gly Asp Asn Leu Cys 1860	Gln Arg Asn
Ala Asp 1865	Cys Ile Asn Ser Pro 1870	Gly Ser Tyr Arg Cys 1875	Glu Cys Ala
Ala Gly 1880	Phe Lys Leu Ser Pro 1885	Asn Gly Ala Cys Val 1890	Asp Arg Asn
Glu Cys 1895	Leu Glu Ile Pro Asn 1900	Val Cys Ser His Gly 1905	Leu Cys Val
Asp Leu 1910	Gln Gly Ser Tyr Gln 1915	Cys Ile Cys His Asn 1920	Gly Phe Lys

Ala 1925	Ser	Gln	Asp	Gln	Thr	Met 1930	Cys	Met	Asp	Val	Asp 1935	Glu	Cys	Glu
Arg 1940	His	Pro	Cys	Gly	Asn	Gly 1945	Thr	Cys	Lys	Asn	Thr 1950	Val	Gly	Ser
Tyr 1955	Asn	Cys	Leu	Cys	Tyr	Pro 1960	Gly	Phe	Glu	Leu	Thr 1965	His	Asn	Asn
Asp 1970	Cys	Leu	Asp	Ile	Asp	Glu 1975	Cys	Ser	Ser	Phe	Phe 1980	Gly	Gln	Val
Cys 1985	Arg	Asn	Gly	Arg	Cys	Phe 1990	Asn	Glu	Ile	Gly	Ser 1995	Phe	Lys	Cys
Leu 2000	Cys	Asn	Glu	Gly	Tyr	Glu 2005	Leu	Thr	Pro	Asp	Gly 2010	Lys	Asn	Cys
Ile 2015	Asp	Thr	Asn	Glu	Cys	Val 2020	Ala	Leu	Pro	Gly	Ser 2025	Cys	Ser	Pro
Gly 2030	Thr	Cys	Gln	Asn	Leu	Glu 2035	Gly	Ser	Phe	Arg	Cys 2040	Ile	Cys	Pro
Pro 2045	Gly	Tyr	Glu	Val	Lys	Ser 2050	Glu	Asn	Cys	Ile	Asp 2055	Ile	Asn	Glu
Cys 2060	Asp	Glu	Asp	Pro	Asn	Ile 2065	Cys	Leu	Phe	Gly	Ser 2070	Cys	Thr	Asn
Thr 2075	Pro	Gly	Gly	Phe	Gln	Cys 2080	Leu	Cys	Pro	Pro	Gly 2085	Phe	Val	Leu
Ser 2090	Asp	Asn	Gly	Arg	Arg	Cys 2095	Phe	Asp	Thr	Arg	Gln 2100	Ser	Phe	Cys
Phe 2105	Thr	Asn	Phe	Glu	Asn	Gly 2110	Lys	Cys	Ser	Val	Pro 2115	Lys	Ala	Phe
Asn 2120	Thr	Thr	Lys	Ala	Lys	Cys 2125	Cys	Cys	Ser	Lys	Met 2130	Pro	Gly	Glu
Gly 2135	Trp	Gly	Asp	Pro	Cys	Glu 2140	Leu	Cys	Pro	Lys	Asp 2145	Asp	Glu	Val
Ala 2150	Phe	Gln	Asp	Leu	Cys	Pro 2155	Tyr	Gly	His	Gly	Thr 2160	Val	Pro	Ser
Leu 2165	His	Asp	Thr	Arg	Glu	Asp 2170	Val	Asn	Glu	Cys	Leu 2175	Glu	Ser	Pro
Gly 2180	Ile	Cys	Ser	Asn	Gly	Gln 2185	Cys	Ile	Asn	Thr	Asp 2190	Gly	Ser	Phe
Arg 2195	Cys	Glu	Cys	Pro	Met	Gly 2200	Tyr	Asn	Leu	Asp	Tyr 2205	Thr	Gly	Val
Arg 2210	Cys	Val	Asp	Thr	Asp	Glu 2215	Cys	Ser	Ile	Gly	Asn 2220	Pro	Cys	Gly
Asn	Gly	Thr	Cys	Thr	Asn	Val	Ile	Gly	Ser	Phe	Glu	Cys	Asn	Cys

2225	2230	2235
Asn Glu Gly Phe Glu Pro Gly 2240	Pro Met Met Asn Cys 2245	Glu Asp Ile 2250
Asn Glu Cys Ala Gln Asn Pro 2255	Leu Leu Cys Ala Leu 2260	Arg Cys Met 2265
Asn Thr Phe Gly Ser Tyr Glu 2270	Cys Thr Cys Pro Ile 2275	Gly Tyr Ala 2280
Leu Arg Glu Asp Gln Lys Met 2285	Cys Lys Asp Leu Asp 2290	Glu Cys Ala 2295
Glu Gly Leu His Asp Cys Glu 2300	Ser Arg Gly Met Met 2305	Cys Lys Asn 2310
Leu Ile Gly Thr Phe Met Cys 2315	Ile Cys Pro Pro Gly 2320	Met Ala Arg 2325
Arg Pro Asp Gly Glu Gly Cys 2330	Val Asp Glu Asn Glu 2335	Cys Arg Thr 2340
Lys Pro Gly Ile Cys Glu Asn 2345	Gly Arg Cys Val Asn 2350	Ile Ile Gly 2355
Ser Tyr Arg Cys Glu Cys Asn 2360	Glu Gly Phe Gln Ser 2365	Ser Ser Ser 2370
Gly Thr Glu Cys Leu Asp Asn 2375	Arg Gln Gly Leu Cys 2380	Phe Ala Glu 2385
Val Leu Gln Thr Ile Cys Gln 2390	Met Ala Ser Ser Ser 2395	Arg Asn Leu 2400
Val Thr Lys Ser Glu Cys Cys 2405	Cys Asp Gly Gly Arg 2410	Gly Trp Gly 2415
His Gln Cys Glu Leu Cys Pro 2420	Leu Pro Gly Thr Ala 2425	Gln Tyr Lys 2430
Lys Ile Cys Pro His Gly Pro 2435	Gly Tyr Thr Thr Asp 2440	Gly Arg Asp 2445
Ile Asp Glu Cys Lys Val Met 2450	Pro Asn Leu Cys Thr 2455	Asn Gly Gln 2460
Cys Ile Asn Thr Met Gly Ser 2465	Phe Arg Cys Phe Cys 2470	Lys Val Gly 2475
Tyr Thr Thr Asp Ile Ser Gly 2480	Thr Ser Cys Ile Asp 2485	Leu Asp Glu 2490
Cys Ser Gln Ser Pro Lys Pro 2495	Cys Asn Tyr Ile Cys 2500	Lys Asn Thr 2505
Glu Gly Ser Tyr Gln Cys Ser 2510	Cys Pro Arg Gly Tyr 2515	Val Leu Gln 2520
Glu Asp Gly Lys Thr Cys Lys 2525	Asp Leu Asp Glu Cys 2530	Gln Thr Lys 2535

Gln His	Asn Cys	Gln Phe	Leu	Cys Val	Asn Thr	Leu	Gly Gly	Phe
2540			2545			2550		
Thr Cys	Lys Cys	Pro Pro	Gly	Phe Thr	Gln His	His	Thr Ala	Cys
2555			2560			2565		
Ile Asp	Asn Asn	Glu Cys	Gly	Ser Gln	Pro Leu	Leu	Cys Gly	Gly
2570			2575			2580		
Lys Gly	Ile Cys	Gln Asn	Thr	Pro Gly	Ser Phe	Ser	Cys Glu	Cys
2585			2590			2595		
Gln Arg	Gly Phe	Ser Leu	Asp	Ala Thr	Gly Leu	Asn	Cys Glu	Asp
2600			2605			2610		
Val Asp	Glu Cys	Asp Gly	Asn	His Arg	Cys Gln	His	Gly Cys	Gln
2615			2620			2625		
Asn Ile	Leu Gly	Gly Tyr	Arg	Cys Gly	Cys Pro	Gln	Gly Tyr	Ile
2630			2635			2640		
Gln His	Tyr Gln	Trp Asn	Gln	Cys Val	Asp Glu	Asn	Glu Cys	Ser
2645			2650			2655		
Asn Pro	Asn Ala	Cys Gly	Ser	Ala Ser	Cys Tyr	Asn	Thr Leu	Gly
2660			2665			2670		
Ser Tyr	Lys Cys	Ala Cys	Pro	Ser Gly	Phe Ser	Phe	Asp Gln	Phe
2675			2680			2685		
Ser Ser	Ala Cys	His Asp	Val	Asn Glu	Cys Ser	Ser	Ser Lys	Asn
2690			2695			2700		
Pro Cys	Asn Tyr	Gly Cys	Ser	Asn Thr	Glu Gly	Gly	Tyr Leu	Cys
2705			2710			2715		
Gly Cys	Pro Pro	Gly Tyr	Tyr	Arg Val	Gly Gln	Gly	His Cys	Val
2720			2725			2730		
Ser Gly	Met Gly	Phe Asn	Lys	Gly Gln	Tyr Leu	Ser	Leu Asp	Thr
2735			2740			2745		
Glu Val	Asp Glu	Glu Asn	Ala	Leu Ser	Pro Glu	Ala	Cys Tyr	Glu
2750			2755			2760		
Cys Lys	Ile Asn	Gly Tyr	Pro	Lys Lys	Asp Ser	Arg	Gln Lys	Arg
2765			2770			2775		
Ser Ile	His Glu	Pro Asp	Pro	Thr Ala	Val Glu	Gln	Ile Ser	Leu
2780			2785			2790		
Glu Ser	Val Asp	Met Asp	Ser	Pro Val	Asn Met	Lys	Phe Asn	Leu
2795			2800			2805		
Ser His	Leu Gly	Ser Lys	Glu	His Ile	Leu Glu	Leu	Arg Pro	Ala
2810			2815			2820		
Ile Gln	Pro Leu	Asn Asn	His	Ile Arg	Tyr Val	Ile	Ser Gln	Gly
2825			2830			2835		
Asn Asp	Asp Ser	Val Phe	Arg	Ile His	Gln Arg	Asn	Gly Leu	Ser
2840			2845			2850		

Tyr Leu His Thr Ala Lys Lys Lys Leu Met Pro Gly Thr Tyr Thr
 2855 2860 2865
 Leu Glu Ile Thr Ser Ile Pro Leu Tyr Lys Lys Lys Glu Leu Lys
 2870 2875 2880
 Lys Leu Glu Glu Ser Asn Glu Asp Asp Tyr Leu Leu Gly Glu Leu
 2885 2890 2895
 Gly Glu Ala Leu Arg Met Arg Leu Gln Ile Gln Leu Tyr
 2900 2905 2910

<210> 220
 <211> 3002
 <212> PRT
 <213> Homo sapiens

<400> 220
 Tyr Phe Ser Arg Glu Lys Pro Leu Arg Gly Arg Tyr Leu Lys Arg Trp
 1 5 10 15
 Gly Lys Glu Gly Ala Ala Gly Ala Ala Ala Glu Thr Val Gly Ala Thr
 20 25 30
 Ser Gly Gln Glu Pro Gln Leu Gly Gln Leu Arg Ala Glu Pro Ser Ser
 35 40 45
 Gly Cys Ser Gly His Asp Trp Glu Gln Pro Pro Pro Pro Pro Arg Glu
 50 55 60
 Ser Glu Pro Pro Leu Leu His Trp Gln Gly Pro Pro Glu Val Gly Ala
 65 70 75 80
 Ala Pro Gly Glu Gly Gly Arg Ser Pro Ala Arg Gly Thr Gly Gly Gly
 85 90 95
 Ile Ala Gly Pro Arg Arg Arg Gly Ala Leu Gln Gly Ala Ala Ala Ala
 100 105 110
 Ala Asp Arg Ala Pro Gly Ala Ala Arg Gly Gly Gly Ser Arg Trp Arg
 115 120 125
 Leu Gly Ile Met Arg Arg Gly Arg Leu Leu Glu Ile Ala Leu Gly Phe
 130 135 140
 Thr Val Leu Leu Ala Ser Tyr Thr Ser His Gly Ala Asp Ala Asn Leu
 145 150 155 160
 Glu Ala Gly Asn Val Lys Glu Thr Arg Ala Ser Arg Ala Lys Arg Arg
 165 170 175
 Gly Gly Gly Gly His Asp Ala Leu Lys Gly Pro Asn Val Cys Gly Ser
 180 185 190
 Arg Tyr Asn Ala Tyr Cys Cys Pro Gly Trp Lys Thr Leu Pro Gly Gly
 195 200 205
 Asn Gln Cys Ile Val Pro Ile Cys Arg His Ser Cys Gly Asp Gly Phe
 210 215 220
 Cys Ser Arg Pro Asn Met Cys Thr Cys Pro Ser Gly Gln Ile Ala Pro

225		230		235		240
Ser Cys Gly Ser Arg Ser Ile Gln His Cys Asn Ile Arg Cys Met Asn						
		245		250		255
Gly Gly Ser Cys Ser Asp Asp His Cys Leu Cys Gln Lys Gly Tyr Ile						
		260		265		270
Gly Thr His Cys Gly Gln Pro Val Cys Glu Ser Gly Cys Leu Asn Gly						
		275		280		285
Gly Arg Cys Val Ala Pro Asn Arg Cys Ala Cys Thr Tyr Gly Phe Thr						
		290		295		300
Gly Pro Gln Cys Glu Arg Asp Tyr Arg Thr Gly Pro Cys Phe Thr Val						
		305		310		315
Ile Ser Asn Gln Met Cys Gln Gly Gln Leu Ser Gly Ile Val Cys Thr						
		325		330		335
Lys Gln Leu Cys Cys Ala Thr Val Gly Arg Ala Trp Gly His Pro Cys						
		340		345		350
Glu Met Cys Pro Ala Gln Pro His Pro Cys Arg Arg Gly Phe Ile Pro						
		355		360		365
Asn Ile Arg Thr Gly Ala Cys Gln Asp Val Asp Glu Cys Gln Ala Ile						
		370		375		380
Pro Gly Leu Cys Gln Gly Gly Asn Cys Ile Asn Thr Val Gly Ser Phe						
		385		390		395
Glu Cys Lys Cys Pro Ala Gly His Lys Leu Asn Glu Val Ser Gln Lys						
		405		410		415
Cys Glu Asp Ile Asp Glu Cys Ser Thr Ile Pro Gly Ile Cys Glu Gly						
		420		425		430
Gly Glu Cys Thr Asn Thr Val Ser Ser Tyr Phe Cys Lys Cys Pro Pro						
		435		440		445
Gly Phe Tyr Thr Ser Pro Asp Gly Thr Arg Cys Ile Asp Val Arg Pro						
		450		455		460
Gly Tyr Cys Tyr Thr Ala Leu Thr Asn Gly Arg Cys Ser Asn Gln Leu						
		465		470		475
Pro Gln Ser Ile Thr Lys Met Gln Cys Cys Cys Asp Ala Gly Arg Cys						
		485		490		495
Trp Ser Pro Gly Val Thr Val Ala Pro Glu Met Cys Pro Ile Arg Ala						
		500		505		510
Thr Glu Asp Phe Asn Lys Leu Cys Ser Val Pro Met Val Ile Pro Gly						
		515		520		525
Arg Pro Glu Tyr Pro Pro Pro Pro Leu Gly Pro Ile Pro Pro Val Leu						
		530		535		540
Pro Val Pro Pro Gly Phe Pro Pro Gly Pro Gln Ile Pro Val Pro Arg						
		545		550		555
						560

Pro Pro Val Glu Tyr Leu Tyr Pro Ser Arg Glu Pro Pro Arg Val Leu
 565 570 575
 Pro Val Asn Val Thr Asp Tyr Cys Gln Leu Val Arg Tyr Leu Cys Gln
 580 585 590
 Asn Gly Arg Cys Ile Pro Thr Pro Gly Ser Tyr Arg Cys Glu Cys Asn
 595 600 605
 Lys Gly Phe Gln Leu Asp Leu Arg Gly Glu Cys Ile Asp Val Asp Glu
 610 615 620
 Cys Glu Lys Asn Pro Cys Ala Gly Gly Glu Cys Ile Asn Asn Gln Gly
 625 630 635 640
 Ser Tyr Thr Cys Gln Cys Arg Ala Gly Tyr Gln Ser Thr Leu Thr Arg
 645 650 655
 Thr Glu Cys Arg Asp Ile Asp Glu Cys Leu Gln Asn Gly Arg Ile Cys
 660 665 670
 Asn Asn Gly Arg Cys Ile Asn Thr Asp Gly Ser Phe His Cys Val Cys
 675 680 685
 Asn Ala Gly Phe His Val Thr Arg Asp Gly Lys Asn Cys Glu Asp Met
 690 695 700
 Asp Glu Cys Ser Ile Arg Asn Met Cys Leu Asn Gly Met Cys Ile Asn
 705 710 715 720
 Glu Asp Gly Ser Phe Lys Cys Ile Cys Lys Pro Gly Phe Gln Leu Ala
 725 730 735
 Ser Asp Gly Arg Tyr Cys Lys Asp Ile Asn Glu Cys Glu Thr Pro Gly
 740 745 750
 Ile Cys Met Asn Gly Arg Cys Val Asn Thr Asp Gly Ser Tyr Arg Cys
 755 760 765
 Glu Cys Phe Pro Gly Leu Ala Val Gly Leu Asp Gly Arg Val Cys Val
 770 775 780
 Asp Thr His Met Arg Ser Thr Cys Tyr Gly Gly Tyr Lys Arg Gly Gln
 785 790 795 800
 Cys Ile Lys Pro Leu Phe Gly Ala Val Thr Lys Ser Glu Cys Cys Cys
 805 810 815
 Ala Ser Thr Glu Tyr Ala Phe Gly Glu Pro Cys Gln Pro Cys Pro Ala
 820 825 830
 Gln Asn Ser Ala Glu Tyr Gln Ala Leu Cys Ser Ser Gly Pro Gly Met
 835 840 845
 Thr Ser Ala Gly Ser Asp Ile Asn Glu Cys Ala Leu Asp Pro Asp Ile
 850 855 860
 Cys Pro Asn Gly Ile Cys Glu Asn Leu Arg Gly Thr Tyr Lys Cys Ile
 865 870 875 880
 Cys Asn Ser Gly Tyr Glu Val Asp Ser Thr Gly Lys Asn Cys Val Asp
 885 890 895

Ile Asn Glu Cys Val Leu Asn Ser Leu Leu Cys Asp Asn Gly Gln Cys
 900 905 910
 Arg Asn Thr Pro Gly Ser Phe Val Cys Thr Cys Pro Lys Gly Phe Ile
 915 920 925
 Tyr Lys Pro Asp Leu Lys Thr Cys Glu Asp Ile Asp Glu Cys Glu Ser
 930 935 940
 Ser Pro Cys Ile Asn Gly Val Cys Lys Asn Ser Pro Gly Ser Phe Ile
 945 950 955 960
 Cys Glu Cys Ser Ser Glu Ser Thr Leu Asp Pro Thr Lys Thr Ile Cys
 965 970 975
 Ile Glu Thr Ile Lys Gly Thr Cys Trp Gln Thr Val Ile Asp Gly Arg
 980 985 990
 Cys Glu Ile Asn Ile Asn Gly Ala Thr Leu Lys Ser Gln Cys Cys Ser
 995 1000 1005
 Ser Leu Gly Ala Ala Trp Gly Ser Pro Cys Thr Leu Cys Gln Val
 1010 1015 1020
 Asp Pro Ile Cys Gly Lys Gly Tyr Ser Arg Ile Lys Gly Thr Gln
 1025 1030 1035
 Cys Glu Asp Ile Asp Glu Cys Glu Val Phe Pro Gly Val Cys Lys
 1040 1045 1050
 Asn Gly Leu Cys Val Asn Thr Arg Gly Ser Phe Lys Cys Gln Cys
 1055 1060 1065
 Pro Ser Gly Met Thr Leu Asp Ala Thr Gly Arg Ile Cys Leu Asp
 1070 1075 1080
 Ile Arg Leu Glu Thr Cys Phe Leu Arg Tyr Glu Asp Glu Glu Cys
 1085 1090 1095
 Thr Leu Pro Ile Ala Gly Arg His Arg Met Asp Ala Cys Cys Cys
 1100 1105 1110
 Ser Val Gly Ala Ala Trp Gly Thr Glu Glu Cys Glu Glu Cys Pro
 1115 1120 1125
 Met Arg Asn Thr Pro Glu Tyr Glu Glu Leu Cys Pro Arg Gly Pro
 1130 1135 1140
 Gly Phe Ala Thr Lys Glu Ile Thr Asn Gly Lys Pro Phe Phe Lys
 1145 1150 1155
 Asp Ile Asn Glu Cys Lys Met Ile Pro Ser Leu Cys Thr His Gly
 1160 1165 1170
 Lys Cys Arg Asn Thr Ile Gly Ser Phe Lys Cys Arg Cys Asp Ser
 1175 1180 1185
 Gly Phe Ala Leu Asp Ser Glu Glu Arg Asn Cys Thr Asp Ile Asp
 1190 1195 1200
 Glu Cys Arg Ile Ser Pro Asp Leu Cys Gly Arg Gly Gln Cys Val

1205				1210				1215			
Asn Thr	Pro Gly	Asp Phe	Glu	Cys Lys	Cys Asp	Glu	Gly Tyr	Glu			
1220			1225			1230					
Ser Gly	Phe Met	Met Met	Lys	Asn Cys	Met Asp	Ile	Asp Glu	Cys			
1235			1240			1245					
Gln Arg	Asp Pro	Leu Leu	Cys	Arg Gly	Gly Val	Cys	His Asn	Thr			
1250			1255			1260					
Glu Gly	Ser Tyr	Arg Cys	Glu	Cys Pro	Pro Gly	His	Gln Leu	Ser			
1265			1270			1275					
Pro Asn	Ile Ser	Ala Cys	Ile	Asp Ile	Asn Glu	Cys	Glu Leu	Ser			
1280			1285			1290					
Ala His	Leu Cys	Pro Asn	Gly	Arg Cys	Val Asn	Leu	Ile Gly	Lys			
1295			1300			1305					
Tyr Gln	Cys Ala	Cys Asn	Pro	Gly Tyr	His Ser	Thr	Pro Asp	Arg			
1310			1315			1320					
Leu Phe	Cys Val	Asp Ile	Asp	Glu Cys	Ser Ile	Met	Asn Gly	Gly			
1325			1330			1335					
Cys Glu	Thr Phe	Cys Thr	Asn	Ser Glu	Gly Ser	Tyr	Glu Cys	Ser			
1340			1345			1350					
Cys Gln	Pro Gly	Phe Ala	Leu	Met Pro	Asp Gln	Arg	Ser Cys	Thr			
1355			1360			1365					
Asp Ile	Asp Glu	Cys Glu	Asp	Asn Pro	Asn Ile	Cys	Asp Gly	Gly			
1370			1375			1380					
Gln Cys	Thr Asn	Ile Pro	Gly	Glu Tyr	Arg Cys	Leu	Cys Tyr	Asp			
1385			1390			1395					
Gly Phe	Met Ala	Ser Glu	Asp	Met Lys	Thr Cys	Val	Asp Val	Asn			
1400			1405			1410					
Glu Cys	Asp Leu	Asn Pro	Asn	Ile Cys	Leu Ser	Gly	Thr Cys	Glu			
1415			1420			1425					
Asn Thr	Lys Gly	Ser Phe	Ile	Cys His	Cys Asp	Met	Gly Tyr	Ser			
1430			1435			1440					
Gly Lys	Lys Gly	Lys Thr	Gly	Cys Thr	Asp Ile	Asn	Glu Cys	Glu			
1445			1450			1455					
Ile Gly	Ala His	Asn Cys	Gly	Lys His	Ala Val	Cys	Thr Asn	Thr			
1460			1465			1470					
Ala Gly	Ser Phe	Lys Cys	Ser	Cys Ser	Pro Gly	Trp	Ile Gly	Asp			
1475			1480			1485					
Gly Ile	Lys Cys	Thr Asp	Leu	Asp Glu	Cys Ser	Asn	Gly Thr	His			
1490			1495			1500					
Met Cys	Ser Gln	His Ala	Asp	Cys Lys	Asn Thr	Met	Gly Ser	Tyr			
1505			1510			1515					

Arg Cys	Leu Cys	Lys Glu	Gly Tyr	Thr Gly	Asp Gly	Phe Thr	Cys
1520			1525		1530		
Thr Asp	Leu Asp	Glu Cys	Ser Glu	Asn Leu	Asn Leu	Cys Gly	Asn
1535			1540		1545		
Gly Gln	Cys Leu	Asn Ala	Pro Gly	Gly Tyr	Arg Cys	Glu Cys	Asp
1550			1555		1560		
Met Gly	Phe Val	Pro Ser	Ala Asp	Gly Lys	Ala Cys	Glu Asp	Ile
1565			1570		1575		
Asp Glu	Cys Ser	Leu Pro	Asn Ile	Cys Val	Phe Gly	Thr Cys	His
1580			1585		1590		
Asn Leu	Pro Gly	Leu Phe	Arg Cys	Glu Cys	Glu Ile	Gly Tyr	Glu
1595			1600		1605		
Leu Asp	Arg Ser	Gly Gly	Asn Cys	Thr Asp	Val Asn	Glu Cys	Leu
1610			1615		1620		
Asp Pro	Thr Thr	Cys Ile	Ser Gly	Asn Cys	Val Asn	Thr Pro	Gly
1625			1630		1635		
Ser Tyr	Ile Cys	Asp Cys	Pro Pro	Asp Phe	Glu Leu	Asn Pro	Thr
1640			1645		1650		
Arg Val	Gly Cys	Val Asp	Thr Arg	Ser Gly	Asn Cys	Tyr Leu	Asp
1655			1660		1665		
Ile Arg	Pro Arg	Gly Asp	Asn Gly	Asp Thr	Ala Cys	Ser Asn	Glu
1670			1675		1680		
Ile Gly	Val Gly	Val Ser	Lys Ala	Ser Cys	Cys Cys	Ser Leu	Gly
1685			1690		1695		
Lys Ala	Trp Gly	Thr Pro	Cys Glu	Met Cys	Pro Ala	Val Asn	Thr
1700			1705		1710		
Ser Glu	Tyr Lys	Ile Leu	Cys Pro	Gly Gly	Glu Gly	Phe Arg	Pro
1715			1720		1725		
Asn Pro	Ile Thr	Val Ile	Leu Glu	Asp Ile	Asp Glu	Cys Gln	Glu
1730			1735		1740		
Leu Pro	Gly Leu	Cys Gln	Gly Gly	Lys Cys	Ile Asn	Thr Phe	Gly
1745			1750		1755		
Ser Phe	Gln Cys	Arg Cys	Pro Thr	Gly Tyr	Tyr Leu	Asn Glu	Asp
1760			1765		1770		
Thr Arg	Val Cys	Asp Asp	Val Asn	Glu Cys	Glu Thr	Pro Gly	Ile
1775			1780		1785		
Cys Gly	Pro Gly	Thr Cys	Tyr Asn	Thr Val	Gly Asn	Tyr Thr	Cys
1790			1795		1800		
Ile Cys	Pro Pro	Asp Tyr	Met Gln	Val Asn	Gly Gly	Asn Asn	Cys
1805			1810		1815		
Met Asp	Met Arg	Arg Ser	Leu Cys	Tyr Arg	Asn Tyr	Tyr Ala	Asp
1820			1825		1830		

Asn	Gln	Thr	Cys	Asp	Gly	Glu	Leu	Leu	Phe	Asn	Met	Thr	Lys	Lys
1835						1840					1845			
Met	Cys	Cys	Cys	Ser	Tyr	Asn	Ile	Gly	Arg	Ala	Trp	Asn	Lys	Pro
1850						1855					1860			
Cys	Glu	Gln	Cys	Pro	Ile	Pro	Ser	Thr	Asp	Glu	Phe	Ala	Thr	Leu
1865						1870					1875			
Cys	Gly	Ser	Gln	Arg	Pro	Gly	Phe	Val	Ile	Asp	Ile	Tyr	Thr	Gly
1880						1885					1890			
Leu	Pro	Val	Asp	Ile	Asp	Glu	Cys	Arg	Glu	Ile	Pro	Gly	Val	Cys
1895						1900					1905			
Glu	Asn	Gly	Val	Cys	Ile	Asn	Met	Val	Gly	Ser	Phe	Arg	Cys	Glu
1910						1915					1920			
Cys	Pro	Val	Gly	Phe	Phe	Tyr	Asn	Asp	Lys	Leu	Leu	Val	Cys	Glu
1925						1930					1935			
Asp	Ile	Asp	Glu	Cys	Gln	Asn	Gly	Pro	Val	Cys	Gln	Arg	Asn	Ala
1940						1945					1950			
Glu	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Arg	Cys	Asp	Cys	Lys	Pro
1955						1960					1965			
Gly	Tyr	Arg	Phe	Thr	Ser	Thr	Gly	Gln	Cys	Asn	Asp	Arg	Asn	Glu
1970						1975					1980			
Cys	Gln	Glu	Ile	Pro	Asn	Ile	Cys	Ser	His	Gly	Gln	Cys	Ile	Asp
1985						1990					1995			
Thr	Val	Gly	Ser	Phe	Tyr	Cys	Leu	Cys	His	Thr	Gly	Phe	Lys	Thr
2000						2005					2010			
Asn	Asp	Asp	Gln	Thr	Met	Cys	Leu	Asp	Ile	Asn	Glu	Cys	Glu	Arg
2015						2020					2025			
Asp	Ala	Cys	Gly	Asn	Gly	Thr	Cys	Arg	Asn	Thr	Ile	Gly	Ser	Phe
2030						2035					2040			
Asn	Cys	Arg	Cys	Asn	His	Gly	Phe	Ile	Leu	Ser	His	Asn	Asn	Asp
2045						2050					2055			
Cys	Ile	Asp	Val	Asp	Glu	Cys	Ala	Ser	Gly	Asn	Gly	Asn	Leu	Cys
2060						2065					2070			
Arg	Asn	Gly	Gln	Cys	Ile	Asn	Thr	Val	Gly	Ser	Phe	Gln	Cys	Gln
2075						2080					2085			
Cys	Asn	Glu	Gly	Tyr	Glu	Val	Ala	Pro	Asp	Gly	Arg	Thr	Cys	Val
2090						2095					2100			
Asp	Ile	Asn	Glu	Cys	Leu	Leu	Glu	Pro	Arg	Lys	Cys	Ala	Pro	Gly
2105						2110					2115			
Thr	Cys	Gln	Asn	Leu	Asp	Gly	Ser	Tyr	Arg	Cys	Ile	Cys	Pro	Pro
2120						2125					2130			
Gly	Tyr	Ser	Leu	Gln	Asn	Glu	Lys	Cys	Glu	Asp	Ile	Asp	Glu	Cys

2135					2140					2145				
Val	Glu	Glu	Pro	Glu	Ile	Cys	Ala	Leu	Gly	Thr	Cys	Ser	Asn	Thr
2150						2155					2160			
Glu	Gly	Ser	Phe	Lys	Cys	Leu	Cys	Pro	Glu	Gly	Phe	Ser	Leu	Ser
2165						2170					2175			
Ser	Ser	Gly	Arg	Arg	Cys	Gln	Asp	Leu	Arg	Met	Ser	Tyr	Cys	Tyr
2180						2185					2190			
Ala	Lys	Phe	Glu	Gly	Gly	Lys	Cys	Ser	Ser	Pro	Lys	Ser	Arg	Asn
2195						2200					2205			
His	Ser	Lys	Gln	Glu	Cys	Cys	Cys	Ala	Leu	Lys	Gly	Glu	Gly	Trp
2210						2215					2220			
Gly	Asp	Pro	Cys	Glu	Leu	Cys	Pro	Thr	Glu	Pro	Asp	Glu	Ala	Phe
2225						2230					2235			
Arg	Gln	Ile	Cys	Pro	Tyr	Gly	Ser	Gly	Ile	Ile	Val	Gly	Pro	Asp
2240						2245					2250			
Asp	Ser	Ala	Val	Asp	Met	Asp	Glu	Cys	Lys	Glu	Pro	Asp	Val	Cys
2255						2260					2265			
Lys	His	Gly	Gln	Cys	Ile	Asn	Thr	Asp	Gly	Ser	Tyr	Arg	Cys	Glu
2270						2275					2280			
Cys	Pro	Phe	Gly	Tyr	Thr	Leu	Ala	Gly	Asn	Glu	Cys	Val	Asp	Thr
2285						2290					2295			
Asp	Glu	Cys	Ser	Val	Gly	Asn	Pro	Cys	Gly	Asn	Gly	Thr	Cys	Lys
2300						2305					2310			
Asn	Val	Ile	Gly	Gly	Phe	Glu	Cys	Thr	Cys	Glu	Glu	Gly	Phe	Glu
2315						2320					2325			
Pro	Gly	Pro	Met	Met	Thr	Cys	Glu	Asp	Ile	Asn	Glu	Cys	Ala	Gln
2330						2335					2340			
Asn	Pro	Leu	Leu	Cys	Ala	Phe	Arg	Cys	Val	Asn	Thr	Tyr	Gly	Ser
2345						2350					2355			
Tyr	Glu	Cys	Lys	Cys	Pro	Val	Gly	Tyr	Val	Leu	Arg	Glu	Asp	Arg
2360						2365					2370			
Arg	Met	Cys	Lys	Asp	Glu	Asp	Glu	Cys	Glu	Glu	Gly	Lys	His	Asp
2375						2380					2385			
Cys	Thr	Glu	Lys	Gln	Met	Glu	Cys	Lys	Asn	Leu	Ile	Gly	Thr	Tyr
2390						2395					2400			
Met	Cys	Ile	Cys	Gly	Pro	Gly	Tyr	Gln	Arg	Arg	Pro	Asp	Gly	Glu
2405						2410					2415			
Gly	Cys	Val	Asp	Glu	Asn	Glu	Cys	Gln	Thr	Lys	Pro	Gly	Ile	Cys
2420						2425					2430			
Glu	Asn	Gly	Arg	Cys	Leu	Asn	Thr	Arg	Gly	Ser	Tyr	Thr	Cys	Glu
2435						2440					2445			

Cys Asn 2450	Asp Gly Phe Thr 2455	Ala Ser Pro Asn Gln Asp 2460	Glu Cys Leu
Asp Asn 2465	Arg Glu Gly Tyr Cys 2470	Phe Thr Glu Val Leu 2475	Gln Asn Met
Cys Gln 2480	Ile Gly Ser Ser Asn 2485	Arg Asn Pro Val Thr 2490	Lys Ser Glu
Cys Cys 2495	Cys Asp Gly Gly Arg 2500	Gly Trp Gly Pro His 2505	Cys Glu Ile
Cys Pro 2510	Phe Gln Gly Thr Val 2515	Ala Phe Lys Lys Leu 2520	Cys Pro His
Gly Arg 2525	Gly Phe Met Thr Asn 2530	Gly Ala Asp Ile Asp 2535	Glu Cys Lys
Val Ile 2540	His Asp Val Cys Arg 2545	Asn Gly Glu Cys Val 2550	Asn Asp Arg
Gly Ser 2555	Tyr His Cys Ile Cys 2560	Lys Thr Gly Tyr Thr 2565	Pro Asp Ile
Thr Gly 2570	Thr Ser Cys Val Asp 2575	Leu Asn Glu Cys Asn 2580	Gln Ala Pro
Lys Pro 2585	Cys Asn Phe Ile Cys 2590	Lys Asn Thr Glu Gly 2595	Ser Tyr Gln
Cys Ser 2600	Cys Pro Lys Gly Tyr 2605	Ile Leu Gln Glu Asp 2610	Gly Arg Ser
Cys Lys 2615	Asp Leu Asp Glu Cys 2620	Ala Thr Lys Gln His 2625	Asn Cys Gln
Phe Leu 2630	Cys Val Asn Thr Ile 2635	Gly Gly Phe Thr Cys 2640	Lys Cys Pro
Pro Gly 2645	Phe Thr Gln His His 2650	Thr Ser Cys Ile Asp 2655	Asn Asn Glu
Cys Thr 2660	Ser Asp Ile Asn Leu 2665	Cys Gly Ser Lys Gly 2670	Ile Cys Gln
Asn Thr 2675	Pro Gly Ser Phe Thr 2680	Cys Glu Cys Gln Arg 2685	Gly Phe Ser
Leu Asp 2690	Gln Thr Gly Ser Ser 2695	Cys Glu Asp Val Asp 2700	Glu Cys Glu
Gly Asn 2705	His Arg Cys Gln His 2710	Gly Cys Gln Asn Ile 2715	Ile Gly Gly
Tyr Arg 2720	Cys Ser Cys Pro Gln 2725	Gly Tyr Leu Gln His 2730	Tyr Gln Trp
Asn Gln 2735	Cys Val Asp Glu Asn 2740	Glu Cys Leu Ser Ala 2745	His Ile Cys
Gly Gly 2750	Ala Ser Cys His Asn 2755	Thr Leu Gly Ser Tyr 2760	Lys Cys Met

Cys Pro Ala Gly Phe Gln Tyr Glu Gln Phe Ser Gly Gly Cys Gln
 2765 2770 2775
 Asp Ile Asn Glu Cys Gly Ser Ala Gln Ala Pro Cys Ser Tyr Gly
 2780 2785 2790
 Cys Ser Asn Thr Glu Gly Gly Tyr Leu Cys Gly Cys Pro Pro Gly
 2795 2800 2805
 Tyr Phe Arg Ile Gly Gln Gly His Cys Val Ser Gly Met Gly Met
 2810 2815 2820
 Gly Arg Gly Asn Pro Glu Pro Pro Val Ser Gly Glu Met Asp Asp
 2825 2830 2835
 Asn Ser Leu Ser Pro Glu Ala Cys Tyr Glu Cys Lys Ile Asn Gly
 2840 2845 2850
 Tyr Pro Lys Arg Gly Arg Lys Arg Arg Ser Thr Asn Glu Thr Asp
 2855 2860 2865
 Ala Ser Asn Ile Glu Asp Gln Ser Glu Thr Glu Ala Asn Val Ser
 2870 2875 2880
 Leu Ala Ser Trp Asp Val Glu Lys Thr Ala Ile Phe Ala Phe Asn
 2885 2890 2895
 Ile Ser His Val Ser Asn Lys Val Arg Ile Leu Glu Leu Leu Pro
 2900 2905 2910
 Ala Leu Thr Thr Leu Thr Asn His Asn Arg Tyr Leu Ile Glu Ser
 2915 2920 2925
 Gly Asn Glu Asp Gly Phe Phe Lys Ile Asn Gln Lys Glu Gly Ile
 2930 2935 2940
 Ser Tyr Leu His Phe Thr Lys Lys Lys Pro Val Ala Gly Thr Tyr
 2945 2950 2955
 Ser Leu Gln Ile Ser Ser Thr Pro Leu Tyr Lys Lys Lys Glu Leu
 2960 2965 2970
 Asn Gln Leu Glu Asp Lys Tyr Asp Lys Asp Tyr Leu Ser Gly Glu
 2975 2980 2985
 Leu Gly Asp Asn Leu Lys Met Lys Ile Gln Val Leu Leu His
 2990 2995 3000

<210> 221

<211> 216

<212> PRT

<213> Homo sapiens

<400> 221

Met Leu Arg Leu Ser Glu Arg Asn Met Lys Val Leu Leu Ala Ala Ala
 1 5 10 15

Leu Ile Ala Gly Ser Val Phe Phe Leu Leu Pro Gly Pro Ser Ala
 20 25 30

Ala Asp Glu Lys Lys Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe

35 40 45
 Asp Leu Arg Ile Gly Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu
 50 55 60
 Phe Gly Lys Thr Val Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala
 65 70 75 80
 Thr Gly Glu Lys Gly Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val
 85 90 95
 Ile Lys Asp Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly
 100 105 110
 Thr Gly Gly Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe
 115 120 125
 Lys Leu Lys His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly
 130 135 140
 Lys Asp Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala
 145 150 155 160
 Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met
 165 170 175
 Glu Val Val Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys
 180 185 190
 Pro Leu Lys Asp Val Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu
 195 200 205
 Lys Pro Phe Ala Ile Ala Lys Glu
 210 215

<210> 222
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 222
 Met Gly Pro Gly Pro Arg Leu Leu Leu Pro Leu Val Leu Cys Val Gly
 1 5 10 15
 Leu Gly Ala Leu Val Phe Ser Ser Gly Ala Glu Gly Phe Arg Lys Arg
 20 25 30
 Gly Pro Ser Val Thr Ala Lys Val Phe Phe Asp Val Arg Ile Gly Asp
 35 40 45
 Lys Asp Val Gly Arg Ile Val Ile Gly Leu Phe Gly Lys Val Val Pro
 50 55 60
 Lys Thr Val Glu Asn Phe Val Ala Leu Ala Thr Gly Glu Lys Gly Tyr
 65 70 75 80
 Gly Tyr Lys Gly Ser Lys Phe His Arg Val Ile Lys Asp Phe Met Ile
 85 90 95
 Gln Gly Gly Asp Ile Thr Thr Gly Asp Gly Thr Gly Gly Val Ser Ile
 100 105 110

Tyr Gly Glu Thr Phe Pro Asp Glu Asn Phe Lys Leu Lys His Tyr Gly
 115 120 125
 Ile Gly Trp Val Ser Met Ala Asn Ala Gly Pro Asp Thr Asn Gly Ser
 130 135 140
 Gln Phe Phe Ile Thr Leu Thr Lys Pro Thr Trp Leu Asp Gly Lys His
 145 150 155 160
 Val Val Phe Gly Lys Val Ile Asp Gly Met Thr Val Val His Ser Ile
 165 170 175
 Glu Leu Gln Ala Thr Asp Gly His Asp Arg Pro Leu Thr Asn Cys Ser
 180 185 190
 Ile Ile Asn Ser Gly Lys Ile Asp Val Lys Thr Pro Phe Val Val Glu
 195 200 205
 Ile Ala Asp Trp
 210
 <210> 223
 <211> 321
 <212> PRT
 <213> Homo sapiens
 <400> 223
 Met Gly Glu Pro Gln Gly Ser Met Arg Ile Leu Val Thr Gly Gly Ser
 1 5 10 15
 Gly Leu Val Gly Lys Ala Ile Gln Lys Val Val Ala Asp Gly Ala Gly
 20 25 30
 Leu Pro Gly Glu Asp Trp Val Phe Val Ser Ser Lys Asp Ala Asp Leu
 35 40 45
 Thr Asp Thr Ala Gln Thr Arg Ala Leu Phe Glu Lys Val Gln Pro Thr
 50 55 60
 His Val Ile His Leu Ala Ala Met Val Gly Gly Leu Phe Arg Asn Ile
 65 70 75 80
 Lys Tyr Asn Leu Asp Phe Trp Arg Lys Asn Val His Met Asn Asp Asn
 85 90 95
 Val Leu His Ser Ala Phe Glu Val Gly Ala Arg Lys Val Val Ser Cys
 100 105 110
 Leu Ser Thr Cys Ile Phe Pro Asp Lys Thr Thr Tyr Pro Ile Asp Glu
 115 120 125
 Thr Met Ile His Asn Gly Pro Pro His Asn Ser Asn Phe Gly Tyr Ser
 130 135 140
 Tyr Ala Lys Arg Met Ile Asp Val Gln Asn Arg Ala Tyr Phe Gln Gln
 145 150 155 160
 Tyr Gly Cys Thr Phe Thr Ala Val Ile Pro Thr Asn Val Phe Gly Pro
 165 170 175
 His Asp Asn Phe Asn Ile Glu Asp Gly His Val Leu Pro Gly Leu Ile
 180 185 190

His Lys Val His Leu Ala Lys Ser Ser Gly Ser Ala Leu Thr Val Trp
 195 200 205
 Gly Thr Gly Asn Pro Arg Arg Gln Phe Ile Tyr Ser Leu Asp Leu Ala
 210 215 220
 Gln Leu Phe Ile Trp Val Leu Arg Glu Tyr Asn Glu Val Glu Pro Ile
 225 230 235 240
 Ile Leu Ser Val Gly Glu Glu Asp Glu Val Ser Ile Lys Glu Ala Ala
 245 250 255
 Glu Ala Val Val Glu Ala Met Asp Phe His Gly Glu Val Thr Phe Asp
 260 265 270
 Thr Thr Lys Ser Asp Gly Gln Phe Lys Lys Thr Ala Ser Asn Ser Lys
 275 280 285
 Leu Arg Thr Tyr Leu Pro Asp Phe Arg Phe Thr Pro Phe Lys Gln Ala
 290 295 300
 Val Lys Glu Thr Cys Ala Trp Phe Thr Asp Asn Tyr Glu Gln Ala Arg
 305 310 315 320

Lys

<210> 224
 <211> 334
 <212> PRT
 <213> Homo sapiens

<400> 224

Met Pro Lys Arg Arg Asp Ile Leu Ala Ile Val Leu Ile Val Leu Pro
 1 5 10 15
 Trp Thr Leu Leu Ile Thr Val Trp His Gln Ser Thr Leu Ala Pro Leu
 20 25 30
 Leu Ala Val His Lys Asp Glu Gly Ser Asp Pro Arg Arg Glu Thr Pro
 35 40 45
 Pro Gly Ala Asp Pro Arg Glu Tyr Cys Thr Ser Asp Arg Asp Ile Val
 50 55 60
 Glu Val Val Arg Thr Glu Tyr Val Tyr Thr Arg Pro Pro Pro Trp Ser
 65 70 75 80
 Asp Thr Leu Pro Thr Ile His Val Val Thr Pro Thr Tyr Ser Arg Pro
 85 90 95
 Val Gln Lys Ala Glu Leu Thr Arg Met Ala Asn Thr Leu Leu His Val
 100 105 110
 Pro Asn Leu His Trp Leu Val Val Glu Asp Ala Pro Arg Arg Thr Pro
 115 120 125
 Leu Thr Ala Arg Leu Leu Arg Asp Thr Gly Leu Asn Tyr Thr His Leu
 130 135 140
 His Val Glu Thr Pro Arg Asn Tyr Lys Leu Arg Gly Asp Ala Arg Asp

145		150		155		160
Pro Arg Ile	Pro Arg Gly Thr Met Gln Arg Asn Leu Ala Leu Arg Trp					
	165			170		175
Leu Arg Glu Thr Phe Pro Arg Asn Ser Ser Gln Pro Gly Val Val Tyr						
	180		185			190
Phe Ala Asp Asp Asp Asn Thr Tyr Ser Leu Glu Leu Phe Glu Glu Met						
	195		200			205
Arg Ser Thr Arg Arg Val Ser Val Trp Pro Val Ala Phe Val Gly Gly						
	210		215			220
Leu Arg Tyr Glu Ala Pro Arg Val Asn Gly Ala Gly Lys Val Val Arg						
	225		230			240
Trp Lys Thr Val Phe Asp Pro His Arg Pro Phe Ala Ile Asp Met Ala						
	245		250			255
Gly Phe Ala Val Asn Leu Arg Leu Ile Leu Gln Arg Ser Gln Ala Tyr						
	260		265			270
Phe Lys Leu Arg Gly Val Lys Gly Gly Tyr Gln Glu Ser Ser Leu Leu						
	275		280			285
Arg Glu Leu Val Thr Leu Asn Asp Leu Glu Pro Lys Ala Ala Asn Cys						
	290		295			300
Thr Lys Ile Leu Val Trp His Thr Arg Thr Glu Lys Pro Val Leu Val						
	305		310			320
Asn Glu Gly Lys Lys Gly Phe Thr Asp Pro Ser Val Glu Ile						
	325		330			

<210> 225
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 225
 Met Lys Leu Lys Leu Lys Asn Val Phe Leu Ala Tyr Phe Leu Val Ser
 1 5 10 15
 Ile Ala Gly Leu Leu Tyr Ala Leu Val Gln Leu Gly Gln Pro Cys Asp
 20 25 30
 Cys Leu Pro Pro Leu Arg Ala Ala Glu Gln Leu Arg Gln Lys Asp
 35 40 45
 Leu Arg Ile Ser Gln Leu Gln Ala Glu Leu Arg Arg Pro Pro Pro Ala
 50 55 60
 Pro Ala Gln Pro Pro Glu Pro Glu Ala Leu Pro Thr Ile Tyr Val Val
 65 70 75 80
 Thr Pro Thr Tyr Ala Arg Leu Val Gln Lys Ala Glu Leu Val Arg Leu
 85 90 95
 Ser Gln Thr Leu Ser Leu Val Pro Arg Leu His Trp Leu Leu Val Glu
 100 105 110

Asp Ala Glu Gly Pro Thr Pro Leu Val Ser Gly Leu Leu Ala Ala Ser
 115 120 125
 Gly Leu Leu Phe Thr His Leu Val Val Leu Thr Pro Lys Ala Gln Arg
 130 135 140
 Leu Arg Glu Gly Glu Pro Gly Trp Val His Pro Arg Gly Val Glu Gln
 145 150 155 160
 Arg Asn Lys Ala Leu Asp Trp Leu Arg Gly Arg Gly Gly Ala Val Gly
 165 170 175
 Gly Glu Lys Asp Pro Pro Pro Pro Gly Thr Gln Gly Val Val Tyr Phe
 180 185 190
 Ala Asp Asp Asp Asn Thr Tyr Ser Arg Glu Leu Phe Glu Glu Met Arg
 195 200 205
 Trp Thr Arg Gly Val Ser Val Trp Pro Val Gly Leu Val Gly Gly Leu
 210 215 220
 Arg Phe Glu Gly Pro Gln Val Gln Asp Gly Arg Val Val Gly Phe His
 225 230 235 240
 Thr Ala Trp Glu Pro Ser Arg Pro Phe Pro Val Asp Met Ala Gly Phe
 245 250 255
 Ala Val Ala Leu Pro Leu Leu Leu Asp Lys Pro Asn Ala Gln Phe Asp
 260 265 270
 Ser Thr Ala Pro Arg Gly His Leu Glu Ser Ser Leu Leu Ser His Leu
 275 280 285
 Val Asp Pro Lys Asp Leu Glu Pro Arg Ala Ala Asn Cys Thr Arg Val
 290 295 300
 Leu Val Trp His Thr Arg Thr Glu Lys Pro Lys Met Lys Gln Glu Glu
 305 310 315 320
 Gln Leu Gln Arg Gln Gly Arg Gly Ser Asp Pro Ala Ile Glu Val
 325 330 335

<210> 226
 <211> 1010
 <212> PRT
 <213> Homo sapiens

<400> 226
 Met Gly Tyr Ala Arg Ala Ser Gly Val Cys Ala Arg Gly Cys Leu Asp
 1 5 10 15
 Ser Ala Gly Pro Trp Thr Met Ser Arg Ala Leu Arg Pro Pro Leu Pro
 20 25 30
 Pro Leu Cys Phe Phe Leu Leu Leu Leu Ala Ala Ala Gly Ala Arg Ala
 35 40 45
 Gly Gly Tyr Glu Thr Cys Pro Thr Val Gln Pro Asn Met Leu Asn Val
 50 55 60
 His Leu Leu Pro His Thr His Asp Asp Val Gly Trp Leu Lys Thr Val
 65 70 75 80

Asp Gln Tyr Phe Tyr Gly Ile Lys Asn Asp Ile Gln His Ala Gly Val
 85 90 95
 Gln Tyr Ile Leu Asp Ser Val Ile Ser Ala Leu Leu Ala Asp Pro Thr
 100 105 110
 Arg Arg Phe Ile Tyr Val Glu Ile Ala Phe Phe Ser Arg Trp Trp His
 115 120 125
 Gln Gln Thr Asn Ala Thr Gln Glu Val Val Arg Asp Leu Val Arg Gln
 130 135 140
 Gly Arg Leu Glu Phe Ala Asn Gly Gly Trp Val Met Asn Asp Glu Ala
 145 150 155 160
 Ala Thr His Tyr Gly Ala Ile Val Asp Gln Met Thr Leu Gly Leu Arg
 165 170 175
 Phe Leu Glu Asp Thr Phe Gly Asn Asp Gly Arg Pro Arg Val Ala Trp
 180 185 190
 His Ile Asp Pro Phe Gly His Ser Arg Glu Gln Ala Ser Leu Phe Ala
 195 200 205
 Gln Met Gly Phe Asp Gly Phe Phe Phe Gly Arg Leu Asp Tyr Gln Asp
 210 215 220
 Lys Trp Val Arg Met Gln Lys Leu Glu Met Glu Gln Val Trp Arg Ala
 225 230 235 240
 Ser Thr Ser Leu Lys Pro Pro Thr Ala Asp Leu Phe Thr Gly Val Leu
 245 250 255
 Pro Asn Gly Tyr Asn Pro Pro Arg Asn Leu Cys Trp Asp Val Leu Cys
 260 265 270
 Val Asp Gln Pro Leu Val Glu Asp Pro Arg Ser Pro Glu Tyr Asn Ala
 275 280 285
 Lys Glu Leu Val Asp Tyr Phe Leu Asn Val Ala Thr Ala Gln Gly Arg
 290 295 300
 Tyr Tyr Arg Thr Asn His Thr Val Met Thr Met Gly Ser Asp Phe Gln
 305 310 315 320
 Tyr Glu Asn Ala Asn Met Trp Phe Lys Asn Leu Asp Lys Leu Ile Arg
 325 330 335
 Leu Val Asn Ala Gln Gln Ala Lys Gly Ser Ser Val His Val Leu Tyr
 340 345 350
 Ser Thr Pro Ala Cys Tyr Leu Trp Glu Leu Asn Lys Ala Asn Leu Thr
 355 360 365
 Trp Ser Val Lys His Asp Asp Phe Phe Pro Tyr Ala Asp Gly Pro His
 370 375 380
 Gln Phe Trp Thr Gly Tyr Phe Ser Ser Arg Pro Ala Leu Lys Arg Tyr
 385 390 395 400
 Glu Arg Leu Ser Tyr Asn Phe Leu Gln Val Cys Asn Gln Leu Glu Ala

405	410	415
Leu Val Gly Leu Ala Ala Asn Val Gly Pro Tyr Gly Ser Gly Asp Ser		
420	425	430
Ala Pro Leu Asn Glu Ala Met Ala Val Leu Gln His His Asp Ala Val		
435	440	445
Ser Gly Thr Ser Arg Gln His Val Ala Asn Asp Tyr Ala Arg Gln Leu		
450	455	460
Ala Ala Gly Trp Gly Pro Cys Glu Val Leu Leu Ser Asn Ala Leu Ala		
465	470	475
Arg Leu Arg Gly Phe Lys Asp His Phe Thr Phe Cys Gln Gln Leu Asn		
485	490	495
Ile Ser Ile Cys Pro Leu Ser Gln Thr Ala Ala Arg Phe Gln Val Ile		
500	505	510
Val Tyr Asn Pro Leu Gly Arg Lys Val Asn Trp Met Val Arg Leu Pro		
515	520	525
Val Ser Glu Gly Val Phe Val Val Lys Asp Pro Asn Gly Arg Thr Val		
530	535	540
Pro Ser Asp Val Val Ile Phe Pro Ser Ser Asp Ser Gln Ala His Pro		
545	550	555
Pro Glu Leu Leu Phe Ser Ala Ser Leu Pro Ala Leu Gly Phe Ser Thr		
565	570	575
Tyr Ser Val Ala Gln Val Pro Arg Trp Lys Pro Gln Ala Arg Ala Pro		
580	585	590
Gln Pro Ile Pro Arg Arg Ser Trp Ser Pro Ala Leu Thr Ile Glu Asn		
595	600	605
Glu His Ile Arg Ala Thr Phe Asp Pro Asp Thr Gly Leu Leu Met Glu		
610	615	620
Ile Met Asn Met Asn Gln Gln Leu Leu Leu Pro Val Arg Gln Thr Phe		
625	630	635
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Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ala Gln Gly Lys Gly
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  130          135          140

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Pro Asp Glu Phe Ile Asp Val Ile Val Gly Asn Arg Val Tyr Met Pro
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 65 70 75 80
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 85 90 95
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115 120 125
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 Cys Met Glu Val Gly Lys Glu Lys Cys Leu Pro Val Tyr Tyr Glu Gln
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 Val Ile Lys Pro Val Asn Leu Glu Ala Leu Ser Lys Trp Thr Gly His
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 545 550 555 560
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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/17382

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/00, 1/68; G01N 33/53; A61K 49/00

US CL : 435/ 4, 6, 7.1; 424/ 9.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/ 4, 6, 7.1; 424/ 9.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
WEST, MEDLINE**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 6,020,135 A (LEVINE et al) 27 March 1998 (27.03.1998)	1-25
A	WO 00/31530 A2 (THE GOVERNMENT OF THE UNITED STATES OF AMERICA REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES) 02 June 2000 (02.06.2000).	1-25
A	US 5,908,750 A (REED et al) 01 June 1999 (.01.06.1999)	1-25

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier application or patent published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T"

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X"

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y"

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&"

document member of the same patent family

Date of the actual completion of the international search

19 September 2002 (19.09.2002)

Date of mailing of the international search report

18 OCT 2002

Name and mailing address of the ISA/US

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